

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
3 January 2003 (03.01.2003)

PCT

(10) International Publication Number
WO 03/000893 A2

(51) International Patent Classification⁷: **C12N 15/12**,
5/10, C07K 14/705, 16/28, C12Q 1/68, G01N 33/50,
A61K 45/00, 39/00

(21) International Application Number: PCT/IB02/02357

(22) International Filing Date: 24 June 2002 (24.06.2002)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/301,095 26 June 2001 (26.06.2001) US
60/333,185 6 November 2001 (06.11.2001) US

(71) Applicant (for all designated States except US): **DECODE GENETICS EHF**. [IS/IS]; Sturlugötu 8, IS-101 Reykjavík (IS).

(72) Inventors; and

(75) Inventors/Applicants (for US only): **MARTINEZ, Roger, Moraga, A.** [ES/DE]; Bleichstrasse 6, 60313 Frankfurt am Main (DE). **SIGURDSSON, Gunnar, Thor** [IS/IS]; Kjarrholmi 8, IS-200 Kopavogur (IS).

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZM, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

— without international search report and to be republished upon receipt of that report

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.



WO 03/000893 A2

(54) Title: NUCLEIC ACIDS ENCODING G PROTEIN-COUPLED RECEPTORS

(57) Abstract: Nucleic acids encoding G protein-coupled receptors are disclosed, and methods of using same.

- 1 -

NUCLEIC ACIDS ENCODING G PROTEIN-COUPLED RECEPTORS

5 RELATED APPLICATIONS

This application claims the benefit of and priority to U.S. Provisional Application 60/301,095, filed June 26, 2001 and to U.S. Provisional Application 60/333,185, filed November 6, 2001, the entire teachings of which are incorporated herein by reference.

10

BACKGROUND OF THE INVENTION

G protein-coupled receptors ("GPCRs") are a superfamily of intrinsic transmembrane cell-surface receptors that mediate the transmission of extracellular signals into the cell to produce a cellular response. There are thought to be
15 anywhere from 400 to over 1000 different members of this family. GPCRs are intrinsic membrane proteins, and operate by a common transduction mechanism. In their inactive state, the GPCRs bind to the G proteins. Upon activation, they stimulate guanine nucleotide exchange on the G proteins, resulting in the release of GDP and the binding of GTP. The G-protein then dissociates from the GPCR, and
20 interacts with the adenylate cyclases, which catalyze the conversion of ATP into cAMP. The cAMP then acts as a second messenger. The G proteins can cause intracellular coupling of the GPCRs with various intracellular enzymes, ion channels and transporters.

GPCRs (and perforce, G proteins) are involved in an enormous range of
25 biological processes, and have been found to regulate such processes as hydrolysis of plasma membrane phospholipids, the K^+ and Ca^{2+} ion channels, yeast mating signals, the signaling by cholera and pertussis toxins, and proliferation in some cancers (e.g., pituitary, adrenal, ovarian). The signal can be endogenous or exogenous or, in the case of rhodopsin receptors, the stimulus can be light. Many
30 drugs bind to a GPCR and either produce a response or block the actions of the normal signal. The GPCR superfamily includes the cannabinoid and opioid receptors, chemokine, histamine, angiotensin, neurotensin, vasopressin, calcitonin, dopamine, glutamate and bombesin receptors, taste and odorant receptors, and many others.

35

SUMMARY OF THE INVENTION

The present invention relates to human G protein-coupled receptor (GPCR) genes, particularly nucleic acids comprising GPCR genes, and the amino acids

-2 -

5 encoded by such nucleic acids. These sequences are shown in Tables I and II. In Tables I and II, each GPCR entry lists the name (*e.g.*, "MOOSE00162"), the University of California at Santa Cruz contig designation from which the sequence was analyzed (*e.g.*, "ctg14797"), the exon locations (*e.g.*, "448003 .. 448092, ..."), followed by the amino acid sequence and the nucleic acid sequence.

10 Sub-family information on the sequences is shown in Table III. For each sequence, the following information is provided: the University of California at Santa Cruz contig designation from which the sequence was analyzed (*e.g.*, "ctg14797"), the name (*e.g.*, "MOOSE00162"), and the subfamily to which the sequence appears to belong. The assignments were made on the basis of the best E-value with which the sequence aligned. Sequences listed as "Class A Orphan" are those that have been characterized, and are known to bind GPCR-proteins.

15 In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-124 (odd numbers), as shown in Tables I and II, and the complements thereof. The invention further relates to a nucleic acid molecule which hybridizes under high stringency conditions to a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-124 (odd numbers), as shown in Tables I and II, and the complements thereof. The invention additionally relates to isolated nucleic acid molecules (*e.g.*, cDNA molecules) encoding a GPCR polypeptide (*e.g.*, encoding a polypeptide selected from the group consisting of SEQ ID NOs:1-124 (even numbers), as shown in Tables I and II).

25 The invention further provides a method for assaying a sample for the presence of a nucleic acid molecule comprising all or a portion of a GPCR in a sample, comprising contacting said sample with a second nucleic acid molecule comprising a nucleotide sequence encoding a GPCR polypeptide (*e.g.*, one of SEQ ID NOs:1-124 (odd numbers), as shown in Tables I and II, or the complement of one of SEQ ID NOs:1-124 (odd numbers); a nucleotide sequence encoding one of SEQ ID NOs:1-124 (even numbers), as shown in Tables I and II), or a fragment or derivative thereof, under conditions appropriate for selective hybridization. The invention additionally provides a method for assaying a sample for the level of expression of a GPCR polypeptide, or fragment or derivative thereof, comprising detecting (directly or indirectly) the level of expression of the GPCR polypeptide, fragment or derivative thereof.

35 The invention also relates to a vector comprising an isolated nucleic acid molecule of the invention operatively linked to a regulatory sequence, as well as to a recombinant host cell comprising the vector. The invention also provides a method for preparing a polypeptide encoded by an isolated nucleic acid molecule described

herein (a GPCR polypeptide), comprising culturing a recombinant host cell of the invention under conditions suitable for expression of said nucleic acid molecule.

The invention further provides an isolated polypeptide encoded by isolated nucleic acid molecules of the invention (*e.g.*, GPCR polypeptide), as well as
5 fragments or derivatives thereof. In a particular embodiment, the polypeptide comprises an amino acid sequence selected from the group consisting of SEQ ID NOs:1-124 (even numbers), as shown in Tables I and II. The invention also relates to an isolated polypeptide comprising an amino acid sequence which is greater than about 90 percent identical to an amino acid sequence selected from the group
10 consisting of SEQ ID NOs:1-124 (even numbers), preferably about 95, 96, 97, 98 and 99 percent identical.

The invention also relates to an antibody, or an antigen-binding fragment thereof, which selectively binds to a polypeptide of the invention, as well as to a method for assaying the presence of a polypeptide encoded by an isolated nucleic
15 acid molecule of the invention in a sample, comprising contacting said sample with an antibody which specifically binds to the encoded polypeptide.

The invention further relates to methods of diagnosing a predisposition to a condition mediated by GPCRs. The methods of diagnosing such a predisposition in an individual include detecting the presence of a mutation in GPCR, as well as
20 detecting alterations in expression of a GPCR polypeptide, such as the presence of different splicing variants of GPCR polypeptides. The alterations in expression can be quantitative, qualitative, or both quantitative and qualitative.

The invention additionally relates to an assay for identifying agents that alter (*e.g.*, enhance or inhibit) the activity or expression of one or more GPCR
25 polypeptides. For example, a cell, cellular fraction, or solution containing a GPCR polypeptide or a fragment or derivative thereof, can be contacted with an agent to be tested, and the level of GPCR polypeptide expression or activity can be assessed. The activity or expression of more than one GPCR polypeptides can be assessed concurrently (*e.g.*, the cell, cellular fraction, or solution can contain more than one
30 type of GPCR polypeptide, such as different splicing variants, and the levels of the different polypeptides or splicing variants can be assessed).

In another embodiment, the invention relates to assays to identify polypeptides that interact with one or more GPCR polypeptides. In a yeast two-hybrid system, for example, a first vector is used which includes a nucleic acid encoding a DNA
35 binding domain and also an GPCR polypeptide, splicing variant, or fragment or derivative thereof, and a second vector is used which includes a nucleic acid encoding a transcription activation domain and also a nucleic acid encoding a polypeptide which potentially may interact with the GPCR polypeptide, splicing

-4 -

variant, or fragment or derivative thereof (*e.g.*, a GPCR polypeptide binding agent or receptor). Incubation of yeast containing both the first vector and the second vector under appropriate conditions allows identification of polypeptides which interact with the GPCR polypeptide or fragment or derivative thereof, and thus can be agents which alter the activity of expression of an GPCR polypeptide.

Agents that enhance or inhibit GPCR polypeptide expression or activity are also included in the current invention, as are methods of altering (enhancing or inhibiting) GPCR polypeptide expression or activity by contacting a cell containing GPCR and/or polypeptide, or by contacting the GPCR polypeptide, with an agent that enhances or inhibits expression or activity of GPCR or polypeptide.

Additionally, the invention pertains to pharmaceutical compositions comprising the nucleic acids of the invention, the polypeptides of the invention, and/or the agents that alter activity of GPCR polypeptide. The invention further pertains to methods of treating conditions mediated by GPCRs, by administering GPCR therapeutic agents, such as nucleic acids of the invention, polypeptides of the invention, the agents that alter activity of GPCR polypeptide, or compositions comprising the nucleic acids, polypeptides, and/or the agents that alter activity of GPCR polypeptide.

DETAILED DESCRIPTION OF THE INVENTION

The present invention relates to nucleic acids comprising G protein-coupled receptors ("GPCRs"), and the GPCR amino acids encoded by those nucleic acids.

The GPCR superfamily includes the receptors for many important signaling pathways, including, but not limited to, hormone receptors, growth factors, viral receptors, neuroreceptors, etc., such as acetylcholine, adrenocorticotropin (ACTH), adenosine, α -adrenergic receptors, β -adrenergic receptors, angiotensin, bombesin, bradykinin, C5a, calcitonin, cAMP, cannabinoid, C-C chemokine, cholecystokinin/gastrin (CCK/gastrin), cytomegalovirus, dopamine, endothelial differentiation gene-1, endothelin, formyl peptide, glutamate (metabotropic), gonadotropin-releasing hormone, growth hormone-releasing hormone, histamine, 5-hydroxytryptamine, interleukin-8, kinin, luteinizing hormone/follicle-stimulating hormone/thyroid-stimulating hormone (LH/FSH/TSH), mas, melanocortin, muscarinic, neuropeptide Y, neurotensin, odorant, opioid, opsins, parathyroid hormone, platelet-activating factor (PAF), prolactin, prostaglandin E, rhodopsins, secretin, serotonin, somatostatin, tachykinin, taste, testis specific, thrombin, thromboxane A₂, thyrotropin-releasing hormone (TRH), tyramine/octopamine, vasoactive intestinal peptide (VIP), vasopressin, viral and yeast mating factor.

These receptors are involved in the treatment of infections and various diseases and conditions, including, but not limited to, bacterial, fungal, protozoan and viral infections, particularly infections caused by HIV-1 or HIV-2; cancers; diabetes; asthma; Parkinson's disease; both acute and congestive heart failure;

5 hypotension; hypertension; urinary retention; osteoporosis; angina pectoris; myocardial infarction; ulcers; asthma; allergies; benign prostatic hypertrophy (benign prostatic hyperplasia); chronic renal failure; renal disease; impaired glucose tolerance; seizure disorder; depression; anxiety; obsessive compulsive disorder; affective neurosis/disorder; depressive neurosis/disorder; anxiety neurosis;

10 dysthymic disorder; behavior disorder; mood disorder; schizophrenia; psychosexual dysfunction; sex disorder; sexual disorder; disturbed biological and circadian rhythms; feeding disorders, such as anorexia, bulimia, cachexia, and obesity; Cushing's syndrome/disease; basophil adenoma; prolactinoma; hyperprolactinemia; hypopituitarism; hypophysis tumor/adenoma; hypothalamic diseases; Froehlich's

15 syndrome; adenohipophysis disease; hypophysis disease; hypophysis tumor/adenoma; pituitary growth hormone; adenohipophysis hypofunction; adenohipophysis hyperfunction; hypothalamic hypogonadism; Kallman's syndrome (anosmia, hyposmia); functional or psychogenic amenorrhea; hypopituitarism; hypothalamic hypothyroidism; hypothalamic-adrenal dysfunctions;

20 idiopathic hyperprolactinemia; hypothalamic disorders of growth hormone deficiency; idiopathic growth hormone deficiency; dwarfism; gigantism; acromegaly; disturbed biological and circadian rhythms; and sleep disturbances associated with such diseases as neurological disorders, heart and lung diseases, mental illness, and addictions; migraine; hyperalgesia; enhanced or exaggerated

25 sensitivity to pain, such as hyperlgesia, causalgia and allodynia; acute pain; burn pain; atypical facial pain; neuropathic pain; back pain; complex regional pain syndromes I and II; arthritic pain; sports injury pain; pain related to infection, *e.g.*, HIV, post-polio syndrome, and post-herpetic neuralgia; phantom limb pain; labour pain; cancer pain; post-chemotherapy pain; post-stroke pain; post-operative pain;

30 neuralgia; and tolerance to narcotics or withdrawal from narcotics; sleep disorders; sleep apnea; narcolepsy; insomnia; parasomnia; jet-lag syndrome; and other neurodegenerative disorders, which includes nosological entities such as disinhibition-dementia-parkinsonism-amyotrophy complex; pallido-ponto-nigral degeneration; and dyskinesias, such as Huntington's disease or Gilles dela Tourett's

35 syndrome.

With the availability of complete genomic sequences for many organisms today, including *Homo sapiens*, it has become clear that there is a need for data mining techniques to extract the information in them, *e.g.*, gene prediction programs.

-6 -

Of these, the most successful ones are those based on the comparison of known protein or protein-derived information, or those that use expressed sequence tags (ESTs) to predict gene location and structure.

One such algorithm is GeneWise. It bases its exon prediction on the use of Hidden Markov Models (HMMs) of proteins to be compared against a genomic sequence, so that the translation of the sequence will match the model in a similar way to other HMM profile searches (Eddy, *Curr. Opin. Struct. Biol.* 6(3):361-5, 1996), and allowing the presence of long insertions as long as they include donor and acceptor site sequences at both ends.

To take advantage of the algorithm, the models for different protein families must be built so that they represent the full-length sequences instead of the most common features in them. This is a major difference with existing HMM databases such as Pfam (Sonnhammer *et al.*, *Proteins* 28(3):405-20, 1997), in which each model is built to represent a family of proteins as broad as possible with minimum overlap between them.

In the present approach, the sequences were subdivided in several families so that the similarity inside of a group of them was over 50%. Given this approach, there are several points of overlap between different families when analyzing a sequence, so the discrimination must be done after the search is completed.

Several resources that include expert-supervised classifications are used to select the best groups of sequences, *e.g.*, the GPCR database (Horn *et al.*, *Nucleic Acids Res.* 26(1):275-9, 1998), PKR (Smith *et al.*, *Trends Biochem. Sci.* 22(11):444-6, 1997), NuclearRdb (Horn *et al.*, *Nucleic Acids Res.* 29:346-349, 2001), IOCH (Le Novere *et al.*, *Nucleic Acids Res.* 27(1):340-2, 1999), Enzyme (Bairoch, *Nucleic Acids Res.* 28:304-305, 2000) and Swiss-Prot (Bairoch *et al.*, *Nucleic Acids Res.* 28:45-48, 2000). When none is available, or the sequences included in some groups are too disrinatly related, the grouping must be done manually, using the ClustalW (Thompson *et al.*, *Nucleic Acids Res.* 22:4673-4680, 1994) package to measure the distance between different sequences.

The present model was built from multiple sequence alignments of the different protein families obtained with DiAlign 2 (Morgenstern, *Bioinformatics* 15(3):211-8, 1999). DiAlign works based on segment-to-segment comparisons instead of arbitrary thresholds for gap opening and extension, which makes it ideally suited for building models that represent an entire, full-length sequence, since the alignments built this way have more match states that would be assigned as insertion states when using other alignment algorithms. The models were built using the standard HMMer package.

-7 -

To search for new genes, a genome-wide scan was done on the University of California at Santa Cruz sequences, using the GeneWise algorithm. It translates the genomic sequence on the fly to proteins and can therefore maintain a reading frame through insertions and deletions. The algorithm also rewards gaps in the genomic sequence relative to the model if they are encapsulated within introns, like splice structure.

For each superfamily of proteins, a classification was obtained in which the sequences are grouped by length and similarity. Each one of these groups was then used to build a HMM profile representing this group of sequences. This approach aims to have models that can represent the full length of the encoded proteins for a whole range of proteins, without being too specific for any one of them or being too general, as would be a HMM built for large groups of sequences. This classification was based either on existing expert-supervised classifications, or by retrieval of sequences and classification based on pairwise alignment distances.

These models were then searched against the October 2000 Fixed Release (with its subsequent corrections) and the April 2001 Fixed Release for data shown in Tables I and II, respectively, of the Santa Cruz contigs using the Paracel GeneMatcher+ Hardware Accelerator with the GeneWise algorithm. The sequences were chopped at 100 Kb with an overlap of 1 Kb. Each one of the superfamilies required between 3 and 6 days to complete and generate results. The results represent the coding regions of the complete final protein as it is found in the organism.

The cross-validation of the results was done in two steps. First, all of the hits with an E-value lower than 10^{-8} that did not overlap with one another were selected, and in the event of overlapping, the one with lowest E-value was selected. After selecting all of those matches, the DNA sequences were compared against the RefSeq database (Pruitt *et al.*, *Trends Genet.* 16(1): 44-47, 2000) using BLAST (Altschul *et al.*, *Nucleic Acids Res.* 25:3389-3402, 1997).

Over 80% of the sequences were 90% or more identical to an existing human RefSeq entry and/or mRNA from GenBank. The differences are usually due to picking the wrong model for a certain sequence that appears as a hit more than once in different families, being a different valid splice variant, which can be tested by comparing to the EST database, or by addition of a small last exon to complete the match instead of accept an stop codon in a previous one. In all of such cases, the results are easily and quickly corrected by eye. Very rarely the algorithm will actually make a wrong prediction, which is consistent with the expected behaviour (Guigo *et al.*, *Genome Res.* 10(10): 1631-42, 2000).

Of the remaining sequences, over 50% have a match over 90% identical in the public domain protein databases, and the differences between those sequences in the databases and the potential translations is basically the same as the differences between the DNA sequences and the RefSeq entries.

5 The full sequences of the GPCR genes and splice variants are shown in Tables I and II as SEQ ID NOs:1-124 (odd numbers). The amino acids encoded by these nucleic acids are shown in Tables I and II as SEQ ID NOs:1-124 (even numbers).

10 A number of the genes were linked to markers known to be associated with human diseases genes. These are shown in Table IV. The diseases were linked to the HMM genes in the following manner: (1) the HMM gene models were compared to the consensus of the human genome sequence, located and the results kept in a relational database; (2) all possible markers (Sequence Tagged Sites (STS's)) (public or deCODE Genetics) are also located in the same consensus using ePCR or BLAT and results kept in a relational database; and (3) LOD scores for
15 diseases are linked to markers. A span of one LOD drop around the marker was also given. A computer program takes each LOD peak and links it to the consensus through the markerhit in the database. The database is then queried for all HMM genes within the span of one LOD drop or a minimum of 15 Mb in each direction from the marker. The output is the name of the peak marker and its distance to the
20 HMM gene.

NUCLEIC ACIDS OF THE INVENTION

Accordingly, the invention pertains to isolated nucleic acid molecules comprising human GPCR genes. The term, "GPCR", as used herein, refers to an
25 isolated nucleic acid molecule selected from the group shown in Tables I and II, and consisting of SEQ ID NOs:1-124 (odd numbers), and also to a portion or fragment of the isolated nucleic acid molecule (e.g., cDNA or the gene) that encodes GPCR polypeptide (e.g., a polypeptide selected from the group shown in Tables I and II, and consisting of SEQ ID NOs:1-124 (even numbers)). In a preferred embodiment,
30 the isolated nucleic acid molecule comprises a nucleic acid molecule selected from the group consisting of SEQ ID NOs:1-124 (odd numbers) or the complement of such a nucleic acid molecule.

The isolated nucleic acid molecules of the present invention can be RNA, for example, mRNA, or DNA, such as cDNA and genomic DNA. DNA molecules can
35 be double-stranded or single-stranded; single stranded RNA or DNA can be the coding, or sense, strand or the non-coding, or antisense, strand. The nucleic acid molecule can include all or a portion of the coding sequence of the gene and can further comprise additional non-coding sequences such as introns and non-coding 3'

and 5' sequences (including regulatory sequences, for example). Additionally, the nucleic acid molecule can be fused to a marker sequence, for example, a sequence that encodes a polypeptide to assist in isolation or purification of the polypeptide. Such sequences include, but are not limited to, those that encode a glutathione-S-transferase (GST) fusion protein and those that encode a hemagglutinin A (HA) polypeptide marker from influenza.

An "isolated" nucleic acid molecule, as used herein, is one that is separated from nucleic acids that normally flank the gene or nucleotide sequence (as in genomic sequences) and/or has been completely or partially purified from other transcribed sequences (*e.g.*, as in an RNA library). For example, an isolated nucleic acid of the invention may be substantially isolated with respect to the complex cellular milieu in which it naturally occurs, or culture medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized. In some instances, the isolated material will form part of a composition (for example, a crude extract containing other substances), buffer system or reagent mix. In other circumstances, the material may be purified to essential homogeneity, for example as determined by PAGE or column chromatography such as HPLC. Preferably, an isolated nucleic acid molecule comprises at least about 50, 80 or 90% (on a molar basis) of all macromolecular species present. With regard to genomic DNA, the term "isolated" also can refer to nucleic acid molecules that are separated from the chromosome with which the genomic DNA is naturally associated. For example, the isolated nucleic acid molecule can contain less than about 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotides which flank the nucleic acid molecule in the genomic DNA of the cell from which the nucleic acid molecule is derived.

The nucleic acid molecule can be fused to other coding or regulatory sequences and still be considered isolated. Thus, recombinant DNA contained in a vector is included in the definition of "isolated" as used herein. Also, isolated nucleic acid molecules include recombinant DNA molecules in heterologous host cells, as well as partially or substantially purified DNA molecules in solution. "Isolated" nucleic acid molecules also encompass *in vivo* and *in vitro* RNA transcripts of the DNA molecules of the present invention. An isolated nucleic acid molecule or nucleotide sequence can include a nucleic acid molecule or nucleotide sequence that is synthesized chemically or by recombinant means. Therefore, recombinant DNA contained in a vector is included in the definition of "isolated" as used herein. Also, isolated nucleotide sequences include recombinant DNA molecules in heterologous organisms, as well as partially or substantially purified DNA molecules in solution. *In vivo* and *in vitro* RNA transcripts of the DNA molecules of the present invention are also encompassed by "isolated" nucleotide

-10 -

sequences. Such isolated nucleotide sequences are useful in the manufacture of the encoded polypeptide, as probes for isolating homologous sequences (*e.g.*, from other mammalian species), for gene mapping (*e.g.*, by *in situ* hybridization with chromosomes), or for detecting expression of the gene in tissue (*e.g.*, human tissue), such as by Northern blot analysis.

The present invention also pertains to nucleic acid molecules which are not necessarily found in nature but which encode a GPCR polypeptide (*e.g.*, a polypeptide having an amino acid sequence comprising an amino acid sequence selected from the group consisting of SEQ ID NOs:1-124 (even numbers)), or another splicing variant of a GPCR polypeptide or polymorphic variant thereof. Thus, for example, DNA molecules which comprise a sequence that is different from the naturally-occurring nucleotide sequence but which, due to the degeneracy of the genetic code, encode a GPCR polypeptide of the present invention are also the subject of this invention. The invention also encompasses nucleotide sequences encoding portions (fragments), or encoding variant polypeptides such as analogues or derivatives of a GPCR polypeptide. Such variants can be naturally-occurring, such as in the case of allelic variation or single nucleotide polymorphisms, or non-naturally-occurring, such as those induced by various mutagens and mutagenic processes. Intended variations include, but are not limited to, addition, deletion and substitution of one or more nucleotides that can result in conservative or non-conservative amino acid changes, including additions and deletions. Preferably the nucleotide (and/or resultant amino acid) changes are silent or conserved; that is, they do not alter the characteristics or activity of a GPCR polypeptide. In one preferred embodiment, the nucleotide sequences are fragments that comprise one or more polymorphic microsatellite markers. In another preferred embodiment, the nucleotide sequences are fragments that comprise one or more single nucleotide polymorphisms in a GPCR gene.

Other alterations of the nucleic acid molecules of the invention can include, for example, labeling, methylation, internucleotide modifications such as uncharged linkages (*e.g.*, methyl phosphonates, phosphotriesters, phosphoamidates, carbamates), charged linkages (*e.g.*, phosphorothioates, phosphorodithioates), pendent moieties (*e.g.*, polypeptides), intercalators (*e.g.*, acridine, psoralen), chelators, alkylators, and modified linkages (*e.g.*, alpha anomeric nucleic acids). Also included are synthetic molecules that mimic nucleic acid molecules in the ability to bind to designated sequences via hydrogen bonding and other chemical interactions. Such molecules include, for example, those in which peptide linkages substitute for phosphate linkages in the backbone of the molecule.

-11 -

The invention also pertains to nucleic acid molecules that hybridize under high stringency hybridization conditions, such as for selective hybridization, to a nucleotide sequence described herein (e.g., nucleic acid molecules which specifically hybridize to a nucleotide sequence encoding polypeptides described herein, and, optionally, have an activity of the polypeptide). In one embodiment, the invention includes variants described herein which hybridize under high stringency hybridization conditions (e.g., for selective hybridization) to a nucleotide sequence comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-124 (odd numbers). In another embodiment, the invention includes variants described herein which hybridize under high stringency hybridization conditions (e.g., for selective hybridization) to a nucleotide sequence encoding an amino acid sequence selected from the group consisting of SEQ ID NOs:1-124 (even numbers) or a polymorphic variant thereof. In a preferred embodiment, the variant that hybridizes under high stringency hybridizations has an activity of a GPCR.

Such nucleic acid molecules can be detected and/or isolated by specific hybridization (e.g., under high stringency conditions). "Specific hybridization," as used herein, refers to the ability of a first nucleic acid to hybridize to a second nucleic acid in a manner such that the first nucleic acid does not hybridize to any nucleic acid other than to the second nucleic acid (e.g., when the first nucleic acid has a higher similarity to the second nucleic acid than to any other nucleic acid in a sample wherein the hybridization is to be performed). "Stringency conditions" for hybridization is a term of art which refers to the incubation and wash conditions, e.g., conditions of temperature and buffer concentration, which permit hybridization of a particular nucleic acid to a second nucleic acid; the first nucleic acid may be perfectly (i.e., 100%) complementary to the second, or the first and second may share some degree of complementarity which is less than perfect (e.g., 70%, 75%, 85%, 90%, 95%). For example, certain high stringency conditions can be used which distinguish perfectly complementary nucleic acids from those of less complementarity. "High stringency conditions", "moderate stringency conditions" and "low stringency conditions" for nucleic acid hybridizations are explained on pages 2.10.1-2.10.16 and pages 6.3.1-6.3.6 in *Current Protocols in Molecular Biology* (Ausubel, F.M. et al., "Current Protocols in Molecular Biology", John Wiley & Sons, 1998 and 2001), the entire teachings of which are incorporated by reference herein). The exact conditions which determine the stringency of hybridization depend not only on ionic strength (e.g., 0.2X SSC, 0.1X SSC), temperature (e.g., room temperature, 42°C, 68°C) and the concentration of destabilizing agents such as formamide or denaturing agents such as SDS, but also on factors such as the length of the nucleic acid sequence, base composition, percent

mismatch between hybridizing sequences and the frequency of occurrence of subsets of that sequence within other non-identical sequences. Thus, equivalent conditions can be determined by varying one or more of these parameters while maintaining a similar degree of identity or similarity between the two nucleic acid molecules.

5 Typically, conditions are used such that sequences at least about 60%, at least about 70%, at least about 80%, at least about 90% or at least about 95% or more identical to each other remain hybridized to one another. By varying hybridization conditions from a level of stringency at which no hybridization occurs to a level at which hybridization is first observed, conditions which will allow a given sequence to
10 hybridize (e.g., selectively) with the most similar sequences in the sample can be determined.

Exemplary conditions are described in Krause, M.H. and S.A. Aaronson, *Methods in Enzymology* 200:546-556, 1991, and in, Ausubel, *et al.*, "*Current Protocols in Molecular Biology*", John Wiley & Sons, 1998 and 2001, which
15 describes the determination of washing conditions for moderate or low stringency conditions. Washing is the step in which conditions are usually set so as to determine a minimum level of complementarity of the hybrids. Generally, starting from the lowest temperature at which only homologous hybridization occurs, each °C by which the final wash temperature is reduced (holding SSC concentration
20 constant) allows an increase by 1% in the maximum extent of mismatching among the sequences that hybridize. Generally, doubling the concentration of SSC results in an increase in T_m of -17°C. Using these guidelines, the washing temperature can be determined empirically for high, moderate or low stringency, depending on the level of mismatch sought.

For example, a low stringency wash can comprise washing in a solution containing 0.2X SSC/0.1% SDS for 10 minutes at room temperature; a moderate stringency wash can comprise washing in a prewarmed solution (42°C) solution containing 0.2X SSC/0.1% SDS for 15 minutes at 42°C; and a high stringency wash can comprise washing in prewarmed (68°C) solution containing 0.1X SSC/0.1% SDS
30 for 15 minutes at 68°C. Furthermore, washes can be performed repeatedly or sequentially to obtain a desired result as known in the art. Equivalent conditions can be determined by varying one or more of the parameters given as an example, as known in the art, while maintaining a similar degree of identity or similarity between the target nucleic acid molecule and the primer or probe used.

35 The percent identity of two nucleotide or amino acid sequences can be determined by aligning the sequences for optimal comparison purposes (e.g., gaps can be introduced in the sequence of a first sequence). The nucleotides or amino acids at corresponding positions are then compared, and the percent identity between

the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % identity = # of identical positions/total # of positions x 100). In certain embodiments, the length of a sequence aligned for comparison purposes is at least 30%, preferably at least 40%, more preferably at least 60%, and even more preferably at least 70%, 80%, 90% or 95% of the length of the reference sequence. The actual comparison of the two sequences can be accomplished by well-known methods, for example, using a mathematical algorithm. A preferred, non-limiting example of such a mathematical algorithm is described in Karlin *et al.*, *Proc. Natl. Acad. Sci. USA* 90:5873-5877, 1993. Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) as described in Altschul *et al.*, *Nucleic Acids Res.* 25:389-3402, 1997. When utilizing BLAST and Gapped BLAST programs, the default parameters of the respective programs (*e.g.*, NBLAST) can be used. In one embodiment, parameters for sequence comparison can be set at score=100, wordlength=12, or can be varied (*e.g.*, W=5 or W=20).

Another preferred, non-limiting example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Myers and Miller *CABIOS* 4(1): 11-17, 1998. Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package (ACCELRYS, Cambridge, UK). When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art and include ADVANCE and ADAM as described in Torellis and Robotti, *Comput. Appl. Biosci.* 10:3-5, 1994; and FASTA described in Pearson and Lipman *Proc. Natl. Acad. Sci. USA* 85:2444-8, 1988.

In another embodiment, the percent identity between two amino acid sequences can be accomplished using the GAP program in the GCG software package using either a BLOSUM63 matrix or a PAM250 matrix, and a gap weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. In yet another embodiment, the percent identity between two nucleic acid sequences can be accomplished using the GAP program in the GCG software package, using a gap weight of 50 and a length weight of 3.

The present invention also provides isolated nucleic acid molecules that contain a fragment or portion that hybridizes under highly stringent conditions to a nucleotide sequence comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-124 (odd numbers), or the complement of such a sequence, and also provides isolated nucleic acid molecules that contain a fragment or portion that hybridizes under highly stringent conditions to a nucleotide sequence encoding an amino acid sequence selected SEQ ID NOs:1-124 (even numbers), or

polymorphic variant thereof. The nucleic acid fragments of the invention are at least about 15, preferably at least about 18, 20, 23 or 25 nucleotides, and can be 30, 40, 50, 100, 200 or more nucleotides in length. Longer fragments, for example, 30 or more nucleotides in length, which encode antigenic polypeptides described herein are particularly useful, such as for the generation of antibodies as described below.

In a related aspect, the nucleic acid fragments of the invention are used as probes or primers in assays such as those described herein. "Probes" or "primers" are oligonucleotides that hybridize in a base-specific manner to a complementary strand of nucleic acid molecules. Such probes and primers include polypeptide nucleic acids, as described in Nielsen *et al.*, *Science* 254:1497-1500, (1991).

Typically, a probe or primer comprises a region of nucleotide sequence that hybridizes to at least about 15, typically about 20-25, and more typically about 40, 50 or 75, consecutive nucleotides of a nucleic acid molecule comprising a contiguous nucleotide sequence selected from the group consisting of SEQ ID NOs:1-124 (odd numbers), or the complement of such a sequence, or a sequence encoding an amino acid sequence selected from SEQ ID NOs:1-124 (even numbers), or polymorphic variant thereof. In preferred embodiments, a probe or primer comprises 100 or fewer nucleotides, preferably from 6 to 50 nucleotides, preferably from 12 to 30 nucleotides. In other embodiments, the probe or primer is at least 70% identical to the contiguous nucleotide sequence or to the complement of the contiguous nucleotide sequence, preferably at least 80% identical, more preferably at least 90% identical, even more preferably at least 95% identical, or even capable of selectively hybridizing to the contiguous nucleotide sequence or to the complement of the contiguous nucleotide sequence. Often, the probe or primer further comprises a label, e.g., radioisotope, fluorescent compound, enzyme, or enzyme co-factor.

The nucleic acid molecules of the invention such as those described above can be identified and isolated using standard molecular biology techniques and the sequence information provided herein. For example, nucleic acid molecules can be amplified and isolated by the polymerase chain reaction using synthetic oligonucleotide primers designed based on one or more of the sequences selected from the group consisting of SEQ ID NOs:1-124 (odd numbers), or the complement of such a sequence, or designed based on nucleotides based on sequences encoding one or more of the amino acid sequences provided herein. See generally *PCR Technology: Principles and Applications for DNA Amplification* (ed. H.A. Erlich, Freeman Press, NY, NY, 1992); *PCR Protocols: A Guide to Methods and Applications* (Eds. Innis *et al.*, Academic Press, San Diego, CA, 1990); Mattila *et al.*, *Nucl. Acids Res.* 19:4967, 1991; Eckert *et al.*, *PCR Methods and Applications*

1:17, 1991; PCR (eds. McPherson *et al.*, IRL Press, Oxford); and U.S. Patent 4,683,202. The nucleic acid molecules can be amplified using cDNA, mRNA or genomic DNA as a template, cloned into an appropriate vector and characterized by DNA sequence analysis.

5 Other suitable amplification methods include the ligase chain reaction (LCR) (see Wu and Wallace, *Genomics* 4:560, 1989, Landegren *et al.*, *Science* 241:1077, 1988, transcription amplification (Kwoh *et al.*, *Proc. Natl. Acad. Sci. USA* 86:1173, 1989), and self-sustained sequence replication (Guatelli *et al.*, *Proc. Nat. Acad. Sci. USA* 87:1874, 1990) and nucleic acid based sequence amplification (NASBA). The
10 latter two amplification methods involve isothermal reactions based on isothermal transcription, which produce both single stranded RNA (ssRNA) and double stranded DNA (dsDNA) as the amplification products in a ratio of about 30 or 100 to 1, respectively.

The amplified DNA can be radiolabelled and used as a probe for screening a
15 cDNA library derived from human cells, mRNA in zap express, ZIPLOX or other suitable vector. Corresponding clones can be isolated, DNA can obtained following *in vivo* excision, and the cloned insert can be sequenced in either or both orientations by art recognized methods to identify the correct reading frame encoding a polypeptide of the appropriate molecular weight. For example, the direct analysis of
20 the nucleotide sequence of nucleic acid molecules of the present invention can be accomplished using well-known methods that are commercially available. See, for example, Sambrook *et al.*, *Molecular Cloning, A Laboratory Manual* (2nd Ed., CSHP, New York 1989); Zyskind *et al.*, *Recombinant DNA Laboratory Manual*, (Acad. Press, 1988)). Using these or similar methods, the polypeptide and the DNA
25 encoding the polypeptide can be isolated, sequenced and further characterized.

Antisense nucleic acid molecules of the invention can be designed using the nucleotide sequences of one or more of SEQ ID NOs:1-124 (odd numbers) and/or the complement of one or more of SEQ ID NOs:1-124 (odd numbers), and/or a portion of one or more of SEQ ID NOs:1-124 (odd numbers), or the complement of
30 one or more of SEQ ID NOs:1-124 (odd numbers) and/or a sequence encoding the amino acid sequences of one or more of SEQ ID NOs:1-124 (even numbers), or encoding a portion of one or more of SEQ ID NOs:1-124 (even numbers), and constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid molecule (*e.g.*,
35 an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate

-16 -

derivatives and acridine substituted nucleotides can be used. Alternatively, the antisense nucleic acid molecule can be produced biologically using an expression vector into which a nucleic acid molecule has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid molecule will be of an antisense orientation to a target nucleic acid of interest).

In general, the isolated nucleic acid sequences of the invention can be used as molecular weight markers on Southern gels, and as chromosome markers which are labeled to map related gene positions. The nucleic acid sequences can also be used to compare with endogenous DNA sequences in patients to identify one or more of the disorders described above, and as probes, such as to hybridize and discover related DNA sequences or to subtract out known sequences from a sample. The nucleic acid sequences can further be used to derive primers for genetic fingerprinting, to raise anti-polypeptide antibodies using DNA immunization techniques, and as an antigen to raise anti-DNA antibodies or elicit immune responses. Portions or fragments of the nucleotide sequences identified herein (and the corresponding complete gene sequences) can be used in numerous ways as polynucleotide reagents. For example, these sequences can be used to: (i) map their respective genes on a chromosome; and, thus, locate gene regions associated with genetic disease; (ii) identify an individual from a minute biological sample (tissue typing); and (iii) aid in forensic identification of a biological sample. Additionally, the nucleotide sequences of the invention can be used to identify and express recombinant polypeptides for analysis, characterization or therapeutic use, or as markers for tissues in which the corresponding polypeptide is expressed, either constitutively, during tissue differentiation, or in diseased states. The nucleic acid sequences can additionally be used as reagents in the screening and/or diagnostic assays described herein, and can also be included as components of kits (*e.g.*, reagent kits) for use in the screening and/or diagnostic assays described herein.

Another aspect of the invention pertains to nucleic acid constructs containing a nucleic acid molecule selected from the group consisting of SEQ ID NOs:1-124 (odd numbers) and the complements thereof (or a portion thereof). Yet another aspect of the invention pertains to nucleic acid constructs containing a nucleic acid molecule encoding an amino acid sequence of SEQ ID NOs:1-124 (even numbers) or polymorphic variant thereof. The constructs comprise a vector (*e.g.*, an expression vector) into which a sequence of the invention has been inserted in a sense or antisense orientation. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of

-17 -

vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (e.g., bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (e.g., non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors, expression vectors, are capable of directing the expression of genes to which they are operably linked. In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (e.g., replication defective retroviruses, adenoviruses and adeno-associated viruses) that serve equivalent functions.

Preferred recombinant expression vectors of the invention comprise a nucleic acid molecule of the invention in a form suitable for expression of the nucleic acid molecule in a host cell. This means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which is operably linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" or "operatively linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (e.g., in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (e.g., polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel, "Gene Expression Technology", *Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells (e.g., tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed and the level of expression of polypeptide desired. The expression vectors of the invention can be introduced into host cells to thereby produce polypeptides, including fusion polypeptides, encoded by nucleic acid molecules as described herein.

The recombinant expression vectors of the invention can be designed for expression of a polypeptide of the invention in prokaryotic or eukaryotic cells, e.g., bacterial cells such as *E. coli*, insect cells (using baculovirus expression vectors), yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel,

-18 -

supra. Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but also to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, a nucleic acid molecule of the invention can be expressed in bacterial cells (*e.g.*, *E. coli*), insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing a foreign nucleic acid molecule (*e.g.*, DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*supra*), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, for resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those that confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid molecules encoding a selectable marker can be introduced into a host cell on the same vector as the nucleic acid molecule of the invention or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid molecule can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) a polypeptide of the invention. Accordingly, the invention further provides methods for producing a polypeptide

-19 -

using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding a polypeptide of the invention has been introduced) in a suitable medium such that the polypeptide is produced. In another embodiment, the method further
5 comprises isolating the polypeptide from the medium or the host cell.

The host cells of the invention can also be used to produce nonhuman transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which a nucleic acid molecule of the invention has been introduced (e.g., an exogenous GPCR gene, or an exogenous
10 nucleic acid encoding a GPCR polypeptide). Such host cells can then be used to create non-human transgenic animals in which exogenous nucleotide sequences have been introduced into the genome or homologous recombinant animals in which endogenous nucleotide sequences have been altered. Such animals are useful for studying the function and/or activity of the nucleotide sequence and polypeptide
15 encoded by the sequence and for identifying and/or evaluating modulators of their activity. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal include a transgene. Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens and amphibians. A
20 transgene is exogenous DNA which is integrated into the genome of a cell from which a transgenic animal develops and which remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, an "homologous recombinant animal" is a non-human animal, preferably a mammal, more preferably
25 a mouse, in which an endogenous gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, e.g., an embryonic cell of the animal, prior to development of the animal.

Methods for generating transgenic animals via embryo manipulation and
30 microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009, U.S. Pat. No. 4,873,191 and in Hogan, *Manipulating the Mouse Embryo* (Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1986). Methods for constructing homologous recombination vectors and homologous recombinant
35 animals are described further in Bradley (1991) *Current Opinion in BioTechnology* 2:823-829 and in PCT Publication Nos. WO 90/11354, WO 91/01140, WO 92/0968, and WO 93/04169. Clones of the non-human transgenic animals described herein

can also be produced according to the methods described in Wilmot *et al.* (1997) *Nature* 385:810-813 and PCT Publication Nos. WO 97/07668 and WO 97/07669.

POLYPEPTIDES OF THE INVENTION

5 The present invention also pertains to isolated polypeptides encoded by GPCRs ("GPCR polypeptides") and fragments and variants thereof, as well as polypeptides encoded by nucleotide sequences described herein (*e.g.*, other splicing variants). The term "polypeptide" refers to a polymer of amino acids, and not to a specific length; thus, peptides, oligopeptides and proteins are included within the
10 definition of a polypeptide. As used herein, a polypeptide is said to be "isolated" or "purified" when it is substantially free of cellular material when it is isolated from recombinant and non-recombinant cells, or free of chemical precursors or other chemicals when it is chemically synthesized. A polypeptide, however, can be joined to another polypeptide with which it is not normally associated in a cell (*e.g.*, in a
15 "fusion protein") and still be "isolated" or "purified."

 The polypeptides of the invention can be purified to homogeneity. It is understood, however, that preparations in which the polypeptide is not purified to homogeneity are useful. The critical feature is that the preparation allows for the desired function of the polypeptide, even in the presence of considerable amounts of
20 other components. Thus, the invention encompasses various degrees of purity. In one embodiment, the language "substantially free of cellular material" includes preparations of the polypeptide having less than about 30% (by dry weight) other proteins (*i.e.*, contaminating protein), less than about 20% other proteins, less than about 10% other proteins, or less than about 5% other proteins.

25 When a polypeptide is recombinantly produced, it can also be substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, less than about 10%, or less than about 5% of the volume of the polypeptide preparation. The language "substantially free of chemical precursors or other chemicals" includes preparations of the polypeptide in which it is separated from chemical precursors or
30 other chemicals that are involved in its synthesis. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of the polypeptide having less than about 30% (by dry weight) chemical precursors or other chemicals, less than about 20% chemical precursors or other chemicals, less than about 10% chemical precursors or other chemicals, or less than about 5%
35 chemical precursors or other chemicals.

 In one embodiment, a polypeptide of the invention comprises an amino acid sequence encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-124 (odd numbers), or the

complement of such a nucleic acid, or portions thereof, *e.g.*, SEQ ID NO:1-124 (even numbers), or a portion or polymorphic variant thereof. However, the polypeptides of the invention also encompass fragment and sequence variants. Variants include a substantially homologous polypeptide encoded by the same genetic locus in an organism, *i.e.*, an allelic variant, as well as other splicing variants. Variants also encompass polypeptides derived from other genetic loci in an organism, but having substantial homology to a polypeptide encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs:1-124 (odd numbers), or a complement of such a sequence, or portions thereof, or having substantial homology to a polypeptide encoded by a nucleic acid molecule comprising a nucleotide sequence selected from the group consisting of nucleotide sequences encoding SEQ ID NOs:1-124 (even numbers), or polymorphic variants thereof. Variants also include polypeptides substantially homologous or identical to these polypeptides but derived from another organism, *i.e.*, an ortholog. Variants also include polypeptides that are substantially homologous or identical to these polypeptides that are produced by chemical synthesis. Variants also include polypeptides that are substantially homologous or identical to these polypeptides that are produced by recombinant methods.

As used herein, two polypeptides (or a region of the polypeptides) are substantially homologous or identical when the amino acid sequences are at least about 45-55%, typically at least about 70-75%, more typically at least about 80-85%, and most typically greater than about 90% or more homologous or identical. A substantially homologous amino acid sequence, according to the present invention, will be encoded by a nucleic acid molecule hybridizing to one or more of SEQ ID NOs:1-124 (odd numbers), or portion thereof, under stringent conditions as more particularly described above, or will be encoded by a nucleic acid molecule hybridizing to a nucleic acid sequence encoding one of SEQ ID NOs:1-124 (even numbers), a portion thereof or polymorphic variant thereof, under stringent conditions as more particularly described thereof.

To determine the percent homology or identity of two amino acid sequences, or of two nucleic acid sequences, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of one polypeptide or nucleic acid molecule for optimal alignment with the other polypeptide or nucleic acid molecule). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in one sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the other sequence, then the molecules are homologous at that position. As used herein, amino acid or nucleic acid "homology" is equivalent

-22 -

to amino acid or nucleic acid "identity". The percent homology between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, percent homology equals the number of identical positions/total number of positions times 100).

5 The invention also encompasses polypeptides having a lower degree of identity but having sufficient similarity so as to perform one or more of the same functions performed by a polypeptide encoded by a nucleic acid molecule of the invention. Similarity is determined by conserved amino acid substitution. Such substitutions are those that substitute a given amino acid in a polypeptide by another
10 amino acid of like characteristics. Conservative substitutions are likely to be phenotypically silent. Typically seen as conservative substitutions are the replacements, one for another, among the aliphatic amino acids Ala, Val, Leu and Ile; interchange of the hydroxyl residues Ser and Thr, exchange of the acidic residues Asp and Glu, substitution between the amide residues Asn and Gln,
15 exchange of the basic residues Lys and Arg and replacements among the aromatic residues Phe and Tyr. Guidance concerning which amino acid changes are likely to be phenotypically silent are found in Bowie *et al.*, *Science* 247:1306-1310 (1990).

 A variant polypeptide can differ in amino acid sequence by one or more substitutions, deletions, insertions, inversions, fusions, and truncations or a
20 combination of any of these. Further, variant polypeptides can be fully functional or can lack function in one or more activities. Fully functional variants typically contain only conservative variation or variation in non-critical residues or in non-critical regions. Functional variants can also contain substitution of similar amino acids that result in no change or an insignificant change in function. Alternatively,
25 such substitutions may positively or negatively affect function to some degree. Non-functional variants typically contain one or more non-conservative amino acid substitutions, deletions, insertions, inversions, or truncation or a substitution, insertion, inversion, or deletion in a critical residue or critical region.

 Amino acids that are essential for function can be identified by methods
30 known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis (Cunningham *et al.*, *Science* 244:1081-1085 (1989)). The latter procedure introduces single alanine mutations at every residue in the molecule. The resulting mutant molecules are then tested for biological activity *in vitro*, or *in vitro* proliferative activity. Sites that are critical for polypeptide activity can also be
35 determined by structural analysis such as crystallization, nuclear magnetic resonance or photoaffinity labeling (Smith *et al.*, *J. Mol. Biol.* 224:899-904 (1992); de Vos *et al.*, *Science* 255:306-312 (1992)).

The invention also includes polypeptide fragments of the polypeptides of the invention. Fragments can be derived from a polypeptide encoded by a nucleic acid molecule comprising one of SEQ ID NOs:1-124 (odd numbers), or a complement of such a nucleic acid (*e.g.*, SEQ ID NOs:1-124 (even numbers), or other variants).

5 However, the invention also encompasses fragments of the variants of the polypeptides described herein. As used herein, a fragment comprises at least 6 contiguous amino acids. Useful fragments include those that retain one or more of the biological activities of the polypeptide as well as fragments that can be used as an immunogen to generate polypeptide-specific antibodies.

10 Biologically active fragments (peptides which are, for example, 6, 9, 12, 15, 16, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) can comprise a domain, segment, or motif that has been identified by analysis of the polypeptide sequence using well-known methods, *e.g.*, signal peptides, extracellular domains, one or more transmembrane segments or loops, ligand binding regions, 15 zinc finger domains, DNA binding domains, acylation sites, glycosylation sites, or phosphorylation sites.

Fragments can be discrete (not fused to other amino acids or polypeptides) or can be within a larger polypeptide. Further, several fragments can be comprised within a single larger polypeptide. In one embodiment a fragment designed for 20 expression in a host can have heterologous pre- and pro-polypeptide regions fused to the amino terminus of the polypeptide fragment and an additional region fused to the carboxyl terminus of the fragment.

The invention thus provides chimeric or fusion polypeptides. These comprise a polypeptide of the invention operatively linked to a heterologous protein or 25 polypeptide having an amino acid sequence not substantially homologous to the polypeptide. "Operatively linked" indicates that the polypeptide and the heterologous protein are fused in-frame. The heterologous protein can be fused to the N-terminus or C-terminus of the polypeptide. In one embodiment the fusion polypeptide does not affect function of the polypeptide *per se*. For example, the 30 fusion polypeptide can be a GST-fusion polypeptide in which the polypeptide sequences are fused to the C-terminus of the GST sequences. Other types of fusion polypeptides include, but are not limited to, enzymatic fusion polypeptides, for example β -galactosidase fusions, yeast two-hybrid GAL fusions, poly-His fusions and Ig fusions. Such fusion polypeptides, particularly poly-His fusions, can 35 facilitate the purification of recombinant polypeptide. In certain host cells (*e.g.*, mammalian host cells), expression and/or secretion of a polypeptide can be increased using a heterologous signal sequence. Therefore, in another embodiment, the fusion polypeptide contains a heterologous signal sequence at its N-terminus.

EP-A-O 464 533 discloses fusion proteins comprising various portions of immunoglobulin constant regions. The Fc is useful in therapy and diagnosis and thus results, for example, in improved pharmacokinetic properties (EP-A 0232 262). In drug discovery, for example, human proteins have been fused with Fc portions for the purpose of high-throughput screening assays to identify antagonists. Bennett *et al.*, *J. Mol. Recog.* 8:52-58 (1995) and Johanson *et al.*, *J. Biol. Chem.* 270:16:9459-9471 (1995). Thus, this invention also encompasses soluble fusion polypeptides containing a polypeptide of the invention and various portions of the constant regions of heavy or light chains of immunoglobulins of various subclasses (IgG, IgM, IgA, IgE).

A chimeric or fusion polypeptide can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of nucleic acid fragments can be carried out using anchor primers which give rise to complementary overhangs between two consecutive nucleic acid fragments which can subsequently be annealed and re-amplified to generate a chimeric nucleic acid sequence (see Ausubel *et al.*, *Current Protocols in Molecular Biology*, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST protein). A nucleic acid molecule encoding a polypeptide of the invention can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the polypeptide.

The isolated polypeptide can be purified from cells that naturally express it, purified from cells that have been altered to express it (recombinant), or synthesized using known protein synthesis methods. In one embodiment, the polypeptide is produced by recombinant DNA techniques. For example, a nucleic acid molecule encoding the polypeptide is cloned into an expression vector, the expression vector introduced into a host cell and the polypeptide expressed in the host cell. The polypeptide can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques.

In general, polypeptides of the present invention can be used as a molecular weight marker on SDS-PAGE gels or on molecular sieve gel filtration columns using art-recognized methods. The polypeptides of the present invention can be used to raise antibodies or to elicit an immune response. The polypeptides can also be used as a reagent, *e.g.*, a labeled reagent, in assays to quantitatively determine levels of the polypeptide or a molecule to which it binds (*e.g.*, a ligand) in biological fluids. The polypeptides can also be used as markers for cells or tissues in which the

-25 -

corresponding polypeptide is preferentially expressed, either constitutively, during tissue differentiation, or in a disease state. The polypeptides can be used to isolate a corresponding binding agent, *e.g.*, ligand, such as, for example, in an interaction trap assay, and to screen for peptide or small molecule antagonists or agonists of the binding interaction.

ANTIBODIES OF THE INVENTION

Polyclonal and/or monoclonal antibodies that specifically bind one form of the gene product but not to the other form of the gene product are also provided.

Antibodies are also provided which bind a portion of either the variant or the reference gene product that contains the polymorphic site or sites. The invention provides antibodies to the polypeptides and polypeptide fragments of the invention, *e.g.*, having an amino acid sequence of one of SEQ ID NOs:1-124 (even numbers) or a portion thereof, or having an amino acid sequence encoded by a nucleic acid molecule comprising all or a portion of SEQ ID NOs:1-124 (odd numbers), or a complement or another variant or portion thereof. The term "antibody" as used herein refers to immunoglobulin molecules and immunologically active portions of immunoglobulin molecules, *i.e.*, molecules that contain an antigen binding site that specifically binds an antigen. A molecule that specifically binds to a polypeptide of the invention is a molecule that binds to that polypeptide or a fragment thereof, but does not substantially bind other molecules in a sample, *e.g.*, a biological sample, which naturally contains the polypeptide. Examples of immunologically active portions of immunoglobulin molecules include F(ab) and F(ab')₂ fragments which can be generated by treating the antibody with an enzyme such as pepsin. The invention provides polyclonal and monoclonal antibodies that bind to a polypeptide of the invention. The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope of a polypeptide of the invention. A monoclonal antibody composition thus typically displays a single binding affinity for a particular polypeptide of the invention with which it immunoreacts.

Polyclonal antibodies can be prepared as described above by immunizing a suitable subject with a desired immunogen, *e.g.*, polypeptide of the invention or fragment thereof. The antibody titer in the immunized subject can be monitored over time by standard techniques, such as with an enzyme linked immunosorbent assay (ELISA) using immobilized polypeptide. If desired, the antibody molecules directed against the polypeptide can be isolated from the mammal (*e.g.*, from the blood) and further purified by well-known techniques, such as protein A

chromatography to obtain the IgG fraction. At an appropriate time after immunization, e.g., when the antibody titers are highest, antibody-producing cells can be obtained from the subject and used to prepare monoclonal antibodies by standard techniques, such as the hybridoma technique originally described by Kohler and Milstein (1975) *Nature* 256:495-497, the human B cell hybridoma technique (Kozbor *et al.* (1983) *Immunol. Today* 4:72), The EBV-hybridoma technique (Cole *et al.* (1985), *Monoclonal Antibodies and Cancer Therapy*, Alan R. Liss, Inc., pp. 77-96) or trioma techniques. The technology for producing hybridomas is well known (see generally *Current Protocols in Immunology* (1994) Coligan *et al.* (Eds.) John Wiley & Sons, Inc., New York, NY). Briefly, an immortal cell line (typically a myeloma) is fused to lymphocytes (typically splenocytes) from a mammal immunized with an immunogen as described above, and the culture supernatants of the resulting hybridoma cells are screened to identify a hybridoma producing a monoclonal antibody that binds a polypeptide of the invention.

Any of the many well known protocols used for fusing lymphocytes and immortalized cell lines can be applied for the purpose of generating a monoclonal antibody to a polypeptide of the invention (see, e.g., *Current Protocols in Immunology, supra*; Galfre *et al.*, *Nature* 266:55052 (1977); R.H. Kenneth, in *Monoclonal Antibodies: A New Dimension In Biological Analyses*, Plenum Publishing Corp., New York, New York (1980); and Lerner, *Yale J. Biol. Med.* 54:387-402 (1981). Moreover, the ordinarily skilled worker will appreciate that there are many variations of such methods that also would be useful.

Alternative to preparing monoclonal antibody-secreting hybridomas, a monoclonal antibody to a polypeptide of the invention can be identified and isolated by screening a recombinant combinatorial immunoglobulin library (e.g., an antibody phage display library) with the polypeptide to thereby isolate immunoglobulin library members that bind the polypeptide. Kits for generating and screening phage display libraries are commercially available (e.g., the Pharmacia *Recombinant Phage Antibody System*, Catalog No. 27-9400-01; and the Stratagene *SurfZAP™* Phage Display Kit, Catalog No. 240612). Additionally, examples of methods and reagents particularly amenable for use in generating and screening antibody display library can be found in, for example, U.S. Patent No. 5,223,409; PCT Publication No. WO 92/18619; PCT Publication No. WO 91/17271; PCT Publication No. WO 92/20791; PCT Publication No. WO 92/15679; PCT Publication No. WO 93/01288; PCT Publication No. WO 92/01047; PCT Publication No. WO 92/09690; PCT Publication No. WO 90/02809; Fuchs *et al.*, *Bio/Technology* 9:1370-1372 (1991);

Hay *et al.*, *Hum. Antibod. Hybridomas* 3:81-85 (1992); Huse *et al.*, *Science* 246:1275-1281 (1989); Griffiths *et al.*, *EMBO J.* 12:725-734 (1993).

Additionally, recombinant antibodies, such as chimeric and humanized monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art.

In general, antibodies of the invention (*e.g.*, a monoclonal antibody) can be used to isolate a polypeptide of the invention by standard techniques, such as affinity chromatography or immunoprecipitation. A polypeptide-specific antibody can facilitate the purification of natural polypeptide from cells and of recombinantly produced polypeptide expressed in host cells. Moreover, an antibody specific for a polypeptide of the invention can be used to detect the polypeptide (*e.g.*, in a cellular lysate, cell supernatant, or tissue sample) in order to evaluate the abundance and pattern of expression of the polypeptide. Antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Antibody detection can be facilitated by coupling it to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{35}S or ^3H .

DIAGNOSTIC AND SCREENING ASSAYS OF THE INVENTION

The present invention also pertains to a method of diagnosing or aiding in the diagnosis of a disease or condition associated with a GPCR gene or gene product in an individual. Diagnostic assays can be designed for assessing GPCR gene expression, or for assessing activity of GPCR polypeptides of the invention. In one embodiment, the assays are used in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or condition associated with a GPCR, or a defect in a GPCR. The invention also provides for prognostic (or predictive) assays for determining whether an

-28 -

individual is susceptible to a disease or condition associated with a GPCR, *e.g.*, if an individual is at risk for addiction to an opioid. For example, mutations in the gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of symptoms associated with a susceptibility to a disease or condition associated with a GPCR. Another aspect of the invention pertains to assays for monitoring the influence of agents (*e.g.*, drugs, compounds or other agents) on the gene expression or activity of polypeptides of the invention, as well as to assays for identifying agents that bind to a polypeptides. These and other assays and agents are described in further detail in the following sections.

DIAGNOSTIC ASSAYS

The nucleic acids, probes, primers, polypeptides and antibodies described herein can be used in methods of diagnosis of a susceptibility to a disease or condition associated with a GPCR, as well as in kits useful for diagnosis of a susceptibility to a disease or condition associated with a GPCR.

In one embodiment of the invention, susceptibility to a disease or condition associated with a GPCR can be diagnosed by detecting a polymorphism in a GPCR as described herein. The polymorphism can be a mutation in a GPCR, such as the insertion or deletion of a single nucleotide, or of more than one nucleotide, resulting in a frame shift mutation; the change of at least one nucleotide, resulting in a change in the encoded amino acid; the change of at least one nucleotide, resulting in the generation of a premature stop codon; the deletion of several nucleotides, resulting in a deletion of one or more amino acids encoded by the nucleotides; the insertion of one or several nucleotides, such as by unequal recombination or gene conversion, resulting in an interruption of the coding sequence of the gene; duplication of all or a part of the gene; transposition of all or a part of the gene; or rearrangement of all or a part of the gene. More than one such mutation may be present in a single gene. Such sequence changes cause a mutation in the polypeptide encoded by a GPCR gene. For example, if the mutation is a frame shift mutation, the frame shift can result in a change in the encoded amino acids, and/or can result in the generation of a premature stop codon, causing generation of a truncated polypeptide. Alternatively, a polymorphism associated with a susceptibility to a disease or condition associated with a GPCR can be a synonymous mutation in one or more nucleotides (*i.e.*, a mutation that does not result in a change in the polypeptide encoded by a GPCR gene). Such a polymorphism may alter splicing sites, affect the stability or transport of mRNA, or otherwise affect the transcription or translation of

-29 -

the gene. A GPCR gene that has any of the mutations described above is referred to herein as a "mutant gene."

In a first method of diagnosing a susceptibility to a disease or condition associated with a GPCR, hybridization methods, such as Southern analysis, Northern analysis, or *in situ* hybridizations, can be used (see *Current Protocols in Molecular Biology*, Ausubel, F. *et al.*, Eds., John Wiley & Sons, including all supplements through 1999). For example, a biological sample from a test subject (a "test sample") of genomic DNA, RNA, or cDNA, is obtained from an individual suspected of having, being susceptible to or predisposed for, or carrying a defect for, a susceptibility to a disease or condition associated with a GPCR (the "test individual"). The individual can be an adult, child, or fetus. The test sample can be from any source which contains genomic DNA, such as a blood sample, sample of amniotic fluid, sample of cerebrospinal fluid, or tissue sample from skin, muscle, buccal or conjunctival mucosa, placenta, gastrointestinal tract or other organs. A test sample of DNA from fetal cells or tissue can be obtained by appropriate methods, such as by amniocentesis or chorionic villus sampling. The DNA, RNA, or cDNA sample is then examined to determine whether a polymorphism in a GPCR is present, and/or to determine which splicing variant(s) encoded by the GPCR is present. The presence of the polymorphism or splicing variant(s) can be indicated by hybridization of the gene in the genomic DNA, RNA, or cDNA to a nucleic acid probe. A "nucleic acid probe", as used herein, can be a DNA probe or an RNA probe; the nucleic acid probe can contain at least one polymorphism in a GPCR or contains a nucleic acid encoding a particular splicing variant of a GPCR. The probe can be any of the nucleic acid molecules described above (*e.g.*, the gene, a fragment, a vector comprising the gene, a probe or primer, etc.).

To diagnose a susceptibility to a disease or condition associated with a GPCR, a test sample containing a GPCR, is contacted with at least one nucleic acid probe to form a hybridization sample. A preferred probe for detecting mRNA or genomic DNA is a labeled nucleic acid probe capable of hybridizing to mRNA or genomic DNA sequences described herein. The nucleic acid probe can be, for example, a full-length nucleic acid molecule, or a portion thereof, such as an oligonucleotide of at least 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to appropriate mRNA or genomic DNA. For example, the nucleic acid probe can be all or a portion of one of SEQ ID NOs:1-124 (odd numbers), or the complement thereof, or a portion thereof; or can be a nucleic acid encoding a portion of one of SEQ ID NOs:1-124 (even numbers). Other suitable probes for use in the diagnostic assays of the invention are described

-30 -

above (see *e.g.*, probes and primers discussed under the heading, "Nucleic Acids of the Invention").

The hybridization sample is maintained under conditions that are sufficient to allow specific hybridization of the nucleic acid probe to a GPCR. "Specific hybridization", as used herein, indicates exact hybridization (*e.g.*, with no mismatches). Specific hybridization can be performed under high stringency conditions or moderate stringency conditions, for example, as described above. In a particularly preferred embodiment, the hybridization conditions for specific hybridization are high stringency.

Specific hybridization, if present, is then detected using standard methods. If specific hybridization occurs between the nucleic acid probe and the GPCR in the test sample, then the GPCR has the polymorphism, or is the splicing variant, that is present in the nucleic acid probe. More than one nucleic acid probe can also be used concurrently in this method. Specific hybridization of any one of the nucleic acid probes is indicative of a polymorphism in the GPCR, or of the presence of a particular splicing variant encoding the GPCR and is therefore diagnostic for a susceptibility to a susceptibility to a disease or condition associated with a GPCR.

In Northern analysis (see *Current Protocols in Molecular Biology*, Ausubel, F. *et al.*, eds., John Wiley & Sons, *supra*) the hybridization methods described above are used to identify the presence of a polymorphism or a particular splicing variant, associated with a susceptibility to a susceptibility to a disease or condition associated with a GPCR. For Northern analysis, a test sample of RNA is obtained from the individual by appropriate means. Specific hybridization of a nucleic acid probe, as described above, to RNA from the individual is indicative of a polymorphism in a GPCR, or of the presence of a particular splicing variant encoded by a GPCR, and is therefore diagnostic for a susceptibility to a susceptibility to a disease or condition associated with a GPCR.

For representative examples of use of nucleic acid probes, see, for example, U.S. Patents No. 5,288,611 and 4,851,330.

Alternatively, a peptide nucleic acid (PNA) probe can be used instead of a nucleic acid probe in the hybridization methods described above. PNA is a DNA mimic having a peptide-like, inorganic backbone, such as N-(2-aminoethyl)glycine units, with an organic base (A, G, C, T or U) attached to the glycine nitrogen via a methylene carbonyl linker (see, for example, Nielsen, P.E. *et al.*, *Bioconjugate Chemistry* 5, American Chemical Society, p. 1 (1994)). The PNA probe can be designed to specifically hybridize to a gene having a polymorphism associated with a susceptibility to a susceptibility to a disease or condition associated with a GPCR.

Hybridization of the PNA probe to a GPCR is diagnostic for a susceptibility to a susceptibility to a disease or condition associated with a GPCR.

In another method of the invention, mutation analysis by restriction digestion can be used to detect a mutant gene, or genes containing a polymorphism(s), if the mutation or polymorphism in the gene results in the creation or elimination of a restriction site. A test sample containing genomic DNA is obtained from the individual. Polymerase chain reaction (PCR) can be used to amplify a GPCR (and, if necessary, the flanking sequences) in the test sample of genomic DNA from the test individual. RFLP analysis is conducted as described (see *Current Protocols in Molecular Biology, supra*). The digestion pattern of the relevant DNA fragment indicates the presence or absence of the mutation or polymorphism in the GPCR, and therefore indicates the presence or absence of this susceptibility to a susceptibility to a disease or condition associated with a GPCR.

Sequence analysis can also be used to detect specific polymorphisms in a GPCR. A test sample of DNA or RNA is obtained from the test individual. PCR or other appropriate methods can be used to amplify the gene, and/or its flanking sequences, if desired. The sequence of a GPCR, or a fragment of the gene, or cDNA, or fragment of the cDNA, or mRNA, or fragment of the mRNA, is determined, using standard methods. The sequence of the gene, gene fragment, cDNA, cDNA fragment, mRNA, or mRNA fragment is compared with the known nucleic acid sequence of the gene, cDNA (e.g., one or more of SEQ ID NOs:1-124 (odd numbers), or a complement thereof, or a nucleic acid sequence encoding one of SEQ ID NOs:1-124 (even numbers) or a fragment thereof) or mRNA, as appropriate. The presence of a polymorphism in the GPCR indicates that the individual has a susceptibility to a susceptibility to a disease or condition associated with a GPCR.

Allele-specific oligonucleotides can also be used to detect the presence of a polymorphism in a GPCR, through the use of dot-blot hybridization of amplified oligonucleotides with allele-specific oligonucleotide (ASO) probes (see, for example, Saiki, R. *et al.*, *Nature* 324:163-166 (1986)). An "allele-specific oligonucleotide" (also referred to herein as an "allele-specific oligonucleotide probe") is an oligonucleotide of approximately 10-50 base pairs, preferably approximately 15-30 base pairs, that specifically hybridizes to a GPCR, and that contains a polymorphism associated with a susceptibility to a susceptibility to a disease or condition associated with a GPCR. An allele-specific oligonucleotide probe that is specific for particular polymorphisms in a GPCR can be prepared, using standard methods (see *Current Protocols in Molecular Biology, supra*). To identify polymorphisms in the gene that are associated with a susceptibility to a

susceptibility to a disease or condition associated with a GPCR, a test sample of DNA is obtained from the individual. PCR can be used to amplify all or a fragment of a GPCR, and its flanking sequences. The DNA containing the amplified GPCR (or fragment of the gene) is dot-blotted, using standard methods (see *Current Protocols in Molecular Biology, supra*), and the blot is contacted with the oligonucleotide probe. The presence of specific hybridization of the probe to the amplified GPCR is then detected. Specific hybridization of an allele-specific oligonucleotide probe to DNA from the individual is indicative of a polymorphism in the GPCR, and is therefore indicative of a susceptibility to a disease or condition associated with a GPCR.

In another embodiment, arrays of oligonucleotide probes that are complementary to target nucleic acid sequence segments from an individual, can be used to identify polymorphisms in a GPCR. For example, in one embodiment, an oligonucleotide array can be used. Oligonucleotide arrays typically comprise a plurality of different oligonucleotide probes that are coupled to a surface of a substrate in different known locations. These oligonucleotide arrays, also described as "Genechips™," have been generally described in the art, for example, U.S. Pat. No. 5,143,854 and PCT patent publication Nos. WO 90/15070 and 92/10092. These arrays can generally be produced using mechanical synthesis methods or light directed synthesis methods which incorporate a combination of photolithographic methods and solid phase oligonucleotide synthesis methods. See Fodor *et al.*, *Science* 251:767-777 (1991), Pirrung *et al.*, U.S. Pat. No. 5,143,854 (see also PCT Application No. WO 90/15070) and Fodor *et al.*, PCT Publication No. WO 92/10092 and U.S. Pat. No. 5,424,186, the entire teachings of each of which are incorporated by reference herein. Techniques for the synthesis of these arrays using mechanical synthesis methods are described in, *e.g.*, U.S. Pat. Nos. 5,384,261; the entire teachings of which are incorporated by reference herein.

Once an oligonucleotide array is prepared, a nucleic acid of interest is hybridized with the array and scanned for polymorphisms. Hybridization and scanning are generally carried out by methods described herein and also in, *e.g.*, Published PCT Application Nos. WO 92/10092 and WO 95/11995, and U.S. Pat. No. 5,424,186, the entire teachings of which are incorporated by reference herein. In brief, a target nucleic acid sequence that includes one or more previously identified polymorphic markers is amplified by well known amplification techniques, *e.g.*, PCR. Typically, this involves the use of primer sequences that are complementary to the two strands of the target sequence both upstream and downstream from the polymorphism. Asymmetric PCR techniques may also be used. Amplified target, generally incorporating a label, is then hybridized with the

array under appropriate conditions. Upon completion of hybridization and washing of the array, the array is scanned to determine the position on the array to which the target sequence hybridizes. The hybridization data obtained from the scan is typically in the form of fluorescence intensities as a function of location on the array.

Although primarily described in terms of a single detection block, *e.g.*, for detection of a single polymorphism, arrays can include multiple detection blocks, and thus be capable of analyzing multiple, specific polymorphisms. In alternate arrangements, it will generally be understood that detection blocks may be grouped within a single array or in multiple, separate arrays so that varying, optimal conditions may be used during the hybridization of the target to the array. For example, it may often be desirable to provide for the detection of those polymorphisms that fall within G-C rich stretches of a genomic sequence, separately from those falling in A-T rich segments. This allows for the separate optimization of hybridization conditions for each situation.

Additional description of use of oligonucleotide arrays for detection of polymorphisms can be found, for example, in U.S. Patents 5,858,659 and 5,837,832, the entire teachings of which are incorporated by reference herein.

Other methods of nucleic acid analysis can be used to detect polymorphisms in a GPCR or variants encoding by a GPCR. Representative methods include direct manual sequencing (Church and Gilbert, *Proc. Natl. Acad. Sci. USA* 81:1991-1995 (1988); Sanger, F. *et al. Proc. Natl. Acad. Sci. USA* 74:5463-5467 (1977); Beavis *et al.*, U.S. Pat. No. 5,288,644); automated fluorescent sequencing; single-stranded conformation polymorphism assays (SSCP); clamped denaturing gel electrophoresis (CDGE); denaturing gradient gel electrophoresis (DGGE) (Sheffield, V.C. *et al. Proc. Natl. Acad. Sci. USA* 86:232-236 (1989)), mobility shift analysis (Orita, M. *et al., Proc. Natl. Acad. Sci. USA* 86:2766-2770 (1989)), restriction enzyme analysis (Flavell *et al.*, *Cell* 15:25 (1978); Geever, *et al.*, *Proc. Natl. Acad. Sci. USA* 78:5081 (1981)); heteroduplex analysis; chemical mismatch cleavage (CMC) (Cotton *et al.*, *Proc. Natl. Acad. Sci. USA* 85:4397-4401 (1985)); RNase protection assays (Myers, R.M. *et al.*, *Science* 230:1242 (1985)); use of polypeptides which recognize nucleotide mismatches, such as *E. coli* mutS protein; allele-specific PCR, for example.

In another embodiment of the invention, diagnosis of a susceptibility to a susceptibility to a disease or condition associated with a GPCR can also be made by examining expression and/or composition of a GPCR polypeptide, by a variety of methods, including enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations and immunofluorescence. A test sample from an individual is

assessed for the presence of an alteration in the expression and/or an alteration in composition of the polypeptide encoded by a GPCR, or for the presence of a particular variant encoded by a GPCR. An alteration in expression of a polypeptide encoded by a GPCR can be, for example, an alteration in the quantitative
5 polypeptide expression (*i.e.*, the amount of polypeptide produced); an alteration in the composition of a polypeptide encoded by a GPCR is an alteration in the qualitative polypeptide expression (*e.g.*, expression of a mutant GPCR polypeptide or of a different splicing variant). In a preferred embodiment, diagnosis of a susceptibility to a disease or condition associated with a GPCR is made by detecting
10 a particular splicing variant encoded by that GPCR, or a particular pattern of splicing variants.

Both such alterations (quantitative and qualitative) can also be present. An "alteration" in the polypeptide expression or composition, as used herein, refers to an alteration in expression or composition in a test sample, as compared with the
15 expression or composition of polypeptide by a GPCR in a control sample. A control sample is a sample that corresponds to the test sample (*e.g.*, is from the same type of cells), and is from an individual who is not affected by a susceptibility to a disease or condition associated with a GPCR. An alteration in the expression or composition of the polypeptide in the test sample, as compared with the control
20 sample, is indicative of a susceptibility to a disease or condition associated with a GPCR. Similarly, the presence of one or more different splicing variants in the test sample, or the presence of significantly different amounts of different splicing variants in the test sample, as compared with the control sample, is indicative of a susceptibility to a disease or condition associated
25 with a GPCR. Various means of examining expression or composition of the polypeptide encoded by a GPCR can be used, including spectroscopy, colorimetry, electrophoresis, isoelectric focusing, and immunoassays (*e.g.*, David *et al.*, U.S. Pat. No. 4,376,110) such as immunoblotting (see also *Current Protocols in Molecular Biology*, particularly Chapter 10). For example, in one embodiment, an antibody
30 capable of binding to the polypeptide (*e.g.*, as described above), preferably an antibody with a detectable label, can be used. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (*e.g.*, Fab or F(ab')₂) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (*i.e.*,
35 physically linking) a detectable substance to the probe or antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently labeled secondary antibody and end-labeling of a

-35 -

DNA probe with biotin such that it can be detected with fluorescently labeled streptavidin.

Western blotting analysis, using an antibody as described above that specifically binds to a polypeptide encoded by a mutant GPCR, or an antibody that specifically binds to a polypeptide encoded by a non-mutant gene, or an antibody that specifically binds to a particular splicing variant encoded by a GPCR, can be used to identify the presence in a test sample of a particular splicing variant or of a polypeptide encoded by a polymorphic or mutant GPCR, or the absence in a test sample of a particular splicing variant or of a polypeptide encoded by a non-polymorphic or non-mutant gene. The presence of a polypeptide encoded by a polymorphic or mutant gene, or the absence of a polypeptide encoded by a non-polymorphic or non-mutant gene, is diagnostic for a susceptibility to a susceptibility to a disease or condition associated with a GPCR, as is the presence (or absence) of particular splicing variants encoded by the GPCR gene.

In one embodiment of this method, the level or amount of polypeptide encoded by a GPCR in a test sample is compared with the level or amount of the polypeptide encoded by the GPCR in a control sample. A level or amount of the polypeptide in the test sample that is higher or lower than the level or amount of the polypeptide in the control sample, such that the difference is statistically significant, is indicative of an alteration in the expression of the polypeptide encoded by the GPCR, and is diagnostic for a susceptibility to a susceptibility to a disease or condition associated with that GPCR. Alternatively, the composition of the polypeptide encoded by a GPCR in a test sample is compared with the composition of the polypeptide encoded by the GPCR in a control sample (*e.g.*, the presence of different splicing variants). A difference in the composition of the polypeptide in the test sample, as compared with the composition of the polypeptide in the control sample, is diagnostic for a susceptibility to a susceptibility to a disease or condition associated with that GPCR. In another embodiment, both the level or amount and the composition of the polypeptide can be assessed in the test sample and in the control sample. A difference in the amount or level of the polypeptide in the test sample, compared to the control sample; a difference in composition in the test sample, compared to the control sample; or both a difference in the amount or level, and a difference in the composition, is indicative of a susceptibility to a susceptibility to a disease or condition associated with that GPCR.

Kits (*e.g.*, reagent kits) useful in the methods of diagnosis comprise components useful in any of the methods described herein, including for example, hybridization probes or primers as described herein (*e.g.*, labeled probes or primers), reagents for detection of labeled molecules, restriction enzymes (*e.g.*, for RFLP

-36 -

analysis), allele-specific oligonucleotides, antibodies which bind to mutant or to non-mutant (native) GPCR polypeptide, means for amplification of nucleic acids comprising a GPCR, or means for analyzing the nucleic acid sequence of a GPCR or for analyzing the amino acid sequence of a GPCR polypeptide, etc.

5

SCREENING ASSAYS AND AGENTS IDENTIFIED THEREBY

The invention provides methods (also referred to herein as "screening assays") for identifying the presence of a nucleotide that hybridizes to a nucleic acid of the invention, as well as for identifying the presence of a polypeptide encoded by a nucleic acid of the invention. In one embodiment, the presence (or absence) of a nucleic acid molecule of interest (*e.g.*, a nucleic acid that has significant homology with a nucleic acid of the invention) in a sample can be assessed by contacting the sample with a nucleic acid comprising a nucleic acid of the invention (*e.g.*, a nucleic acid having the sequence of one of SEQ ID NOs:1-124 (odd numbers), or the complement thereof, or a nucleic acid encoding an amino acid having the sequence of one of SEQ ID NOs:1-124 (even numbers), or a fragment or variant of such nucleic acids), under stringent conditions as described above, and then assessing the sample for the presence (or absence) of hybridization. In a preferred embodiment, high stringency conditions are conditions appropriate for selective hybridization. In another embodiment, a sample containing the nucleic acid molecule of interest is contacted with a nucleic acid containing a contiguous nucleotide sequence (*e.g.*, a primer or a probe as described above) that is at least partially complementary to a part of the nucleic acid molecule of interest (*e.g.*, a GPCR nucleic acid), and the contacted sample is assessed for the presence or absence of hybridization. In a preferred embodiment, the nucleic acid containing a contiguous nucleotide sequence is completely complementary to a part of the nucleic acid molecule of interest.

In any of these embodiments, all or a portion of the nucleic acid of interest can be subjected to amplification prior to performing the hybridization.

In another embodiment, the presence (or absence) of a polypeptide of interest, such as a polypeptide of the invention or a fragment or variant thereof, in a sample can be assessed by contacting the sample with an antibody that specifically hybridizes to the polypeptide of interest (*e.g.*, an antibody such as those described above), and then assessing the sample for the presence (or absence) of binding of the antibody to the polypeptide of interest.

In another embodiment, the invention provides methods for identifying agents (*e.g.*, fusion proteins, polypeptides, peptidomimetics, prodrugs, other receptors associated with GPCRs, binding agents, antibodies, small molecules or other drugs, or ribozymes which alter (*e.g.*, increase or decrease) the activity of the polypeptides

-37 -

described herein, or which otherwise interact with the polypeptides herein. For example, such agents can be agents which bind to polypeptides described herein (e.g., GPCR binding agents); which have a stimulatory or inhibitory effect on, for example, activity of polypeptides of the invention; or which change (e.g., enhance or inhibit) the ability of the polypeptides of the invention to interact with GPCR binding agents (e.g., G-proteins, other receptors associated with GPCRs, or other binding agents); or which alter posttranslational processing of the GPCR polypeptide (e.g., agents that alter proteolytic processing to direct the polypeptide from where it is normally synthesized to another location in the cell, such as the cell surface; agents that alter proteolytic processing such that more polypeptide is released from the cell, etc.

In one embodiment, the invention provides assays for screening candidate or test agents that bind to or modulate the activity of polypeptides described herein (or biologically active portion(s) thereof), as well as agents identifiable by the assays. Test agents can be obtained using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the 'one-bead one-compound' library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to polypeptide libraries, while the other four approaches are applicable to polypeptide, non-peptide oligomer or small molecule libraries of compounds (Lam, K.S., *Anticancer Drug Des.* 12:145 (1997)).

In one embodiment, to identify agents which alter the activity of a GPCR polypeptide, a cell, cell lysate, or solution containing or expressing a GPCR polypeptide (e.g., one of SEQ ID NOs:1-124 (even numbers), or another splicing variant encoded by a GPCR), or a fragment or derivative thereof (as described above), can be contacted with an agent to be tested; alternatively, the polypeptide can be contacted directly with the agent to be tested. The level (amount) of GPCR activity is assessed (e.g., the level (amount) of GPCR activity is measured, either directly or indirectly), and is compared with the level of activity in a control (i.e., the level of activity of the GPCR polypeptide or active fragment or derivative thereof in the absence of the agent to be tested). If the level of the activity in the presence of the agent differs, by an amount that is statistically significant, from the level of the activity in the absence of the agent, then the agent is an agent that alters the activity of a GPCR polypeptide. An increase in the level of GPCR activity relative to a control, indicates that the agent is an agent that enhances (is an agonist of) GPCR activity. Similarly, a decrease in the level of GPCR activity relative to a control, indicates that the agent is an agent that inhibits (is an antagonist of) GPCR activity.

-38 -

In another embodiment, the level of activity of a GPCR polypeptide or derivative or fragment thereof in the presence of the agent to be tested, is compared with a control level that has previously been established. A level of the activity in the presence of the agent that differs from the control level by an amount that is statistically significant indicates that the agent alters GPCR activity.

The present invention also relates to an assay for identifying agents which alter the expression of a GPCR gene (*e.g.*, antisense nucleic acids, fusion proteins, polypeptides, peptidomimetics, prodrugs, other receptors associated with GPCRs, G-proteins, binding agents, antibodies, small molecules or other drugs, or ribozymes) which alter (*e.g.*, increase or decrease) expression (*e.g.*, transcription or translation) of the gene or which otherwise interact with the nucleic acids described herein, as well as agents identifiable by the assays. For example, a solution containing a nucleic acid encoding a GPCR polypeptide (*e.g.*, a GPCR gene) can be contacted with an agent to be tested. The solution can comprise, for example, cells containing the nucleic acid or cell lysate containing the nucleic acid; alternatively, the solution can be another solution that comprises elements necessary for transcription/translation of the nucleic acid. Cells not suspended in solution can also be employed, if desired. The level and/or pattern of GPCR expression (*e.g.*, the level and/or pattern of mRNA or of protein expressed, such as the level and/or pattern of different splicing variants) is assessed, and is compared with the level and/or pattern of expression in a control (*i.e.*, the level and/or pattern of the GPCR expression in the absence of the agent to be tested). If the level and/or pattern in the presence of the agent differ(s), by an amount or in a manner that is statistically significant, from the level and/or pattern in the absence of the agent, then the agent is an agent that alters the expression of GPCR. Enhancement of GPCR expression indicates that the agent is an agonist of GPCR activity. Similarly, inhibition of GPCR expression indicates that the agent is an antagonist of GPCR activity. In another embodiment, the level and/or pattern of GPCR polypeptide(s) (*e.g.*, different splicing variants) in the presence of the agent to be tested, is compared with a control level and/or pattern that have previously been established. A level and/or pattern in the presence of the agent that differs from the control level and/or pattern by an amount or in a manner that is statistically significant indicates that the agent alters GPCR expression.

In another embodiment of the invention, agents which alter the expression of a GPCR gene or which otherwise interact with the nucleic acids described herein, can be identified using a cell, cell lysate, or solution containing a nucleic acid encoding the promoter region of the GPCR gene operably linked to a reporter gene. After contact with an agent to be tested, the level of expression of the reporter gene (*e.g.*,

the level of mRNA or of protein expressed) is assessed, and is compared with the level of expression in a control (*i.e.*, the level of the expression of the reporter gene in the absence of the agent to be tested). If the level in the presence of the agent differs, by an amount or in a manner that is statistically significant, from the level in the absence of the agent, then the agent is an agent that alters the expression of the GPCR, as indicated by its ability to alter expression of a gene that is operably linked to the GPCR gene promoter. Enhancement of the expression of the reporter indicates that the agent is an agonist of GPCR activity. Similarly, inhibition of the expression of the reporter indicates that the agent is an antagonist of GPCR activity. In another embodiment, the level of expression of the reporter in the presence of the agent to be tested, is compared with a control level that has previously been established. A level in the presence of the agent that differs from the control level by an amount or in a manner that is statistically significant indicates that the agent alters expression.

Agents which alter the amounts of different splicing variants encoded by a GPCR (*e.g.*, an agent which enhances activity of a first splicing variant, and which inhibits activity of a second splicing variant), as well as agents which are agonists of activity of a first splicing variant and antagonists of activity of a second splicing variant, can easily be identified using these methods described above.

In other embodiments of the invention, assays can be used to assess the impact of a test agent on the activity of a polypeptide in relation to a GPCR binding agent. For example, a cell that expresses a compound that interacts with a GPCR (herein referred to as a "GPCR binding agent", which can be a polypeptide or other molecule that interacts with a GPCR, such as a G-protein) is contacted with a GPCR in the presence of a test agent, and the ability of the test agent to alter the interaction between the GPCR and the GPCR binding agent is determined. Alternatively, a cell lysate or a solution containing the GPCR binding agent, can be used. An agent which binds to the GPCR or the GPCR binding agent can alter the interaction by interfering with, or enhancing the ability of the GPCR to bind to, associate with, or otherwise interact with the GPCR binding agent. Determining the ability of the test agent to bind to a GPCR or a GPCR binding agent can be accomplished, for example, by coupling the test agent with a radioisotope or enzymatic label such that binding of the test agent to the polypeptide can be determined by detecting the labeled with ^{125}I , ^{35}S , ^{14}C or ^3H , either directly or indirectly, and the radioisotope detected by direct counting of radioemmission or by scintillation counting. Alternatively, test agents can be enzymatically labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product. It is

also within the scope of this invention to determine the ability of a test agent to interact with the polypeptide without the labeling of any of the interactants. For example, a microphysiometer can be used to detect the interaction of a test agent with a GPCR or a GPCR binding agent without the labeling of either the test agent, GPCR, or the GPCR binding agent. McConnell, H.M. *et al.*, *Science* 257:1906-1912 (1992). As used herein, a "microphysiometer" (e.g., Cytosensor™) is an analytical instrument that measures the rate at which a cell acidifies its environment using a light-addressable potentiometric sensor (LAPS). Changes in this acidification rate can be used as an indicator of the interaction between ligand and polypeptide. Thus, these receptors can be used to screen for compounds that are agonists for use in treating a susceptibility to a disease or condition associated with a GPCR or antagonists for studying a susceptibility to a disease or condition associated with a GPCR. Drugs could be designed to regulate GPCR activation that in turn can be used to regulate signaling pathways and transcription events of genes downstream.

In another embodiment of the invention, assays can be used to identify polypeptides that interact with one or more GPCR polypeptides, as described herein. For example, a yeast two-hybrid system such as that described by Fields and Song (Fields, S. and Song, O., *Nature* 340:245-246 (1989)) can be used to identify polypeptides that interact with one or more GPCR polypeptides. In such a yeast two-hybrid system, vectors are constructed based on the flexibility of a transcription factor that has two functional domains (a DNA binding domain and a transcription activation domain). If the two domains are separated but fused to two different proteins that interact with one another, transcriptional activation can be achieved, and transcription of specific markers (e.g., nutritional markers such as His and Ade, or color markers such as lacZ) can be used to identify the presence of interaction and transcriptional activation. For example, in the methods of the invention, a first vector is used which includes a nucleic acid encoding a DNA binding domain and also a GPCR polypeptide, splicing variant, or fragment or derivative thereof, and a second vector is used which includes a nucleic acid encoding a transcription activation domain and also a nucleic acid encoding a polypeptide which potentially may interact with the GPCR polypeptide, splicing variant, or fragment or derivative thereof (e.g., a GPCR polypeptide binding agent or G-protein). Incubation of yeast containing the first vector and the second vector under appropriate conditions (e.g., mating conditions such as used in the Matchmaker™ system from Clontech (Palo Alto, California, USA)) allows identification of colonies that express the markers of interest. These colonies can be examined to identify the polypeptide(s) that interact with the GPCR polypeptide or fragment or derivative thereof. Such polypeptides

may be useful as agents that alter the activity of expression of a GPCR polypeptide, as described above.

In more than one embodiment of the above assay methods of the present invention, it may be desirable to immobilize either GPCR, the GPCR binding agent, or other components of the assay on a solid support, in order to facilitate separation of complexed from uncomplexed forms of one or both of the polypeptides, as well as to accommodate automation of the assay. Binding of a test agent to the polypeptide, or interaction of the polypeptide with a binding agent in the presence and absence of a test agent, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtiter plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein (*e.g.*, a glutathione-S-transferase fusion protein) can be provided which adds a domain that allows GPCR or a GPCR binding agent to be bound to a matrix or other solid support.

In another embodiment, modulators of expression of nucleic acid molecules of the invention are identified in a method wherein a cell, cell lysate, or solution containing a nucleic acid encoding a GPCR is contacted with a test agent and the expression of appropriate mRNA or polypeptide (*e.g.*, splicing variant(s)) in the cell, cell lysate, or solution, is determined. The level of expression of appropriate mRNA or polypeptide(s) in the presence of the test agent is compared to the level of expression of mRNA or polypeptide(s) in the absence of the test agent. The test agent can then be identified as a modulator of expression based on this comparison. For example, when expression of mRNA or polypeptide is greater (statistically significantly greater) in the presence of the test agent than in its absence, the test agent is identified as a stimulator or enhancer of the mRNA or polypeptide expression. Alternatively, when expression of the mRNA or polypeptide is less (statistically significantly less) in the presence of the test agent than in its absence, the test agent is identified as an inhibitor of the mRNA or polypeptide expression. The level of mRNA or polypeptide expression in the cells can be determined by methods described herein for detecting mRNA or polypeptide.

This invention further pertains to novel agents identified by the above-described screening assays. Accordingly, it is within the scope of this invention to further use an agent identified as described herein in an appropriate animal model. For example, an agent identified as described herein (*e.g.*, a test agent that is a modulating agent, an antisense nucleic acid molecule, a specific antibody, or a polypeptide-binding agent) can be used in an animal model to determine the efficacy, toxicity, or side effects of treatment with such an agent. Alternatively, an agent identified as described herein can be used in an animal model to determine the

-42 -

mechanism of action of such an agent. Furthermore, this invention pertains to uses of novel agents identified by the above-described screening assays for treatments as described herein. In addition, an agent identified as described herein can be used to alter activity of a polypeptide encoded by a GPCR, or to alter expression of a GPCR, by contacting the polypeptide or the gene (or contacting a cell comprising the polypeptide or the gene) with the agent identified as described herein.

PHARMACEUTICAL COMPOSITIONS

The present invention also pertains to pharmaceutical compositions comprising nucleic acids described herein, particularly nucleotides encoding the polypeptides described herein; comprising polypeptides described herein (*e.g.*, one or more of SEQ ID NOs:1-124 (even numbers)); and/or comprising other splicing variants encoded by a GPCR; and/or an agent that alters (*e.g.*, enhances or inhibits) GPCR gene expression or GPCR polypeptide activity as described herein. For instance, a polypeptide, protein (*e.g.*, a G-protein), an agent that alters GPCR gene expression, or a GPCR binding agent or binding partner, fragment, fusion protein or prodrug thereof, or a nucleotide or nucleic acid construct (vector) comprising a nucleotide of the present invention, or an agent that alters GPCR polypeptide activity, can be formulated with a physiologically acceptable carrier or excipient to prepare a pharmaceutical composition. The carrier and composition can be sterile. The formulation should suit the mode of administration.

Suitable pharmaceutically acceptable carriers include but are not limited to water, salt solutions (*e.g.*, NaCl), saline, buffered saline, alcohols, glycerol, ethanol, gum arabic, vegetable oils, benzyl alcohols, polyethylene glycols, gelatin, carbohydrates such as lactose, amylose or starch, dextrose, magnesium stearate, talc, silicic acid, viscous paraffin, perfume oil, fatty acid esters, hydroxymethylcellulose, polyvinyl pyrrolidone, etc., as well as combinations thereof. The pharmaceutical preparations can, if desired, be mixed with auxiliary agents, *e.g.*, lubricants, preservatives, stabilizers, wetting agents, emulsifiers, salts for influencing osmotic pressure, buffers, coloring, flavoring and/or aromatic substances and the like which do not deleteriously react with the active agents.

The composition, if desired, can also contain minor amounts of wetting or emulsifying agents, or pH buffering agents. The composition can be a liquid solution, suspension, emulsion, tablet, pill, capsule, sustained release formulation, or powder. The composition can be formulated as a suppository, with traditional binders and carriers such as triglycerides. Oral formulation can include standard carriers such as pharmaceutical grades of mannitol, lactose, starch, magnesium

stearate, polyvinyl pyrrolidone, sodium saccharine, cellulose, magnesium carbonate, etc.

Methods of introduction of these compositions include, but are not limited to, intradermal, intramuscular, intraperitoneal, intraocular, intravenous, subcutaneous, topical, oral and intranasal. Other suitable methods of introduction can also include gene therapy (as described below), rechargeable or biodegradable devices, particle acceleration devices ("gene guns") and slow release polymeric devices. The pharmaceutical compositions of this invention can also be administered as part of a combinatorial therapy with other agents.

The composition can be formulated in accordance with the routine procedures as a pharmaceutical composition adapted for administration to human beings. For example, compositions for intravenous administration typically are solutions in sterile isotonic aqueous buffer. Where necessary, the composition may also include a solubilizing agent and a local anesthetic to ease pain at the site of the injection. Generally, the ingredients are supplied either separately or mixed together in unit dosage form, for example, as a dry lyophilized powder or water free concentrate in a hermetically sealed container such as an ampule or sachette indicating the quantity of active agent. Where the composition is to be administered by infusion, it can be dispensed with an infusion bottle containing sterile pharmaceutical grade water, saline or dextrose/water. Where the composition is administered by injection, an ampule of sterile water for injection or saline can be provided so that the ingredients may be mixed prior to administration.

For topical application, nonsprayable forms, viscous to semi-solid or solid forms comprising a carrier compatible with topical application and having a dynamic viscosity preferably greater than water, can be employed. Suitable formulations include but are not limited to solutions, suspensions, emulsions, creams, ointments, powders, enemas, lotions, sols, liniments, salves, aerosols, etc., which are, if desired, sterilized or mixed with auxiliary agents, *e.g.*, preservatives, stabilizers, wetting agents, buffers or salts for influencing osmotic pressure, etc. The agent may be incorporated into a cosmetic formulation. For topical application, also suitable are sprayable aerosol preparations wherein the active ingredient, preferably in combination with a solid or liquid inert carrier material, is packaged in a squeeze bottle or in admixture with a pressurized volatile, normally gaseous propellant, *e.g.*, pressurized air.

Agents described herein can be formulated as neutral or salt forms. Pharmaceutically acceptable salts include those formed with free amino groups such as those derived from hydrochloric, phosphoric, acetic, oxalic, tartaric acids, etc., and those formed with free carboxyl groups such as those derived from sodium,

-44 -

potassium, ammonium, calcium, ferric hydroxides, isopropylamine, triethylamine, 2-ethylamino ethanol, histidine, procaine, etc.

The agents are administered in a therapeutically effective amount. The amount of agents which will be therapeutically effective in the treatment of a particular disorder or condition will depend on the nature of the disorder or condition, and can be determined by standard clinical techniques. In addition, *in vitro* or *in vivo* assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the symptoms of a susceptibility to a disease or condition associated with a GPCR, and should be decided according to the judgment of a practitioner and each patient's circumstances. Effective doses may be extrapolated from dose-response curves derived from *in vitro* or animal model test systems.

The invention also provides a pharmaceutical pack or kit comprising one or more containers filled with one or more of the ingredients of the pharmaceutical compositions of the invention. Optionally associated with such container(s) can be a notice in the form prescribed by a governmental agency regulating the manufacture, use or sale of pharmaceuticals or biological products, which notice reflects approval by the agency of manufacture, use of sale for human administration. The pack or kit can be labeled with information regarding mode of administration, sequence of drug administration (*e.g.*, separately, sequentially or concurrently), or the like. The pack or kit may also include means for reminding the patient to take the therapy. The pack or kit can be a single unit dosage of the combination therapy or it can be a plurality of unit dosages. In particular, the agents can be separated, mixed together in any combination, present in a single vial or tablet. Agents assembled in a blister pack or other dispensing means is preferred. For the purpose of this invention, unit dosage is intended to mean a dosage that is dependent on the individual pharmacodynamics of each agent and administered in FDA approved dosages in standard time courses.

METHODS OF THERAPY

The present invention also pertains to methods of treatment (prophylactic and/or therapeutic) for a susceptibility to a disease or condition associated with a GPCR, using a GPCR therapeutic agent. A "GPCR therapeutic agent" is an agent that alters (*e.g.*, enhances or inhibits) GPCR polypeptide activity and/or GPCR gene expression, as described herein (*e.g.*, a GPCR agonist or antagonist). GPCR therapeutic agents can alter GPCR polypeptide activity or gene expression by a variety of means, such as, for example, by providing additional GPCR polypeptide

-45 -

or by upregulating the transcription or translation of the GPCR gene; by altering posttranslational processing of the GPCR polypeptide; by altering transcription of GPCR splicing variants; or by interfering with GPCR polypeptide activity (*e.g.*, by binding to a GPCR polypeptide), or by downregulating the transcription or translation of a GPCR gene. Representative GPCR therapeutic agents include the following:

nucleic acids or fragments or derivatives thereof described herein, particularly nucleotides encoding the polypeptides described herein and vectors comprising such nucleic acids (*e.g.*, a gene, cDNA, and/or mRNA, such as a nucleic acid encoding a GPCR polypeptide or active fragment or derivative thereof, or an oligonucleotide; for example, one of SEQ ID NOs:1-124 (odd numbers), or a complement thereof, or a nucleic acid encoding one of SEQ ID NOs:1-124 (even numbers), or fragments or derivatives thereof);

polypeptides described herein (*e.g.*, one or more of SEQ ID NOs:1-124 (even numbers), and/or other splicing variants encoded by a GPCR, or fragments or derivatives thereof);

other polypeptides (*e.g.*, G-proteins); GPCR binding agents; peptidomimetics; fusion proteins or prodrugs thereof; antibodies (*e.g.*, an antibody to a mutant GPCR polypeptide, or an antibody to a non-mutant GPCR polypeptide, or an antibody to a particular splicing variant encoded by a GPCR, as described above); ribozymes; other small molecules; and

other agents that alter (*e.g.*, enhance or inhibit) GPCR gene expression or polypeptide activity, or that regulate transcription of GPCR splicing variants (*e.g.*, agents that affect which splicing variants are expressed, or that affect the amount of each splicing variant that is expressed).

More than one GPCR therapeutic agent can be used concurrently, if desired.

A GPCR therapeutic agent that is a nucleic acid is used in the treatment of a susceptibility to a disease or condition associated with a GPCR. The term, "treatment" as used herein, refers not only to ameliorating symptoms associated with the disease, but also preventing or delaying the onset of the disease, and also lessening the severity or frequency of symptoms of the disease. The therapy is designed to alter (*e.g.*, inhibit or enhance), replace or supplement activity of a GPCR polypeptide in an individual. For example, a GPCR therapeutic agent can be administered in order to upregulate or increase the expression or availability of the GPCR gene or of specific splicing variants of GPCR, or, conversely, to downregulate or decrease the expression or availability of the GPCR gene or specific splicing variants of the GPCR. Upregulation or increasing expression or availability of a native GPCR gene or of a particular splicing variant could interfere

-46 -

with or compensate for the expression or activity of a defective gene or another splicing variant; downregulation or decreasing expression or availability of a native GPCR gene or of a particular splicing variant could minimize the expression or activity of a defective gene or the particular splicing variant and thereby minimize the impact of the defective gene or the particular splicing variant.

The GPCR therapeutic agent(s) are administered in a therapeutically effective amount (*i.e.*, an amount that is sufficient to treat the disease, such as by ameliorating symptoms associated with the disease, preventing or delaying the onset of the disease, and/or also lessening the severity or frequency of symptoms of the disease). The amount which will be therapeutically effective in the treatment of a particular individual's disorder or condition will depend on the symptoms and severity of the disease, and can be determined by standard clinical techniques. In addition, *in vitro* or *in vivo* assays may optionally be employed to help identify optimal dosage ranges. The precise dose to be employed in the formulation will also depend on the route of administration, and the seriousness of the disease or disorder, and should be decided according to the judgment of a practitioner and each patient's circumstances. Effective doses may be extrapolated from dose-response curves derived from *in vitro* or animal model test systems.

In one embodiment, a nucleic acid of the invention (*e.g.*, a nucleic acid encoding a GPCR polypeptide, such as one of SEQ ID NOs:1-124 (odd numbers), or a complement thereof; or another nucleic acid that encodes a GPCR polypeptide or a splicing variant, derivative or fragment thereof, such as a nucleic acid encoding one of SEQ ID NOs:1-124 (even numbers)) can be used, either alone or in a pharmaceutical composition as described above. For example, a GPCR or a cDNA encoding a GPCR polypeptide, either by itself or included within a vector, can be introduced into cells (either *in vitro* or *in vivo*) such that the cells produce native GPCR polypeptide. If necessary, cells that have been transformed with the gene or cDNA or a vector comprising the gene or cDNA can be introduced (or re-introduced) into an individual affected with the disease. Thus, cells which, in nature, lack native GPCR expression and activity, or have mutant GPCR expression and activity, or have expression of a disease-associated GPCR splicing variant, can be engineered to express the GPCR polypeptide or an active fragment of the GPCR polypeptide (or a different variant of the GPCR polypeptide). In a preferred embodiment, nucleic acid encoding a GPCR polypeptide, or an active fragment or derivative thereof, can be introduced into an expression vector, such as a viral vector, and the vector can be introduced into appropriate cells in an animal. Other gene transfer systems, including viral and nonviral transfer systems, can be used. Alternatively, nonviral gene transfer methods, such as calcium phosphate

coprecipitation, mechanical techniques (e.g., microinjection); membrane fusion-mediated transfer via liposomes; or direct DNA uptake, can also be used.

Alternatively, in another embodiment of the invention, a nucleic acid of the invention; a nucleic acid complementary to a nucleic acid of the invention; or a
5 portion of such a nucleic acid (e.g., an oligonucleotide as described below); can be used in "antisense" therapy, in which a nucleic acid (e.g., an oligonucleotide) which specifically hybridizes to the mRNA and/or genomic DNA of a GPCR is administered or generated *in situ*. The antisense nucleic acid that specifically hybridizes to the mRNA and/or DNA inhibits expression of the GPCR polypeptide,
10 e.g., by inhibiting translation and/or transcription. Binding of the antisense nucleic acid can be by conventional base pair complementarity, or, for example, in the case of binding to DNA duplexes, through specific interaction in the major groove of the double helix.

An antisense construct of the present invention can be delivered, for example,
15 as an expression plasmid as described above. When the plasmid is transcribed in the cell, it produces RNA that is complementary to a portion of the mRNA and/or DNA which encodes the GPCR polypeptide. Alternatively, the antisense construct can be an oligonucleotide probe that is generated *ex vivo* and introduced into cells; it then inhibits expression by hybridizing with the mRNA and/or genomic DNA of the
20 GPCR. In one embodiment, the oligonucleotide probes are modified oligonucleotides that are resistant to endogenous nucleases, e.g. exonucleases and/or endonucleases, thereby rendering them stable *in vivo*. Exemplary nucleic acid molecules for use as antisense oligonucleotides are phosphoramidate, phosphothioate and methylphosphonate analogs of DNA (see also U.S. 5,176,996;
25 5,264,564; and 5,256,775). Additionally, general approaches to constructing oligomers useful in antisense therapy are also described, for example, by Van der Krol *et al.*, (*Biotechniques* 6:958-976 (1988)); and Stein *et al.* (*Cancer Res.* 48:2659-2668 (1988)). With respect to antisense DNA, oligodeoxyribonucleotides derived from the translation initiation site are preferred.

30 To perform antisense therapy, oligonucleotides (mRNA, cDNA or DNA) are designed that are complementary to mRNA encoding the GPCR. The antisense oligonucleotides bind to GPCR mRNA transcripts and prevent translation. Absolute complementarity, although preferred, is not required. A sequence "complementary" to a portion of an RNA, as referred to herein, indicates that a sequence has sufficient
35 complementarity to be able to hybridize with the RNA, forming a stable duplex; in the case of double-stranded antisense nucleic acids, a single strand of the duplex DNA may thus be tested, or triplex formation may be assayed. The ability to hybridize will depend on both the degree of complementarity and the length of the

antisense nucleic acid, as described in detail above. Generally, the longer the hybridizing nucleic acid, the more base mismatches with an RNA it may contain and still form a stable duplex (or triplex, as the case may be). One skilled in the art can ascertain a tolerable degree of mismatch by use of standard procedures.

5 The oligonucleotides used in antisense therapy can be DNA, RNA, or chimeric mixtures or derivatives or modified versions thereof, single-stranded or double-stranded. The oligonucleotides can be modified at the base moiety, sugar moiety, or phosphate backbone, for example, to improve stability of the molecule, hybridization, etc. The oligonucleotides can include other appended groups such as
10 peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, *Proc. Natl. Acad. Sci. USA* 86:6553-6556 (1989); Lemaitre *et al.*, *Proc. Natl. Acad. Sci. USA* 84:648-652 (1987); PCT International Publication No. WO 88/09810) or the blood-brain barrier (see, *e.g.*, PCT International Publication No. WO 89/10134), or hybridization-
15 triggered cleavage agents (see, *e.g.*, Krol *et al.*, *Bio/Techniques* 6:958-976 (1988)) or intercalating agents. (See *e.g.*, Zon, *Pharm. Res.* 5: 539-549 (1988)). To this end, the oligonucleotide may be conjugated to another molecule (*e.g.*, a peptide, hybridization triggered cross-linking agent, transport agent, hybridization-triggered cleavage agent).

20 The antisense molecules are delivered to cells that express GPCR *in vivo*. A number of methods can be used for delivering antisense DNA or RNA to cells; *e.g.*, antisense molecules can be injected directly into the tissue site, or modified antisense molecules, designed to target the desired cells (*e.g.*, antisense linked to peptides or antibodies that specifically bind receptors or antigens expressed on the
25 target cell surface) can be administered systemically. Alternatively, in a preferred embodiment, a recombinant DNA construct is utilized in which the antisense oligonucleotide is placed under the control of a strong promoter (*e.g.*, pol III or pol II). The use of such a construct to transfect target cells in the patient results in the transcription of sufficient amounts of single stranded RNAs that will form
30 complementary base pairs with the endogenous GPCR transcripts and thereby prevent translation of the GPCR mRNA. For example, a vector can be introduced *in vivo* such that it is taken up in a cell and directs the transcription of an antisense RNA. Such a vector can remain episomal or become chromosomally integrated, as long as it can be transcribed to produce the desired antisense RNA. Such vectors
35 can be constructed by recombinant DNA technology methods standard in the art and described above. For example, a plasmid, cosmid, YAC or viral vector can be used to prepare the recombinant DNA construct that can be introduced directly into the tissue site. Alternatively, viral vectors can be used which selectively infect the

desired tissue, in which case administration may be accomplished by another route (e.g., systemically).

Endogenous GPCR expression can be reduced by inactivating or "knocking out" GPCR or its promoter using targeted homologous recombination (e.g., see Smithies *et al.*, *Nature* 317:230-234 (1985); Thomas & Capecchi, *Cell* 51:503-512 (1987); Thompson *et al.*, *Cell* 5:313-321 (1989)). For example, a mutant, non-functional GPCR (or a completely unrelated DNA sequence) flanked by DNA homologous to the endogenous GPCR (either the coding regions or regulatory regions of GPCR) can be used, with or without a selectable marker and/or a negative selectable marker, to transfect cells that express the GPCR *in vivo*. Insertion of the DNA construct, via targeted homologous recombination, results in inactivation of the GPCR. The recombinant DNA constructs can be directly administered or targeted to the required site *in vivo* using appropriate vectors, as described above. Alternatively, expression of non-mutant GPCRs can be increased using a similar method: targeted homologous recombination can be used to insert a DNA construct comprising a non-mutant, functional GPCR, e.g., a gene having one of SEQ ID NOs:1-124 (odd numbers), or the complement thereof, or a portion thereof, in place of a mutant GPCR in the cell, as described above. In another embodiment, targeted homologous recombination can be used to insert a DNA construct comprising a nucleic acid that encodes a GPCR polypeptide variant that differs from that present in the cell.

Alternatively, endogenous GPCR expression can be reduced by targeting deoxyribonucleotide sequences complementary to the regulatory region of a GPCR (i.e., the GPCR promoter and/or enhancers) to form triple helical structures that prevent transcription of the GPCR in target cells in the body. (See generally, Helene, C., *Anticancer Drug Des.* 6(6): 569-84 (1991); Helene, C., *et al.*, *Ann. N.Y. Acad. Sci.* 660:27-36 (1992); and Maher, L. J., *Bioassays* 14(12):807-15 (1992)). Likewise, the antisense constructs described herein, by antagonizing the normal biological activity of one of the GPCR proteins, can be used in the manipulation of tissue, e.g., tissue differentiation, both *in vivo* and *for ex vivo* tissue cultures. Furthermore, the anti-sense techniques (e.g., microinjection of antisense molecules, or transfection with plasmids whose transcripts are anti-sense with regard to a GPCR mRNA or gene sequence) can be used to investigate the role of one or GPCR in developmental events, as well as the normal cellular function of the GPCRs in adult tissue. Such techniques can be utilized in cell culture, but can also be used in the creation of transgenic animals.

In yet another embodiment of the invention, other GPCR therapeutic agents as described herein can also be used in the treatment or prevention of a susceptibility to

-50 -

a disease or condition associated with a GPCR. The therapeutic agents can be delivered in a composition, as described above, or by themselves. They can be administered systemically, or can be targeted to a particular tissue. The therapeutic agents can be produced by a variety of means, including chemical synthesis;
5 recombinant production; *in vivo* production (*e.g.*, a transgenic animal, such as U.S. Pat. No. 4,873,316 to Meade *et al.*), for example, and can be isolated using standard means such as those described herein.

A combination of any of the above methods of treatment (*e.g.*, administration of non-mutant GPCR polypeptide in conjunction with antisense therapy targeting
10 mutant GPCR mRNA; administration of a first splicing variant encoded by a GPCR in conjunction with antisense therapy targeting a second splicing encoded by a GPCR), can also be used.

The teachings of all publications cited herein are incorporated herein by
15 reference in their entirety.

While this invention has been particularly shown and described with references to preferred embodiments thereof, it will be understood by those skilled in the art that various changes in form and details may be made therein without departing from the scope of the invention encompassed by the appended claims.

MIQTISNVSEA VVQPIASQMPDGDNTDFRYFIYAVTYTVILVPGLIGNILALWV
FYGYMKETKRAVIFMINLAIALDLLQVLSPLRIFYYLNHDPFGPGLCMFCFYLYKYV
NMYASIFYLVCISVRRFWFLMYPFRFHDCKQKYDLYISAGWLIICLACVLFPLLRTS
DDTSGNRTKCFVDLPTRNVNLAQSVMMTIGELIGFVTPLLIVLYCTWKTVLSLQDK
YPMAQDLGEKQKALKMILTCAGVFLICFAPYHFSFPLDFLVKSNEIKSCLARRVILIFH
SVALCLASLNSCLDPVTTYFSTNEFKKSFLEQFRVIASQTQEDHSSAEERISELEDRLLEN
IOSEETKEKRIKNE (SEO ID NO: 2)

MOOSE00638 ctg16465 1516512..1517438, 1589966..1590028

35
40
45

aaaagcgtcctgctctacacgctctcttcatttaccatttcatcttgcacatggcgcgatgattgccaactcgtggtggtctgggt
gaaatccaggccaagaccacaggctatgacacgcactgctacatctgaacctggccattgccgacctgtgggtgtctcaccatcc
cagtctgggtggtcagctctgtgcagcacaaccagtgcccatgggcgagctcacgtgcaagtacacacctcattcttccatcaa
cctcttcggcagcattttcttctcagctgatgagcgtggaccgtacctctccatcacctacttaccacacccccagcagcaggaa
gaagatggtacgcgctgtcgtcgtcctctgggtgtggtgtggtcttctgctgtctctgctgacctactacctgaagaccgtcac
gtctgctccaacaatgagacctactgccggctcttctacccgagcacagcatcaaggagtggctgacggcatggagctggtctcc
gttgtcttgggtcttgcggttcccttccattatcgctgtcttacttctgctgtggcagagccatctcggcgtccagtgcaggagaa
gcacagcagccggaagatcatcttctctacgtgtgtggtcttcttctgtctgctgacctaccagtggtgggtgtctgtggacatct
ctccatctgcactacatcccttccacctgccggctggagcacgcccttccagccctgcatgtcacacagtgcctgtcgtgtgtgca
ctgctgcgtcaacctgtcctctacagcttcatcaatcgcaactacaggtacgaagctgatgaaggccttcatcttcaagtactcggcaa
aacagggctcaccaagctcatcgatgcctccagagcacacacgcgcgatgcacacacacacatgcacacatgcacacacacatac
attcttcttct (SEQ ID NO: 3)

IPLKMHYLPVTYGIIFLVGFPGNAVVISITYFKMRPWKSSSTIMLNLACTDLLYL
TSLPFLIHYYASGENWIFGDFMCKFIRFSFHENLYSSILFLTCTFSIERYCVIIHPMSCFSIH

gtcgccttgaaaagtactaccttccatttttattgggattgagctcgtgtgggagtccttggaaataccattgtgttacggc
tacaatctctctcgaagaactggaacagcagtaataattatctctttaaaccctctgtctctgactagctttctgtgcaccctcccatgtg
20 ataaggaggtatgccaatggaactggatataatggagacgtgctctgcataagcaaccgatattgtctcatgccaacctctataccagc
attctcttctcactttatcagcatagatcgatacttgataaataagtatccttccgagaacacctctgcaaaaaagaagagtttgctatttta
atctcttggccatttgggttttagtaaccttagagttactaccatacttccccttataaatcctgttataactgacaatggcaccacctgtaa
tgatttgcaggtctggagaccccaactacaacctattacagcatgtgtctaacactgttggggcttattctctcttttggatgtgttt
ctttattacaagattgctctcttctaagcagaggaataggcaggttgctactgctctgccccttgaaaagcctctcaacttggctcatcat
25 ggagtggtaatctctctgtcttttacacctatcacgtatcggaatgtgaggatcgcttcacgcctggggagttggaa gcagtat
cagtgactcaggctgcatcaactcctttacattgtgacacggccttggccttctgaacagtgatcaaacctgtctctatctttctttg
ggagatcacttcaggacatgtgtgaatcaactgagacacaactcaaatcccttatcatccttagcagatgggctcatgaactccta
ctttcattcagagaaaatgattctccttctaccctcctcaaatgggtgcgattacagaagtgcaccaccgcag (SEQ ID NO:
11)

[illegible]

-54-

MOOSE00772 ctg78 1060263..1060374, 1105772..1106011, 1106507..1107105

SLAHGIIRSTVLVIFLAASFVGNIVLALVLQRKPQLLQVTNRIFIFNLLVTDLLQI
SLVAPWVWVATSVPLFWPLNSHFCTALVSLTHLFAFASVNTIVVSVDRYLSIIHPLSY
PSKMTQRRGYLLLYGTWIVAILQSTPPLYGWGQAAFDERNALCSMIWGASPSYTLS
5 VVSFIVIPLIVMIACYSVVFCAARRQHALLCYQCKAAKVIFIIFSYVLSLGPYCFLAVL
AVWVDVETQVPQWVITIIWLFLLQCCIHPYVYGYMHKTIKKEIQDMLKKQLNQSS
SDSGSSSSSEDERPMSHVKNGEVGRRRRH (SEQ ID NO: 16)

agcctggccacggcatcatccgctcaaccgtgctggtatcttctcgcgcctctttcgtcggcaacatagtgctggcgct
agtgttgacggcaagccgcagctgctgcaggtgaccaaccgtttatcttaacctctcgtcaccgacctgctgcagattc
10 gctcgtggccccctgggtggtggccacctgtgctctctcttctggccctcaacagccactctgcacggccctggttagcctcacc
acctgttcgcttcgccagcgtcaacaccattgtcgtggtgcatggtgctactgtccatcatccacctctcttaccgctcaa
gatgaccacagcgccgcggttacctgctccttatggcacctgattgtggccatcctgcagagcactctccactctacggctggggc
caggctgcctttgatgagcgaatgctctctgctccatgatctggggggccagccccagctacactattctcagcgtggtgctctcatc
gtcattccactgattgtcatgattgctgctactccgtggtgtctgtgcagccggaggcagcatgctctgctgtgctaccagtgcgaag
15 ctgctaaagtgtatctcatcatcttctctatgtgctatccctggggccctactgcttttagcagctcctggccgtggtggatgctga
aaccagggtacccagtggtgatcaccataatcatctggcttttctctcagtgctgcatccacctatgtctatggtacatgcac
aagaccattaagaaggaatccaggacatgctgaagaacaactaaaccagcagcttcatctgactctggtcctcctcctctcaga
agatgaacgacccatgagatcccatgtgaagaatggtgaggtggcaggcgccggagacat (SEQ ID NO: 15)

20 MOOSE00775 ctg15540 14488015..14488239, 14488744..14488768,
14488985..14489082, 14491445..14491621, 14495389..14495435, 14499020..14499178,
14539721..14539940

PGRAKMALVLTGVLIFALALFGNALVFYVVTRSKTMRTVTNIFICSLALSDML
ITLFCIPVTMLQNISDNWLGGAFICKMVPFVQSTAVVTEILTMTCIAVERHQGLVHPF
25 KMKWQYTNRRRAFTMLGVVWLVAIVVGSMPMWHIKYDFLYEKEHICCLEEWTSPVHQ
KIYTTFILVILFLPLMVMLILYSKIGYELWIKRKKRAVIMMVTVVALFAVCWAPFH
VVHMMIEYSEFLSHVTPSMIFAIVQIIGFSNSICNPIVYAFMNENFKKNVLSAVCYCIV
NKTFSPAQRHGNSGITMMRKKAKFSLRENPEET (SEQ ID NO: 18)

ccgggacgcgccaagatggccctcgtgctcaccggcgtgctcatattcgcctggcgctctttggcaatgctctggtgtttta
30 cgtggtgacccgcagcaagaccatgcgcaccgtcaccaacatcttatatgctccctggcgctcagtgacatgctcaccctctttg
catcccgctcaccatgctccagaacattccgacaactggctggggggtgcttcatttgcaagatggtgccattgtccagctaccgct
gttgtagacagaatcctcactatgacctgcattgctgtggaaggcaccagggaactgtgcaccttttaaatgaatggcgaatacacc
aaccgaagggtttcacaatgctaggtgtggtcgtggtggcagctcgttaggatcaccatgtggcacatcaaatgacttcta
tatgaaaaggaacacatctgctgcttagaagagtgaccagccctgtgcaccagaagatctacacccttcatcctgtcatcctctc
35 ctctgcctcttatggtgatgcttattctgtacagtaaaattggtatgaacttggataaagaaagaaagaaagagctgtcattatgatg
gtgacagtggtggctctcttctgtgtgctgggcaccattccatgttgcctatgatgattgaatacagtgaattcctctccatgttactc
cttctatgattttgtatcgtgcaaatatttgatttccaactccatctgtaatccattgtctatgcattatgaatgaaactcaaaaaaa
tgtttgtctgcagttgttattgcatagtaataaaaccttctcaccagacaaaggcatggaaattcaggaattacaatgatcggaaga
aagcaaaatttccctcagagagaatccagtgaggaaacc (SEQ ID NO: 17)

40 MOOSE00779 ctg16537 5292218..5292340, 5438500..5438551, 5450751..5450956,
5450981..5451284, 5462460..5462773

FFAAKIVIGIALAGIMLVCGIGNVFIAALTRYKKLRNLTNLLIANLAISDFLVA
IICCPFEMDYVVRQLSWEHGHVLCASVNYLRTVSLYVSTNALLAIAIDRYLAIVHPL
45 KPRMNYQTASFLIALVWMVSILIAIPSAYFATETVLFIVKSQEKIFCGQIWPVDQQLY
YKSYFLFIFGVEFVGPVVTMTLCYARISRELWFKAIRKRLRCRRKTVLVLMCILTAYV
LCWAPFYGFTTVRDFFTVVFVEKHYLTAFYVVECIAMSNMINTVPFLYFWLRWGF
TIFLRLTSLQKKKKRRRRKRKRTERDSNRYLYTHVPSSIIHSTPAW (SEQ ID NO: 20)

ttcttcgacgccaagatgctcattggcattgcactggcaggcatcatgctggtcgtcgccatcggttaacttgcctttatcgtg

-55-

ccccaccgctataagaagttgcgcaacctcaccaatctgctcattgccaacctggccatctccgacttctggtggccatcatctgct
gccccttcgagatggactactacgttggtacggcagctctcctgggagcatggccacgtgctctgtgctccgtcaactacctgcgcac
cgtctccctctacgtctccaccaatgccttgctggccattgccattgacagatatctgccatcgttcaccccttgaaaccacggatgaatt
atcaaacggcctcctcctgctgccttggtctggatggtgtcattctcattgccatccatcggcttactttgcaacagaacggctctc
5 ttattgtcaagagccaggagaagatcttctgtggccagatctggcctgtggatcagcagctctactacaagcttacttctcttcatcttt
ggtgtcagagttcgtggccctgtggtcaccatgacctgtgctatgccaggatctccgggagctctggtcaaggcaattcgcaagc
ggctgcgtgccgaggaagacggctcgtggtcctatgtgcattctacggcctatgtgctgtgctgggcaccccttctacggttcacc
atcgttctgacttctccccactgtgtcgtgaaggaaaagcactacctcactgccttctacgtggtcgaagtcatcgccatgagcaaca
gcatgatcaacaccgtccattttgtattttggttgagatggggttcactatattctcaggctgactctgtctcaaaaaaaaaaaaaa
10 gaagaagaagaaaaaagaactgaagcagagactcaacagatattgtacactcatgttcttagcagcattattcacagcact
ccagc ctgg (SEQ ID NO: 19)

MOOSE00804 ctg30162 16180..16299, 37790..38066, 71494..71629, 82561..82975
SWELQMFFFMVFSLLYVATMVGNSLIVITVIVDPHLHSPMYFLLTNLSIDMSL
15 ASFATPKMITDYL TGHKTISFDGCLTQIFFLHLFTGTEILLMAMSFDRYIAICKPLHYA
SVISPQVCVALVVASWIMGVMHSMTPFIEYLLIRVSFLHCLSLLTLLKNSWLQVRGF
VFGFCILFYCLSFTFSLLVSSYIILVTWVWKSSAAMAKAFSTLASHIAVVILFFGPCIFI
YVWPFTISPLDKFLAIFYTVFTPVLNPIIYTLRNRDMKAAVRKIRTSISHFRQRTDHL
KNSAKKTNTKRTLHDVLDPSHRT (SEQ ID NO: 22)

20 tcttggaactacagatgttttcttatggtgtttcattgctttatgtggcaacaatggtgggtaacagcctcatagtcacaca
gttatagtggaccctcacctacactctctatgtatttctgcttaccatcttcaatcattgatgtctcttcttcccccacaaag
atgattacagattacctaacaggtcacaaaaccatctctttgatggctgccttaccagatattcttccaccccttctactggaactgaga
tcatcttactcatggccatgtcctttgataggtatattgcaatatgcaagccctgcactatgcttctgctcattagtcacccagggtgtgtgtgt
ctcgtggtggcttctcgattatgggagttatgcattcaatgacaccatttattgaatatttattgattagagtgctcttctccattgcttctt
25 tgttgacttactaaagaacagctggttacaggtagtggtgtttgtttgggtctgtattctgttctattgtctatcttctacttctctcttgg
tcagctctacatcattattctgttacagtttggtcctcaagcttcagctgcaatggcaaggcatttctacgctggttcccatattgcagt
agtaattatttcttggaccttgcatcttctctatgtgtggcccttaccatctctcttggataaattcttggcatattttactgtttcac
ccccgtcctaaacccattattatacactaaggaataggatagaaggctgccgtaaggaaaattaggactcaatactcacttctgg
caaaggacagatcatctagacaaaaattcagccaaaaaacaacaatacaaggcactctagatcatgtggacctaccagatagtc
30 acagaaca (SEQ ID NO: 21)

MOOSE00814 ctg15378 3973801..3973891, 3975545..3975625, 4023376..4023510,
4032595..4032652, 4060801..4060926, 4186201..4186358, 4227631..4227840,
4235835..4235929
35 SVVDTVILPSMIGIICSTGLVGNILIVFTIIRSRRKKTVPDIYICNLAVADLVHIVG
MPFLIHQWARGGEWVFGGPLCTIITSLDTCNQFACSAIMTVMSVDRYFALVQPFRLT
RWRTRYKTIRINLGLWAASFILALPVWVYSKVIKFDGVESCLSNLLIFSCKKYFISLIF
CIFFISISFISALIFITFLLLFLEKQQQKQKKHTSQVMHLLLSSTFLVSWIPRYFILFEAI
VNGSSLMIWLSVCLLLVYKNACDFCTIHYFDVKCVFRNRYRQLSKKKSHGFSVPTTQ
40 TESLSSTPTQHRKVVFGLARPLWAT (SEQ ID NO: 24)

agtggtgtagatacagtcactcctccctccatgattgggattatctgttcaacagggtggttggcaacatcctcattgtattcac
tataataagatccaggaaaaaacagtccttgacatctatactgcaacctggctgtggtgattggtccacatagttggaatgcctttc
ttattaccaatggggccggagggggagagtggtgtttggggggcctctctgcaccatcatcacatccctggatactgttaaccaattg
cctgtagtgccatcatgactgtaatgagtggtgacaggtagctttgccctcgtccaaccatttcgactgacacgttgagagaacaaggtaga
45 agaccatccggatcaatttggcccttgggcagcttcttattcctggcattgctgtctgggtctactcgaagggtcatcaaatttaagac
ggtgttgagagttgttgcataattgcttattcttcaagaaatatttatttcttgatctttgtatttttttatttcaatttatttctgtct
ctgatctttattacatttcttactattcttagaaaaacaacaacaacaaaaaaaaaacacacgtcacagggtcatgcatctcctactctgt
cttccacattccttgtaaggtaggtcctaggtattttattcttgaagcaattggaatgggagttcactcatgatttggctctctgtttgtct
gttattggtgtataagaatgctgtgattttgaccattcattattttagtgtaaatgtgtcttaggagaattacagacaattgtcaagaa

-56-

aaaaagccatggaagctttgtgccacaccccaacagaaagttatctccaccccaacacacaggaaagtggtgttttggttt
ggccagaccactatgggctact (SEQ ID NO: 23)

MOOSE00818 ctg15907 32727057..32727450, 32800163..32800610,
32874979..32875093

5 WPHLEVVLFVVILIFYLITLIGNLFIILSYLDSHLHTPMYFFLSNLSFLDLCYTT
SSIPQLLVNLWGPEKTISYAGCTVQLYFVLALGTAECVLLVMSYDRYAAVCRPLH
YTVLMHPRFCRLAAASWVTLHSSFTFWVPLCGHRLVDHFFCEVPALLRLSCVDTH
ANELTLMVMSSIFVLIPLILITAYGAIAARAVLSMQSTTGLQKVFTCGAHLMMVVSIF
10 FIPVMCMYLQPPSENSPDQGKFIALFYTVVTPSLNPLIYTLRNKHVKGAARKLLGACR
PMQSQPRTVRSSFFDRKATGCEPGSCVTPAAQTC (SEQ ID NO: 26)

tgccctcatctggaagtagttctttgtggttatcttgatcttctacttgataacactgataaggaaacctgttcatcatcctgt
catacctggactcccatctccacactcccatgtacttctcttcaaatctctcatttctggatctctgctacaccaccagctctatccctca
gttgctggtgaatctctggggcccgaaaagaccatctcttatgtggtgtacagtca
15 acttiactttgttctgcactgggaaccgcagagtgtgctactggtggtgatgctctatgatcggtatgcagctgtgttagaccttgca
ttactgtcctcatgcacccctgttctgccgctgtggtgctggttctgggtaacacttctccttacttctgggtaccccttg
tggacatcgctagtggatcacttctgtgaagttcagcacttctgcttctatcatgtgtgacacccatgcaaatgagctgacctcat
ggtcatgagctccattttgttctacacctctcattctgattctcactgctatggtgccattgccgggctgtactgagcatgcaatcaacc
actgggcttcagaaagtgttaggacatgtggagcccatctatggtgtatctctcttttctcattccagctatgtcatgtatctccagccac
20 catcagaaaattctcctgatcagggaagttcattgccctctttatactgtgtcacaccgagcttaactcttaactacactctcagaaa
caagcatgtaaaaggggcagcgaagagactattgggtgctgcccccatgcagagccagccagaactgtgaggtcaagtttctt
tgatagaaaggcaacaggtgtgagcctggctcctgtgtgaggactccggcagcacagactgt (SEQ ID NO: 25)

MOOSE00822 ctg14294 995965..996055, 1019834..1020641, 1219431..1219494

25 VRVVPRTVFFLFFFLFILVLVSNILTVIILSQLVARRQKSSYNYLLALAAADILV
LFFIVFVDFLLEDFILNMQMPQVPDKIEVLEFSSIHTSIWITVPLTIDRYIAVCHPLKYH
TVSYPARTRKVIVSVYITCFLTSIPYYWWPNWTEYISTSVHHVLIWIHCFTVYLVP
SIFFILNSIIVYKLRRKSNFRLRGYSTGKTTAILFTTTSIFATLWAPRIIMLYHLYGAPIQ
NRWL VHIMSDIANMLALLNTAINFFLYCFISKFRFTMAAATLKAFFKCQKQPVIQPF
30 KQISLSPHTHTHTHTHTHTHTSKDT (SEQ ID NO: 28)

gttcgtgctggtccccgcaccgtgtttttttgtttttttgtttttttgtttttgttttcaaatatcttgacagtgatcatcctctcc
cagctggtggcaagaagacagaagtcctctacaactatcttggcactcgtgctgctgacatcttggtcctcttttcatagtgtgt
ggacttctgttgaagatttcatctgaacatgcagatgctcaggtccccgacaagatcatagaagtgtggaattctcatccatccac
accctcatatggattactgtaccgttaaccattgacaggtatctgctgtctgccaccgctcaagtaccacacgggtcctacaccagccc
35 gcacccggaaagtcattgttaagtgtttacatcacctgcttctgaccagatccccattactggtggcccaacatctggactgaagacta
catcagcacctctgtgcatcacgtcctcatctggtaccactgcttcacccgtctacctggtgccctgctccatcttctcatcttgaactcaat
cattgtgtacaagtcaggaggagagcaatttctcctgctggtactccacggggaagaccaccgcatctgttcaccattacctc
catcttggcacactttgggccccgcacatcatgatttaccacctctatggggcggccatccagaaccgctggtggttacacatc
atgtccgacattgccaacatgtagcccttctgaacacagccatcaacttcttcttactgcttcacagcaagcgggtccgcaccatgg
40 cagccgccacgctcaaggctttctcaagtgcagagcaacctgtacaaattcaaccttcaagcagatatcttaagccaacacaca
cacacacacacacacacacacacacacacacacttctaaagacact (SEQ ID NO: 27)

MOOSE00826 ctg15968 677807..678430, 679388..679470, 683881..684142

45 MGPGEALLAGLLVMVLAVALLSNALVLLCCAYSaelRTRASGVLLVNLslG
HLLLAALDMPFTLLGVMRGRTPSAPGACQVIGFLDTFLASNAALSVAALSADQWLA
VGfPLRYAGRLRPryAGLLGCAWQSLAFSGAALGCSWLGYSSAFASCSLRLPPEP
ERPRFAAFTATLHAVGFVLPLAVLCLTSLQVHRVARRHCQRMdTRRRHRATRKIGIA
IATFLICFAPYVMTRLAELVPFVTVNAQWGILSKCLTYSKAVADPFTYSLRRPFRQV
LAGMVHRLlKRTPRPASTHDSSLDVAGMVHQLlKRTPRPASTHN (SEQ ID NO: 30)

15 LEGIKHWIFIPFFFMYMVAISGNCFILIIKTNPRLHTPMYYLLSLLALTDLGLC
VSTLPTTMGIFWFNSQSIYFGACQIQMFCSIHSFSMESSVLLMMSFDRFVAICHPLRYS
VIITGQQVVRAGLIVIFRGPVATIPIVLLLKAFPYCGSVVLSHSFCLHQEVIQLACTDIT
FNNLYGLMVVFTVMLDLVLIALSYGLILHTVAGLASQEEQRRAFQTCTAHLCAVL
VFFVPMMGSLVHRFGKHAPPAIHLMLANVYLFVPPMLNPPIYSIKTKEIHRAIKLLE
20 CRLSRQCQNQLEERVSVMEDEMNMKQEEKFREKRIKR (SEQ ID NO: 32)

ttggaaggcatcaaacactggattttcatcccttttctttatgtacatgggtgccatctcaggcaatgtttcattctgatcattatt
aagaccaaccctcgtctgcacacaccatgtactatctactatccttgcctgccctcactgacctggggctgtgtgtccacgttgccca
ccactatggggatcttctgtttaactccagagtatctactttggagcgtgtcaaatccagatgttctgcattccactcttttcttcatgga
gtcctcagtgtcctcatgatgtcctttgaccgccttgggccatctgccacctctgaggtattcggtcattatcactggccagcaagtgg
25 tcagagcaggcctaattgtcatctccggggacctgtggccactatccctattgtcctcctcctgaaggctttccctactgtggatctgtg
gtcctctcccactcatttgcctgcaccaggaagtatacagctggcctgcacagataccaccttcaataatctgtatggactgatgtgtg
tagttttcactgtgatgtcggacctgggtctcatcgcactgtcctatggactcatcctgcacacagtagcaggcctggcctcccaagagg
agcagcgccgtgccttcagacatgcaccgctcatctctgtgtgtgtagtattcttggcccatgatggggctgtccctgggtgcaccg
tttgggaagcatgcccaacctgtattcatcttcttattggccaatgtctaccttttggcctcccattgtaaccaatcatatatacagcatt
30 agaccaaggagatccaccgtgccattatcaaacctcctagaatgcagaagctcaggagccaatgcaatcaactggaagaaagggat
cagtgtatggaagatgaatgaatgaatgaagcaagaagagaagttagagaaaaaagaataaaaaaga (SEQ ID NO: 31)

35 HSTADLVLSVVMVAVFTVALCGNVLLIFLIYMDPHLHTPMYFFLSQLSLMDL
MLVCTNVPKMAANFLSGRKSSISFVGCGIQIGLFVCLVGSEGLLLGLMAYDRYVAISH
PLHYPILMNQVRVCLQITGSSWAFGIIDGLIQMVVVMNFPYCGLRKVNHFFCEMLSLL
KLACVIFACCVFMILLFPFSIIVASYAHILGTVLQMHSAQAWKKALATCSSHLTAFFFC
QLPYQILSHQVVCSEFYWVILGHRCDKSSLSSTVSLSFVAVLNPILYGSVARSFRRRAG
40 ALLVCRKKPQNSENFTFTPTSFLLSPYITHTHTHTHAHTHV (SEQ ID NO: 34)

45 cacagtgactgctgacctgtgctcttctccgtgggtatggcggcttcacagtggccctctgtgggaatgtcctctcatcttct
catctacatggacccctcaccttcacaccccatgtacttctctcagccagctctccctcatggacccatgttggtctgtaccaatgtgc
caaagatggcagccaacttctgtctggcagggaagtcacatctcttctgtggctgtggcatacaaatggcctcttctgtctgtgtggga
tctgaggggctctgtctgggactcatggcttatgaccgctatgtggccattagccacccttccactatcccctctcatgaatcagagg
gtctgtctccagattactgggagctcttgggcttgggataatcagatggcttgatccagatggtggtagtaatgaatttcccctactgtgg
cttgaggaaggtgaaccatttctctgtgagatgctatccttgttgaagctggcctgtgtgataattgcttctgtcttcatgcttcttccc
atttcccatcatctgtggcctctatgctcacattctagggactgtgtctgcgaatgcactctgtctcaggcctggaaaaaggccctggccac
ctgtctctccacctgacagcttttttttggcaactaccttaccaaatcttcccaicaagtgctgtgtcattttatgggtgatttgggg
catagatgtgacaaatctcatgtcaatcaagtcacagtgtcatttcttgggttctaataccaattctatatggcagcgtgcgccgctct

LCFLQTEQLITLWVLFVFTIVGNSVVLFSWRRKKKSRMTFFVTQLAITVGFI
LDLFLILFIMPLHFSLVYLFHYESSPDFWCLQSYFFCVLLYASTYVLVLSIDRYHAIV
YPMKFLQGEKQARVLIVIAWSLSFLFSIPTLIIFGKRTLNNGEVQCWALWPDDSYWTP
10 YMTIVAFLVYFIPLTISIMYGIVIRTTWIKSKTYETAKIKAIKYSIIILAFICWSPYFLF
DILDNFNLLPDTQERFYASVIIQNLPALNSAINPLIYYSVSQKNKRKRKRSSRRKKKE
KERRRRKKRRRRKKKEGRRGGEGRGKKEEERRKE (SEQ ID NO: 36)

25 MOOSE00846 ctg15944 960216..961037, 988991..989137

aacctggagctgtggaaaaatattttctgctgtgtttctgtcatgtatgtagccacagtgctggaaaaatcacttatgtggttaact
attatcacaaagtcagagctgtgaggtcacctatgtattttttcttaccttctgtcccttttggatgtcatgtttcatctgtcgttgccccaagg
35 tgaattgtagacacctctccaagagcactaccatctctcaaaggctgcctcaccagctgtttgtggagcatttcttgggtgtgtggg
gatcatctctcactgtgatggcctatgaccgtacgtggcctatctgaagccccgcactacacgatcatatgattccacgggtgtg
ctgcctaagtgtggaagggtgtgggtggggggaattatgcacgcaatgatacaacttctctcatgtatcaaataccttctgtgttccta
atatcatagatcaccttataatgtattgtttcagttgtgtacacttgctgtcacggacaccacatcctgggcctcttaagtaccctaacag
tgggatgatgtgtgtggccatcttcttaactaaattgcctctacacgggtacatctatgtcctcgaagtcttacagctctaaagggcggca
40 caaagccctctctacctgcagctcccacctcacgggtgtgtattgttctttgtccctgtattttctgtacatgaggcctgtgtgtcactcac
cccatagacaaggcaatggctgtgtcagactcaatcatcacacccatgttaaatcccttgatctatacactgaggaatgcagaggacata
agagagatactgaggctgatgtttcgtgccccctttgtccttattttattttttcagggtgtgtctcaaaatcctgagctcaggctgcc
ctcctcggcctcccaaagtctggagttacaggtgtgagccactgc (SEQ ID NO: 37)

45 MOOSE00855 ctg14333 2003002..2003122, 2024409..2025211
VHTAYLVLSSLAMFTCLCGMAGNSMVTWLLGFRMHRNPFCTIYILNLAAADLL
FLFSMASTLSLETQPLVNTTDKVHELMKRLMYFAYTVGLSLLTAISTQRCLSVLPFIW
FKCHRPRHLSAWVCGLLWTLCLLMNGLTSSFCSKFLKFNEIDRCFRVDMVQAALIMG
VLTPVMTLSSLTLFVWVRRSSQQWRROPTRLFVVVLASVLVFLICSLPLSIYWEVLY

WLSLPPEMQVLCFSLSRLSSSVSSSANPVYFLVGSRRSHRLPTRQGRCLTLSTRFREN
SITRTAPRGKSTPRIQSPSTRPHILQ (SEQ ID NO: 40)

gtgcacacggcctacctgggtgctgagctccctggccatgttcacctgctgtcggggatggcaggcaacagcatgggtgatc
tggctgctgggctttcgaatgcacaggaaccccttctgcatctatatcctcaacctggcggcagccgacctctcttcttcagcatgg
5 ctccacgctcagcctggaaacccagccctggtaataccactgacaaggctccacgagctgatgaagagactgatgtactttgcctac
acagtgggctgagcctgctgacggccatcagcaccagcgcgtgtctctgtcctctccctatctggttcaagtgtcaccggccag
gcacctgtcagcctgggtgtgtggcctgctgtggacactgtctcctgatgaacgggtgacctctccttctgcagcaagttctgaaat
tcaatgaagatcgggtgtcagggtggacatgggtcaggccgcccctcatctgggggtcttaacccagtgatgactgttcagcctg
acctctttgtctgggtgcggaggagctcccagcagtgccggcggcagcccacagcgtgttcgtgtggctggcctctgtcctgg
10 tgttctctatctgttccctgctcagcatctactggttgtgtctactggttgagcctgcggccgagatgcagggtcctgtgtcctgagct
tgtcacgctctcctgctcgaagcagcagcgaacccgctcatctacttctggtggcagccggaggagccacaggtgccc
ccagacaggggggtgctcactgtcaacccgattccgtgagaactctatcacgagaacagcaccagggggaaatccaccccc
aggatccaatcaccttccaccaggccacacatctacaa (SEQ ID NO: 39)

15 MOOSE00861 ctg16279 54051..54182, 115058..115808, 116858..116925
PCVAGVIPVITYSVLLGLGLPGDLLTAVALARLATRTRRPSYYYLLALTASDII
IQVVIVFAGFLLQGAVALARQVPQAVVRTANILEFAANHASVWIAILLTVDRYTALCH
PLHHRAASSPGRTRRAIAA VLSAALLTGIPFYWWLDMWRDTPRDLDEVLKW AHC
LTVYFIPCGVFLVTNSAIHRLRRRGRSGLQPRVGKSTAILLGITTLFTLLWAPRVFVM
20 LYHMYVAPVHRDWRVHLALDVANMVAMLHTAANFGLYCFVSKTFRATFCSCCPS
CSAMGRSQTATSSSRVQAVLLPQPPEELGLQARATT (SEQ ID NO: 42)

ccgtgtgtggctggcgtcatccctgtcatctactacagtgtcctgctgggcttgggctgctggtgacctcctgaccgcagt
ggccctggcgcgccttggccaccaggaaccaggaggccctctactactaccttctggcgcctcacagcctcggatacatcatccagggtg
gtcatcgtgttcgggcttctcctcctgcaggagcagtgctggcccgccagggtgccccaggctgtgtgtgcgcacggccaacatcctg
25 gaggttgtgccaaccacgcctcagctggatcgccatcctgtctacgggtgacctgacctgacctgtgccccctgcaccatcg
ggccgctcgtccccaggccggaccgcccggccatgtgtgtgtcctgagtgctgacctgtgacctgacctgtctactgtgtg
ctggacatgtggagagacaccgactcaccagaacactggacgagggtcctcaagtgggctcactgtctactgtctattcatccctgt
ggcgtgttctgtgtcaccaactggccatcatccaccggctacggaggggggagggtgggctgcagccccgggtgggcaaga
gcacagccatctcctggccatcaccacactgttaccctcctgtggcgccccgggtcttctgtcatgtctaccacatgtacgtggcc
30 cctgtccaccgggactggagggtccacctggccttggatgtggccaatatggtggccatgtccacacggcagccaacttggcctct
actgtcttgcagcaagactttccggccacttttgccttgttggccaagctgtagtgaatggggcgatctcagctcactgcaacctcc
tctcccggttcaagcagttctcctgcctcagcctcccaggagctgggactacaggcgcgtgccaccaca (SEQ ID NO:
41)

35 MOOSE00872 ctg18147 32565..32680, 45290..45647, 45666..46148
DPELKLIPFSLFLSMYLVTLGNLLILLAVIDSHLHTPMYFLFLNLSFTDICLTT
TTVPKILVNIQAQNSITYTGCLTQICLVLVFAGLESCFLAVMAYDRYVAICHPLRYT
VLMNVHFWGLLLSMFMSTMDALVQSLMVLQLSFCKNVEIPLFFCELACSDTLINN
ILIYFASSVFGAIPLSGIIFSYSQIVTSVLRMP SARGKYKAFSTCGCHLSVFSLFYGTAF
40 GVISSAVAESSRITAVASVMYTVVPQMMNPFYSLRNKEMKKALRLKIECLTLCFV
LFFSLRWLSLSLSPRLECN GTTSAHCNFRRLRV (SEQ ID NO: 44)

gaccagaactgaagtaatcccttcagcctgttctgtccatgtacctggcaccatcctggggaacctgtcattctcctg
gctgtcatctctgactcccacccacacccccatgtacttctctttaaactctcttactgacatctgttaaccacaaccacagtc
aaagatcctagtgaacatccaagctcagaatcagagtacttacacaggctgctcaccagatctgtctgtcttgggttggct
45 tggaaagttgcttcttcagctcatggctacgaccgctatgtggccattggccaccactgaggtacacagtcctcatgaatgtccattc
tggggctgtgattctctctccatgtcatgacactatggatgacctgttcagagtctgatgtgattgcagctgtccttctgaaaaac
gttgaatccctttgttctgtgaactgcctgttctgacacctcatcaacaacatctcatattttgcaagtagtgatttgggtgaatt
cctctctctggaataattttcttattctcaaatgtcacctctgtctgagaatgccatcagcaaggaggaaagtataaagcgtttccacct
gtggctgtcaccctctgtttttctgttctatgggacagcttttgggtgtacattgtctgtgtgctgagcttcccgaattactgtgt

-60-

ggcttcagtgatgtactgtggccctcaaatgatgaacccctcatctacagcctgagaaataaggagatgaagaaagcttgagga
aacttattgaatgcctgactctttgtttgtttttctctgagatggagcttctctgtctcccaggctggagtgcaatggcacgacctc
ggctcactgcaactccgctccgggtt (SEQ ID NO: 43)

5 MOOSE00880 ctg15944 3962338..3962443, 4014447..4014532, 4029024..4029117,
4033619..4034316

ATEFQVLLFLLFLLLYLMILCGNTAIWVVCVTHSLRTPMYFFLSNLSFLELCY
TTVVVPLMLSNILGAQKPISLAGCGAQMFFVTLGSTDCFLLAJMA YDRYVAICHPL
HYTLIMTRELCTQMLGGALGLALFPSLQLTALIFTLPFCGHHQEINHFLCDVPPVRL
10 ACADIRVHQA VLYVVSILVLTIPFLLCVSYVFITCAILSIRSAEGRRRRAFSTCSFHLTV
VLLHFPPLQVHHFFKNSAPFKTLLIPFIQPFQYVNVIPMLNPLIYSLRNKEVKEALRKIL
NRAKTQVTQTHRETGSHHRQTDGCRPQRTGRYLHRQTE (SEQ ID NO: 46)

ggcactgaattccaggttctctctctctctctctctctacttgatgatcctctgtggcaacacagccatcatctgggtg
gtgtgcacacacagcaccctccgcaccccgatgatttctctgtccaacctgtcttctggaactctgtacaccaccgtggtgtagtac
15 cctgatgctttcaacattttggggggccagaagccatttctgttggtggtggtggggcccaatgttcttctgtcacccctcggcagc
acggactgttctcttggcgatcatggcctatgaccgctatgtggctatctgccaccgctgcactacacccctcatcatgaccgcgag
ctgtgcacgcagatgtgggtggggccctgggctggccctcttccctcctgcagctcaccgccttaattcttaccctgcccttttgc
ggccaccaccaggaaatcaaccacttctctgcgatgtgctcctccgctcctgcgctggcctgcgctgacatccgcgtgcaccaggt
gtcctctatgtctgagcatcctctgtgtgaccatccctcctgtcctcctcctgtctcctacgtgttcatcactgtgccatcctgagcatc
20 cgttctgccgagggccgccggccttctccacctgtccttccacctcaccgtggtcctgtgcacttct
ctccctgcaggttcaccacttcttaaaattctgtccttctcaaaacctgtccttccctcctcagccatttgggtatgtgaatgtcatc
cccatgtgaatccctcatctacagcctgaggaacaaggagtgaggagccctgagaaaaattctcaatagagccaagacacag
gtgacacagacacatagagagactggtgtagcacatacacaggcagacagatgggtgcaggcctaggcagacaggcagatatctgc
atagacagacagaa (SEQ ID NO: 45)

25 MOOSE00882 ctg15944 1984917..1985024, 2124131..2124428, 2127756..2127837,
2273894..2274344

DPQMEIIFVFLIVYL VNVVGNIGMILITTDQLHTPMYFFLCNLSFVDLGY
SAIAPRMLADFLTNHKVISFSSCATQFAFFVGFVDAECYVLAAMAYGRFVAICRPLH
30 YSTFMSKQVCLALMLGSLAGLVSLVAHTTLTFSLSYCGCCYILKERAGHRKLNYSI
FFILFSLFFSLIILISYIFILAILRMRSAESRRKAFSTCGSHLVAVTVFYGTLCMYVRP
PTDRSVEQSKVIAVFYTFVSPMLNPITYSLRNKDVKQAFWKLIRRNKSMACGRVGKT
KCSERPEKDPSCSDSEIVAAVVKE (SEQ ID NO: 48)

gaccctcagatggagatcatcttctctgtgtcttctctcatgtttacctggtaatgtagtgagggaatattgggtatgattatcctg
35 attacaacagacactcagcttcacacacccatgtatttttctctgtcaacctctccttgttgacctgggctactctcagccattgcccc
aggatgctggctgacttcttaacaaatcaaaagtatctcttctccagctgtgccaccagtttgctttttgtagggtttgtggtgctg
agtgtatgtcctggcagccatggcctatggctgtttgtggcatttgcgaccctccactatgacacctcatgtccaagcaggctgtg
ttggctctcatgtgggcttacctggctgtgtgtagttagttagccacactaccctcacctcagcctgattactgtgtgtgtgtg
atatatttaaggaaagagcaggacatagaaaattaaattatagatctttttatccttttttcttttttctccctcatataatctcatctc
40 tacaattcatttctattgccatcctgaggatgcgttctgtgaaagtaggcgcaaagcgttctccacctgcgggtccacctgtggca
gtgactgtgtttatggaacctgttctgcatgtacgttagacctccacggacaggtcagtggaacagtcctcaagtcattgtgtttcta
cattttgtaagccctatgtgaaccccatcatctatgttaggaacaaggatgtgaaacaagcttttggaaactgatcagaagaac
aaaagcatggcctgtggcagggtgggaaagacaaaattgtcagagaggccagagaaagacccatccatttgcagcgacagtgaaat
tgtgtgtgtgtgtgaaggaa (SEQ ID NO: 47)

45 MOOSE00886 ctg15296 1927198..1927675, 1927700..1928051, 1949720..1949831
NSEVQRVLFFVFLIYVVTVCGNMLIVVTITSSPTLASPVYFFLANLSFIDTFYS
SSMAPKLIADSLYEGRTISYECCMAQLFGAHLGGVEILLTVMA YDRYVAICKPLHN
TTIMTRHLCAMLVGVAWLGGFLHSLVQLLLVLWLPFCGPNVINHFAFACTNTYVIG

15 MOOSE00899 ctg17659 60714..60781, 124639..124720, 298068..298255,
298292..298925

[illegible]

40 SQDWRITIPALLVAVCLVGVGNLCVIGILLHNAWKGPMSIHSLILNLSLAD
LSLLLFSAPIRATAYSKSVWDLGWVCKSSDWFHTCMAAKSLTIVVAVKVCIFYA
SDPAKQVSIHNYTTWSVLVAIWTVASLLPLPEWFFSTIRHHEGVEMCLVDVPAVAEE
FMSMFGKLYPLLAFLPLFFASFYFWRAYDQCKKRGTKTQNLNRNQIRSKQVTVMML
SLAIIISALLWLPEWVAWLWVWHLKAAGPAPPQGFIALSQVLMFSISSANPLIFLVMSE
EFREGLKDSILRIHFVCSSMRSSYSSVKVFLCDSSNSGTSSDSTSNARS (SEQ ID NO:
54)

45 tccaggacttggaaccatcatcccggctctcttggtggctgtctgcctgggtgggcttcgtgggaacctgtgtgtattgg
catctccttcacaatgcttggaaaggaaagccatccatgatccactccctgattctgaatctcagcctgggtgatctccctcctgctgt
ttctgcacctatccgagctacggcgtactccaaaagtgttgggaatctaggctggtttgtctgcaagtcctctgactggtttatcacacat
gcatggcagccaaggagcctgacaatcgttgggtggccaaagtatgcttcattgatgcaagtaccagcccaagcaagtgaatatcca
caactacaccatctggtcagtctgggtggccatctggactgtggctagcctgttaccctgccggaatggttcttagcaccatcaggca
tcatgaagggtgtggaatgtgcctcgtggatgtaccagctgtggctgaaagattatgtcgatgttggtaagctctaccactcctggca

10 CYKQTLSTFTGLTCIVSLVALTGNVVLWLLGCRMRRNAVSIYILNLVAADFL
FLSGHIICSPRLRLNIRHPISKILSPVMTFPYFIGLSMLSIASTERCLIKHCISALWPIWYH
CRRPHTLSAVLCALLWAPSLLLAFLEGYYCAFLFKIGDYSWFQTFDFITGTWLIFKFV
VLFYVPLKIMFCSEIGITSVSHRAQPTISLTHMVASYLGVMLLFLICSLPLGIKWFLFLF
WILVDFDIFLCHLQPVSDVLSSLNSSANPIYFFMGSFRQRVFCCCCCCCCCFTKFL
15 GITFVSRRGGSHLHSGHSRHVPSHSRH (SEQ ID NO: 56)

30 ERLRLISAGVCGLLLVGLSANGMLLVVGRGPGSPHPLHSLTHSLMMNITP
SDLLFLACVVPVLLSFLQHNWWLGAICTISQATNTATTFCIFYSMVATALLRHVA
VARPDLAFPAGWGTLTLLCGAMWALGLTESLPNWLFRVAVEEETAGAPKTQACL
LLSPAGTSCYISLLGALAFLPCTLGLGCSFSHVGWLLWTQPQENIGLSLVVLVVFVL
MWGPCSMLGYVAAMGYLPATPAAFVASSLCTILAYSNCAVSPILCFYLSRPFQAGLR
35 DLFCRPMMARHPRGPGQQRDSVSNNKTKTKTHTHTHTHTHTHTH (SEQ ID NO: 58)

[illegible]

-63 -

MOOSE00994 ctg17802 159288..159335, 297487..298009, 298142..298330,
313005..313117

5 SLALYNVFPFFFWLLFVGALLGNGALLVVVLRTPGLRDALYLAHL CVVDLLA
AASIMPLGLLAAPPPGLGRVRLGPAPCRAARFLSAALLPACTLGVAALGLARYRLIV
HPLRPGSRPPPVLVLTAVWAAAGLLGALSLLGPPPAPPPAPARCSVLGGLGPFRL
WALLAFALPALLLLGAYGGIFVVA PLAVGQFAACWLPYGCAC LAPAARAAEAEAA
VTWVAYSFAAHPFLYGLLQRPVRLALGRLSRLRSSWAVRTTSGSRLLRGPCSVLD
QTLSSSGPSLAGSS (SEQ ID NO: 60)

10 tcttagcactctacaatgtcttccattttttctggctcttttgggggactgctgggcaacggcgctgctggtcgtg
gtgctgcgcacggcgggactgcgcgacgcgctctacctggcgacactgtgctgctggactgctggcgccgctccatcatgcc
gctgggctgctggcgacggcgcccgggctggcgcgctgctgctggcgccgcatgccgcccgtcgtctcctctcc
ggcgctctgctggcgctgcacgctggggtggcgacgtggcctggcacgctaccgctcatcgtgcacccgctgcggccagg
ctcgcggcgccgctgctgctgctcaccggcggtggcgccgggactgctggcgcgctctccctgctcggcgccg
cccgcacggccccctgctcctgctgctcggctctggctggggcgctggcgccctccggcgctctgggcctgctggccttc
15 gcgctggcgccctcctgctgctcggcgctacggcgcatctcgtggtggcgccgctggcgccgctggcccaattgcagcctgctgg
ctgccttatggctgcgcgtgctggcgcccgacgcggcgccggaagcgaagcggtgcacctgggtcgcctactcggcctt
cgcggctcaccctctctgtacgggctgctgcagcgccccgtgcgttggcactggcgccctctcgcctgaggagcagctggcg
ggtgaggaccacatcgtgatcaagactgctcagaggccctgcagtgcttgaccaaagcgtgtcaagttcaggggccagcctggct
gggtcctcc (SEQ ID NO: 59)

20 MOOSE01139 ctg12634 1689941..1690075, 1696196..1696364, 1729541..1729632,
1731449..1731515, 1744203..1744423, 1748034..1748243, 1777967..1778134,
1813481..1813504, 1865325..1865428, 1868201..1868336

25 THLPSASSQIPALEESCEAVEAREIMWFKTRQGQIAKQPCPAGTIGVSTYLCLA
PDGIWDPQGPDLSCSSPWVNHTQKRSCRAYVQSEENFNPNCSFWSYSKRTMTGY
WSTQGCRLLTTNKTHHTCSCNHLTNFAVLMAHVEHSDAVHDLDDLVTWVGILLSL
VCLLICIFTFCFRGLQSDRNTIHKNLCSLFAELLFLIGINRTDQPIACAVFAALLHFF
FLAFTWMFLEGVQLYIMLVEVFESEHSRRKYFYL VGYGMPALIVAVSAVDYRSY
GTDKVCWLRRLDTYFIWSFIGPATLIIMLVIFLGIALYKMFHHTAILKPESGLDNIKS
30 WVIGAIALLCGLTWAFLMYINESTVIMAYLFTIFNSLQGMFIFHCVLQKKVRK
EYGKCLRTHCCSGKSTESSIGSKTSGSRTPGRYSTGSQVNN (SEQ ID NO: 62)

acacacctccatcagcatcgtcccaatccagctctcgaagagagctgtgaggctgtggaagcccagaaaaatcatgtgg
tttaagactcgtcaaggacagatagcaaaagcagccatgccctgcaggaactataggtgtatcaacttatctatgcctgctcctgatgga
atttgggatcccaaggctcagatctcagcaactgtctctccttgggtcaatcataaacacagaagcgctcttcagagccatgtcc
35 agtcagaggaaaaattcaaccctaactgttcattttggagctactccaagcgtaaatgacaggtatttggtcaacacaaggctgtcggct
cctgacaacaaataagacacatactacatgctctgttaaccacctaacaatttgcagtactgatggcacatgtggaacacagtgatgc
ggtccatgacctctcttgatgtgacgtgggttgaatttgcgtccttgttgcctcgtattgcatcttcacatttgcctttccgg
gggtccagagtgcacgttaaccacatccacaagaacctctgcacagctctttagcagagctgctctcctgattgggatcaaccga
actgaccaaccaattgcctgtgctgtttcgtgcccgtgtacatttcttcttggctgcccctcctggtgagggggtgcag
40 ctttatcatcgtggtggaggttttgagagtgaacattcacgtaggaaatactttatctggtcggctatgggatgcctgcactcatttg
gctgtgtcagctgcagtagactacaggatgtggaacagataaagtattgtggtccgacttgacacctacttcatttggagtttatagg
accagcaatttgataattatgcttaattgaattccttgggattgctttataaaatgtttcatcactgctatactgaacctgaatcagg
ctgtctgataacatcaagtcaggttataggtgcaatagctcttctgcctattaggattgacctgggccccttgactcatgtatataat
gaaagcacagtcacatggcctatctctcaccattttcaattctctacagggaattgttatattttccattgtgctcctacagaagaaggt
45 acgaaaagagtatgggaaatgcctgcgaacacattgctgtagtggcaaaagtacagagagttccattggttcagggaacacatctggtt
ctcgaacctcctggacgtactccacaggctcacaggtaaacat (SEQ ID NO: 61)

MOOSE01146 ctg15998 3076899..3076950, 3227362..3227381, 3254354..3254409,
3255136..3255184, 3257523..3257602, 3334521..3334629, 3354815..3354918,

3355747..3355867, 3358761..3358914, 3368419..3368485, 3370880..3370950,
3371577..3371604, 3415043..3415096, 3441342..3441468, 3442278..3442323,
3512965..3513101

5 HRRLKQENHLNPGGRGCMGLWGGGLCWVPTAPGSCGAPPGRRLCPDWFSAL
LSSTSMMSGPSLSLCCPHGPRCLQTHWSPRMQATVSGEGVWSNHGCALTRGNLTY
SVCRCCTLNFAILMQLARGHQVALSSISYVGCSSLVLCLVATLVTFVAVLSTIRNQRY
HIHANLSFAVLVAQVLLLSIFRLEPGTVSGRSSTPCQVMAVLLHYFFLSAFAWMLVE
GLHLYSMVIKVFSGSEDSKHRYYYGMGWGFPLLICISLSFAMDSYGTSSNCWLSLAS
GAIWAFVAPALFVIVPNFVFLVETGPVLLTGLASQDPSVRSTQLTAKAAAVLLPILG
10 TSWVFGVLAVNGCAVVFQYMFATLNSLQGLFIFLHCLLNSEVQGLEELQKKWWG
GDPELGISRKPLPSGAAGAGKGEHSQGLGKSRA (SEQ ID NO: 64)

5 caccaggaggctgaagcaggagaaatcactgaacccgggagcagaggtgcatgggctttgggggtgggggtctttgct
gggtgcccaccgcgcagggagctgcgggtgctccccgggcccgcctgoggtgccccgactggttctctgccctgctcaactagc
atgatgtcaggctccttactctccctctgctgctcctcacggaccaggtgtctgcagacaggacactggagccccaggatgcaggcca
15 ctgtctccggagaaggggtctggtcgaaccacggctgtgctcctcacgagaggaaacctcacctactccgtctgccgtgcactcacct
caccacatttgccatcctcatgcagcttgacgcggacaccaggtggcgctgtctctatcagctatgtgggctgctccctctccgtgct
ctgcctggtggccacgctggtcaccttgcctgctgctccaccatccggaaccagcgctaccacatccacgccaacctgtccttccgcc
gtgctgggtggccaggctcctgctgctcattgttccgcctcagccgggacaggtgagtggtggcgagctccacccctgccaaagt
atggcgtgctcctacactacttctcctgagtgcttgcctgcatggtgctggtggaggggctgcacctctacagcatggtgatcaaggct
20 ttgggtcggaggacagcaagcaccgtactactatgggatgggatggggttttcttctctgctgctcatcttactgctcatttgcctat
gacagttacggaacaagcaacaattgctggctgtcgttggcgagtgccgccatctgggctttgtagccctgccctgttgcctatcgtg
gtacctaatgttatgttttagtagagacgggtccagtttgccttactggaactagcagccaagaccttctgtgcgtccaccaggtgac
ggccaaggcagcggcctgctgctgctccatcctgggtacctcgtgggtctttggcggtgctgctgcaacggttgcctgctggtttcca
gtacatgtttgccacgctcaactccctgcagggactgtcatattccttcttctgctcctgaattcagaggtacaggggctggaggag
25 ctgcagaagaatggtggggcggtgacctgagttaggcatcagcaggaagccactgccatccgggctgcaggggcccgggaag
ggtgagcacagccaggcctgggtggcaagtccaggga (SEQ ID NO: 63)

MOOSE01148 ctg12559 20179213..20179257, 20217038..20217100,
20401216..20401250, 20420415..20420483, 20567869..20567971, 20571553..20571656,
30 20572335..20572624, 20573833..20573929, 20576381..20576664, 20593994..20594078,
20661185..20661284

YYQEQLAQKDPLTYLNDNCFILPDIFTCRFTCPWQGSCSLCPYLCPWFQFLFP
SAQVIRSCTKWSGTWDTFFGGWNTSGCVAHRRSDASETVCCLNHFTHFGVLM
LDARNTKVLTFISYIGCGISAFSAATLLTYVAFEFLLSFRRKLRRDYPSKILMNLSTAL
35 LFLNLLFLLDGWITSFNVDGLCIAVAVLLHFFLLATFTWMGLEAHIMYIALVKVFNT
YIRRYILKFCIGWGLPALVVSVVLASRNNNEVYGKESYGKEKGDEFWCWQDPVIFYV
TCAGYFGVMFFLNIAFMFVVMVQICGRNGKRSNRTLREEVLRNLRVSVSLTFLGMT
WGFAFFAWGPLNIPFMYLFSIFNSLQGLFIFIFHCAMKENVQKQWRQHLCCGRFRGTI
SAHCKLRLPGSRHSPASASQVAGTTGTSHH (SEQ ID NO: 66)

40 tttatcaggaacaattggcacagaaagacctttgacgtactaaatgataattgctttattcttctgataatttactttgtagatt
cacctgccccatggggccaatctttagtctttgcccatacctatgtcctgaatggttccagttgttcttctgctcaggttatcagaagctg
cacaagtggtctggtacttgggacacttttttgaggatggaacacgtcaggatgtgtgcacacagagattcagatgcaagtgaga
cagctgctgctgtgaaccttcacacactttgaggttctgatgttagatgaagaaactaaagtccctcactttcatcagctatattgggt
gtggaatatctgctatttttcagcagcaactcctgacatatgttgcctttgaattcctttttcatttttaggaaattgcgaagggtattatcc
45 ctccaaaatcttgatgaacctgagcacagccctgctgttctgaatctccttctcctcctagatggctggatcacctcctcaatgtggatg
gactttgcatgtgtgagctcgttgcatttctccttctggaacaccttacctggatggggctagaagcaattcacatgtacattgctct
agttaaagtatttaacacttacatcgccgatacattcaaaattctgcatcattgtgctgggttgcctgcttagtggtgtcagttgttctag
cgagcagaaacaacaatgaagtctatggaaagaaagtatgggaaagaaaggatgaattcgttggattcaagatccagtcata
ttttatgtgacctgtgctgggtatttggagtcatttttgaacattgccatgttcatgttggtatgtgcagatctgtgggaaggaatgg

10

15

20

25

30

35

40

15

catTTTgacgaagTctctgaaaattttgctagccttcagcttTgatccaaattacagaatttctgaaTgTgcctctatagaccgatccttata
tcttcactTgcacgggcacTccaggtTgtcattTgcacactctggcTaaTctTgcagcacctactgtagaggtgaatgtctcctTgccaga
gtcatcatcctggagTgtgaggaggatccatactTgcattTggcaccatgctgggctacatTgccatcctggcctcattTgctcatatt
gctttcaaggcaaatatgagaattacaatgaaggccaaattcattacattTggcatgctcattTactcatagctTggatcacattcatcccta

tctatgctaccacatttggcaaatatgtaccagctgtggagattattgtcatattatctaactatggaatcctgtattgcacattcatcccc
aaatgctatgttatttgaagcaagagattaacacaaagtctgcctttctcaag (SEQ ID NO: 67)

MOOSE01172 ctg14779 1950842..1951724, 1953313..1953437, 1953760..1953972,
1954995..1955756, 1959173..1959470, 1967494..1967524, 1970244..1970307

5 GRLVVGALFNLESWYQEACPEIYCFHPPTCLGFNEHGYHLFQAMRLGVEEIN
NSTALLPNITLGYQLYDVCSDSANVYATLRVLSLPGQHHELQGDLLHYSPTVLA VIG
PDSTNRAATTAALLSPFLVPMISYAASSETLSVKRQYPSFLRTIPNDKYQVETMVL
QKFGWTWISLVGSSDDYQGLGVQALENQATGQGICIAFKDIMPFAQVGDERMQCL
10 MRHLAQAGATVVVVFSSRQLARVFFESVVLTNLTGKVWVASEAWALSRHITGVP
QRIGMVLGVAIQKRAVPGLKAFEEAYARADKKAPRCHKGSWCSSNQLCRECQAF
MAHTMPKLKAFSMSSAYNAYRAVYAVAHGLHQLLGACSGACSRGRVYPWQLLEQI
HKVHFLHLHKDTVAFNDNRDPLSSYNIAWDWNGPKWTFVTLGSSTWSPVQLNINET
KIQWHGKDNQVPKSVCSDDCLEGHQVRVTGFHHCCEFCVPCGAGTFLNKSQECQPC
15 GKEEWAPEGSQTCFPRTVVFLALREHTSWVLLAANTLLLLLLGTAGLFAWHLDT
VVRSAAGRLCFLMLGSLAAGSGSLYGFFGEPTRPACLLRQALFALGFTIFLSCLTVRS
FQLIIIFKFKSTKVPTFYHAWVQNHGAGL FVMISSAAQLLICLTWL VVWTPLPAREYQR
FPHLVMLECTETNSLGFILAFLYNGLLSISAFACSYLGKDLPENYNEAKCVTFSLFN
VSWIAFFTASVYDGYLPAANMMAGLSSLSGFGGYFLPKCYVILCRPDNSTEHF
20 QA (SEQ ID NO: 70)

ggcagactagctgtaggagcccttttaatctagaaagttggtagccaagaagcatgctctgagattattgtttcatcctccca
cctgcttaggctcaatgagcatggctaccacctctccaggctatgcggcttggggtgaggagataaacaactccacggccctgctg
ccaacatcacctggggtaccagctgtatgtgtgtctgactctgccaatgtgtatgccacgctgagagtgctctccctgccagg
caacaccacatagagctccaaggagaccttctccactattccctacggctgctggcagtgattgggctgacagaccaaccgtgctg
25 ccaccacagccgctgctgagcccttctggtgcccattgattgctatggccagcagcagacgctcagcgtgaagcggcag
atcccttctctgctgcaccatccccaatgacaagtaccaggtggagaccatggctgctgctgagagaagttcgggtggacctggatc
tctctggttggcagcagtgactatggcagctaggggtgagcagcactggagaaccaggccactggtcaggggatctgcatgtg
ttcaaggacatcatgccccttctgcccaggtgggcgatgagaggtgagtgccctatgcgccacctggccaggccggggccac
cgctggtgtgtttttccagccggcagttggccaggggtgttttgcagtcggtgctgaccaacctgactggcaaggtgtgggtgc
30 ctgagaagcctgggcccctctccaggcacatcactggggtgcccgggatccagcgcattgggatggtgctggcgtggccatccaga
agagggctgtccctggcctgaagggcgtttgaagaagcctatgccggcagacaagaagccctaggcctggccacaaggcctcc
tggtgcagcagcaatcagctctgcagagaatgccaagcttcatggcacacacgatgcccaagctcaagccttctcatgattctgc
ctacaacgcataccgggctgtgtatcggtggcccattggcctccaccagctcctgggctgtgcctctggagctgttccaggggccga
gtctaccctggcagcttttgagcagatccacaaggctcatttctctacacaaggacactgtggcgttaatgacaacagagatccc
35 ctgtagctataacataattgcctgggactggaatggaccacaggtggaccttcacggtcctcggttctccacatggtctccagttcag
ctaaacataaatgagacaaaatccagtgccacggaaaggacaaccaggtgcctaagctgtgtgttcagcagactgtctgaaggcc
accagcgagtggttacgggttccatcactgctgctttagtggtgtgcccgtggtgggctgggaccttctcaacaagagtggtgaatgcc
agcctgtgggaaagaagagtgggcacctgagggagccagacctgtcccgccgactgtgtgttttggccttgcgtgagcacac
ctctgggtgctgtggcagctaacacgctgctgctgctgctgtgggactgtggcctgttgcctggcacctagacaccctgt
40 ggtgaggtcagcagggggccgctgtgttcttatgctgggctccctggcagcaggtagtgccagcctctatggcttcttggggaac
ccacaaggcctgctgtgtgtctacgccaggcccttctggccttgggttaccatcttctgtcctgctgacagttcgtctatccaacta
atcatcatcttcaagtttccaccaaggtacctatcttaccacgctgggtccaaaaccaggtgctggcctgtttgtgatgatcagctc
agcggcccagctgttatctgtctaacttggctgtgtgtgtggacccactgctgctagggaaataccagcgcttccccatctgtgtat
gttgagtgacagagaccaactccctgggttcatactggccttctctacaaatggcctcctctccatcagtgcccttgcctgacgtac
45 ctgggtaaggacttgccagagaactacaacgagcccaatgtgtcaccttcagcctgctcttcaacttctgtcctggatcgcccttctca
ccacggccagcgtctacgacggcaagtacctgctgcccgaacatgatggctgggctgagcagcctgagcagcggcttcgggtg
gtatttctgcctaagtgtacgtgatcctctgcccagacctcaacagcacagacacttcaggcc (SEQ ID NO: 68)

-67 -

MOOSE01176 ctg17658 40622..41514, 41641..41761, 41896..42099, 42214..43015,
49551..49850, 49952..50046

GDYVLGGLFPLGEAEEAGLSRTRPSSPVCTRFSSNGLLWALAMKMAVEEIN
NKSDLLPGLRLGYDLFDTCSEPVVAMKPSLMFLAKAGSRDIAAYCNYTQYQPRVLA
5 VIGPHSSELAMVTGKFFSFFLMPQCLLALQVSYGASMELLSARETFPSFFRTVPSPDRV
QLTAAAEELLQEFGWVNWVAALGSDDEYGRQGLSIFSALAAARGICIAHEGLVPLPRA
DDSRLGKVQDVLHQVNQSSVQVLLFASVHAHALFNYSISSRLSPKVWVASEAWL
TSDLVMGLPGMAQMGTVLGFQRGAQLHEFPQYVKTHLALATDPAFCSALGEREQ
GLEEDVVQQRCPQDCITLQNVSAGLNHHQTFSVYAAVYSVAQALHNTLQCNASG
10 CPAQDPVKPWQLLENMYNLTFFHVGGPLRFDSSGNVDMYDLKLWVWQGSVPRL
HDVGRFNGSLRTERLKIRWHTSDNQKPVSRCSRQCQEGQVRRVKGFHSCCYDCVDC
EAGSYRQNPDDIACFTCGQDEWSPERSTRCFRRRSRFLAWGEPAVLLLLLLLLSLALG
LVLAALGLFVHHRDSPLVQASGGPLACFGLVCLGLVCLSVLLFPQSPARCLAQQP
LSHLPLTGCLSTLFLQAAEIFVESELPLSWADRLSGCLRGPWAWLVVLLAMLVEVAL
15 CTWYLVAFPPEVVTDWHMLPTEALVHCRTSRWSVFGLAHATNATLAFLCFLGTFLV
RSQPGCYNRARGLTFAMLAYFITWVSFVPLLANVQVVLPAVQMGALLLCVLGILA
AFHLPRCYLLMRQPGLNTPPEFFLG (SEQ ID NO: 72)

ggggactacgtgctgggggggctgttccccctgggcgagggcagggaggtggcctccgcagccggacacggcccag
cagccctgtgtgaccaggttctcctcaaacggcctgtcttgggcactggccatgaaatggccgtggaggagatcaacaacagtc
20 ggatctgtgtcccgggctgcgcctgggctacgacctctttgatactgtctggagcctgtgtggccatgaagccagcctcatgttcc
tggccaaggcagggcagccgcgacatcgccgctactgcaactacacgcagtagccagccccgtgtgtgctgtcatcgggccccac
tcgtcagagctcgccatggtcaccgggaagtctcagcttcttctcatgccccaatgctcttggccttgacgtcagctacgggtgcta
gcatggagctgtgagcgcccgggagaccttccccctcttcttcgcaccgtgcccagcgaccgtgtgcagctgacggccggcgcg
gagctgtgtcaggaggttcggctggaactgggtggcgccctgggcagcgacgacgagtagggccggcagggcctgagcatcttct
25 cggccctggccgcggcagcgccatctgcatcgcgacgagggcctgggtccgctgccccgtgcccgtgactcgggctggggga
aggtgcaggagctcctgcaccaggtgaaccagagcagcggtcaggtgtgtgtgtgtgttcgctcctcgtgcacggcccccacgcccct
ttcaactacagcatcagcagcaggtctcgcaccaaggtgtgggtggccagcgagggcctggctgaccttgacctggatcggggctg
cccggcatggccagatgggcacgggtgtgtgttctcctcagaggggtgcccagctgcacgagttccccagtagtgaaagacgca
cctggccctggccaccgacccggccttctgctctgcccctggcgagagggagcaggggtctgaggaggagcgtgtgggcccagcg
30 ctgcccgcagtgtagtgcacacgctgcagaacgtgagcgagggcctaataccaccagacgttctgtctacgcagctgtgtat
agcgtggcccaggccctgcacaacactcttcagtgaacgcctcaggctgccccgcgcaggaccccgtgaagccctggcagctcct
ggagaacatgtacaacctgaccttccacgtggcggggctgccgtgcggttcgacagcagcggaacgtggacatggagtacgac
ctgaagctgtgggtgtggcagggctcagtgccagggctccacgacgtgggaggttcaacggcagcctcaggacagagcgccctga
agatccgctggcacacgtctgacaaccagaagcccggtgtccgggtctcgcggcagtgccaggaggccaggtgcggcggtgtaa
35 ggggttccactcctgtgtctacgactgtgtggactgcgagggcgggcagctaccggcaaaaccagacgacatcgctgcacctttgt
ggccaggatgagtggtccccggagcgaagcacacgctgcttccgcccaggtctcgggtcctggcatggggcgagccggctgtgtct
gtgtgtctcctgtgtgtgagcctggcgctgggcccctgt
ggcctcggggggggccctggcctgt
40 cctgcccgatgctgcccagcagccctgttccacctccgctcacgggtgctgagcacacttctcctgcagggcgccgagatc
ttcgtggagtcagaactgcctctgagctgggcagaccggctgagtggtgctgctggggggccctgggctgggtgtgtgtgtgt
gcatgtgtgtggaggtgcactgtgcacctgttacctgtgtgcttccgccggaggtgtgtgacggactggcacatgtgtcccacg
gaggcgctgtgtgactgcgcacacgctcctgggtcagcttccgctagcgacgccaccaatgccacgtggcctttctgtgttcc
tgggcacttctgtgtgcggagccagccgggctgtacaacctgtcccgtggcctacaccttggcatgtgtgcttctcatcacctgg
gtctccttctgtcccctcctggccaatgtgcaggtgtgtctcagggccgctgtcagatggggcgccctcctgtgtgtgtgtgtgt
45 cctggtgtccttccacctgcccaggtgttacctgtcatcgggcagccaggggtcaacacccccgagttcttctgtggga (SEQ ID
NO: 71)

MOOSE01371 ctg13655 22484333..22486189

ALALLQRSSGAAAASAKELACQEITVPLCKGIGYNYTYMPNQFNHDTQDEAG

[illegible]

35 MOOSE01451 ctg17341.5903471..5903744, 5904206..5904356, 5910947..5911003,
5919010..5919127, 5934289..5934313, 5939959..5940053, 5941313..5941394,
5947946..5948017, 5948441..5948532

40 LARSSNPFEKRRHSGFLNFQLFCSGFSPSLCCQTGTFRSAEVFYCLLFSCALLT
DQKEKMALHFLFHQTLQLIHLELEKMILKNLFMPYWDVWHHQQFYANQILGKGLY
CFFRVVFVYSCSFVELAVSRDRATALQPGRQSETLSQKKKKRNATDFCMLSLCIEGT
YLQIIRAIKCKPTATGVPVFTQCVTKGSFKAQWQETTYNLFTECCFLPLLTAMVICYS
RIVLSVIFSKFLAPAGEFALPRSFDCNCPVRRLRALRLALLILTLFILCWTPPYLLGMWY
WFSPTMLTEVPPSLSHILFLLGLLNAPLDPLLYGAFTL (SEQ ID NO: 76)

45 ctggcaaggagcagcaatcctttgaggagaagaggcactctggtttttgaatttcagcttttctgctgtggtttctcccatct
ttgtgctgtcagacaggacatttaggtctgcagaagtttctattgctctttttgtcagctgtgccctgtcacagaccagaaggagaaat
ggccttacattttctttccatcagacacttcaactcatatttgaggcttggaagaatgattttaaaaaatctttcatgccctattgggatgt
gtggcatcatcagttcaatatgcaaatcaaattttgggaagggtctatactgcttctcagggtatttgtttctatctctgtagctttgtga
gcttgcagtgcggagatctgtccactgcactccagcctgggcgcacagagcgcagactctgtctcaaaaaaaaaaaaaaagaaatg
caactgattttgcatgtgtctttgtgtattgaaggaacatacctccaataataagaccattttgtgcaacccacagccactggccca

gtccctttcactcagtggtgaccaaaggcagcttcaaggctcaatggcaagagaccacctataacctcttcaccttctgctgctctttct
gctgccactgactgccaatggtcatctgctatagccgcatgtgctcagtggtatattttctaaattcctagccctgctggtgaattgccctc
ccccgctccttgacaattgtccccgtgttcgtctccgggccccgagactggccctgcttatctgctgacctcatcctctgctggacacc
ttattacactagggtatggtgactggttcctcccccaccatgctaactgaagtcctccagcctgagccacatcctttctcttgggct
5 cctcaatgctccttgatcctctctctatggggccttcacctt (SEQ ID NO: 75)

MOOSE01609 ctg37 223820..223885, 415276..416383, 418102..418139

LGAVTTPVIPALGDAEAGRSSEVIVLHNYTGKLRGARYQPGAGLRADAVVC
LAVCAFTVLENLAVLLVLGRHPRFHAPMFLLLGSLTSLDLLAGAAAYAANILLSGPLTL
10 KLSPALWFAREGGVFVALTASVLSLLAIALERSLTMARRGPAPVSSRGRTLMAAAA
AWGVSLLLGLLPALGWNCLGRLDACSTVLPYAKAYVLCVLAFAVVGILAAICALYA
RIYCQVRANARRLPARPGTAGTTSTRARRKPRSLALLRTL SVVLLAFVACWGPFLL
LLLDVACPARTCPVLLQADPFLGLAMANSLLNPIIYTLTNRDLRHALLRLVCCGRHS
CGRDPSGSQQSASAAEASGGLRRLCPPGLDGSFSGSERSSPQRDGLDTSGSTGSPACV
15 MKSCLLGKHK (SEQ ID NO: 78)

ctgggagcagtgactacgcctgtaatcccagcacttggggagcgcaggcagggcaggtcatctgaggtcatcgtcctgca
ttacaactacaccggcaagctccgggtgcgcgtaccagccgggtgcccgtcgcgcggacgcccgtggtgctgctggcgtgt
gcgcctcatcgtgctagagaatctagccgtgtgtgtgctcggagccacccgcgttccacgctcccatgtctctgctggca
gcctcacgtgtgctggaatgctgctggcagggcgccttacgcccacacatcctactgtcggggccgctcacgctgaaactgtccccg
20 cgtctgtgttcgcacgggagggagggcgtcttcgtggaactcactgcgtccgtgctgagcctcctggccatcgcgtggagcgcagcc
tcaccatggcgcgcagggggcccgcgccgtctccagtcggggggcgcagcgtggcgtgagcagccggcctggggcgtgtc
ctgctcctcgggctcctgcccagcgtgggtggaattgcctgggtgcctggagcgttgcctcactgtcttgcgctctacgccaaggc
ctacgtgctcttctgctgctgccttcgtgggcatcctggcgctatctgtgactctacgcgcgcatctactgccaggtacgcgcaa
cgcggggcgcctgcccgcacggccgggactgcggggaccacctgacccgggcgcgtcgcaagccgcgctcgtggcctgtgt
25 gcgcacgctcagcgtgtgctcctgtggtcttggcctgtggtggccccctcttctgctgctgtgtgctgacgtggtgcccggcgc
gcacctgtcctgtactctgcagggcgatccctctgggactggccatggccaaactacttctgaaccccatcatctacagctcacca
accgcgacctgcgccacgcgtctcgcctggtctgctgcggagccactcctgcggcagagaccgagtggtcccagcagtc
ggcgagcgcggctgaggtctccggggcctgcgcgctgctgccccgggccttgatgggagcttcagcggtcggagcgtca
tcgccccagcgcgacgggctggacaccagcggtccacaggcagccccgcctgtgtgatgaatcatgtcttttagaaaacataag
30 (SEQ ID NO: 77)

MOOSE02359 ctg15037 7933711..7933760, 7963115..7963181, 7973661..7973682,
7983319..7983352, 7998114..7998223, 7999445..7999609, 8000036..8000207,
8000817..8001020, 8001339..8001472, 8003204..8003358

SPQAPGTWAAA WVPLPTVDVDPDHAHYTLGTVILLVGLTGMLGNLTVIYTFGR
SRSLRTPANMFILNLA VSDFLMSFTQAPVFFTSSLYKQWLFGETGCEFYAFCGALFGIS
SMITLTAIALDRYL VITRPLATFGVASKRRAAFVLLGVWLYALAWSLPPFFGWSAYV
PEGLLTSCSWDYMSFTPAVRA YTMLCCFVFFLPLLIICYIFIFRAIRETGRALQTFG
ACKNGESLWQRQLQSECKMAKIMLLVILLFVLSWAPYSAVALVAFAGYAHVLT
40 YMSSVPAVIAKASAIHNPIYAIHPKYRSDAVASWQSRRLGVHLYPWSLVFCHPSEF
ENHNWSTRDVAPGHLMTMETRVL SILSQ (SEQ ID NO: 80)

ctccgcagggcacctgggacttgggctgctgctgggtccccctccccacggtgatgttcagaccatgcccactataccc
tgggcacagtgatcttctggtgggactcacgggagtgctgggcaacctgacggtcatctataccttctgcaggagcagaagcctccg
gacacctgccaacatgttcatatcaacctcgcggtcagcgacttctcatgtccttaccagggccctgtcttctaccagtagcctct
45 ataagcagtggtcttggggagacaggctgcgagttctatgcttctgtggagctcttggcatttctccatgacacctgacggc
catcgccctggaccgctacctggaatcacacgcccgtggccaccttgggtggcgtccagaggcgtgcggcattgtcctgctg
ggcgttggctctatgacctggcctggagctcgcacaccttctggctggagcgcctacgtgcccagggggtgctgacatcctgctc
ctgggactacatgagcttccgcccgtgcgtgcctacacatgcttctgctgcttcttctcctcctgctatcatcatcta
ctgctacatcttcatctcagggccatccgggagacaggacgggctctccagacctcggggcctgcaaggccaatggcagtcct

-70-

gtggcagcggcagcggctgcagagcagtgcaagatggccaagatcatgctgctggtcatcctcctcttctgctctcctgggctccc
tattccgctgtggccctgggtggccttctgctgggtacgcacacgtcctgacaccctacatgagctcgggtgccagccgtcatcgccaaggc
ctctgcaatccacaaccccatcattacgccatcaccaccccaagtacaggtcagatgctgtggctcctggcagtcagacgtcttgg
ggtacacttgatccctgggtcctggtgtctgccaccctagcgagttgaaaaccacaactggagcaccaggatgtgtcccgaggc
5 cacctgatgacagaaatggagactagagtggtgtctatactaaagccaa (SEQ ID NO: 79)

MOOSE02360 ctg15907 53482006..53482053, 53509199..53509251,
53519616..53519786, 53524954..53525124, 53528381..53528715, 53541306..53541470,
53636121..53636147, 53655914..53655948, 53805160..53805178, 53813699..53813772,
10 53992100..53992118
SLLKIQKISRTWWRVPSTDVSLPMWGDFAVSSSELEILVLTIGIFIFLVLGILS
TFNGYVLYMSSRRKKLRPAEIMTNLAVCDLISVVGKPFTHSCFHRWVFGWIG
CRWYGWAGFFFGCGLITMTAVSLDRYLKICYLSYGVWLKRKHAYICLAATWAY
ASFWTTMPLVGLGDYVPEPFGTSCTLDWWLAQASVGGQVFILNLFCLLLPTAVIV
15 FSYVKIIAKVKSSSKEVAHFDSRIHSSHVLEMKLTKVAMLICAGFLIAWIPYAVVSVW
SAFGRPDSIPIQLSVVPTLLAKSAAMYNPIYQQNFSISNFRDSLQSSVPWIQCCYY
QESRGQLERVVESRDFVRMSAVSADLQKFQRN (SEQ ID NO: 82)

ctctactaaaaatacaaaaaattagtcggacgtggtggcgggtgcctagcacagatgtgagctgcttacctatgtggggag
acttcagggctgtgagtagtggaactcgaatcttagtttaacgattggaattttatttttctttagggattctgtccacatttgaaatg
20 gatattgctttatcatgtcttctagacgaaagaagaagctgagaccgctgaaataatgactatcaatttagcagctctgtgaictggggatt
tcagttgtaggcaagccgttcaccatcatcttctgttctgaccgctgggtgttggctggatcggtcgccgctggatggatgggctg
gatttttcttggctgtggaagccttatcaccatgactgctgtcagcctggatcgatattgaaaatctgctatttcttatggggttggctg
aaaagaagacacgcctacatctgcctggcagccatctgggcctatgcttcttctggaccaccatgccctggtaggtctgggggacta
cgtacctgagcccttcggaacctgtgcacctggactgggtggtggccaggcctcggtagggggccagggtttcatctgaacatc
25 ctcttcttctgccttcttctccaacggctgtgatcgtgttctctactgaaagatcattgccaaggtaagtcctcttccaagaagtagct
catttcagagctggatccatagcagccatgtgctggaatgaaactgacaaaggtagc gatgttgattgtgctgattcctgattgcct
ggattccttatgcatgtgtgtctgtgtggtcagcttttggaaaggccagactccattccatacagctcctgtgtggtgccaacctacttga
aaatctgcagcgatgtacaatcccatcattaccaacaaaacttcaatacaaatcttctgattccctagctcagagctcagtccttgg
30 attcagtgctgttattatcctcaagagagcaggggacagctagaaagggtttagaatcgagagattttgtaggatgtcagcagtttagc
gcagatctacaaaaattccagaggaat (SEQ ID NO: 81)

Table II

MOOSE02352 ctg12376 2508254..2508274, 2512637..2512697, 2596061..2596100,
35 2609217..2609251, 2697256..2697388, 2697901..2698120, 2702134..2702373,
2703765..2703914, 2704936..2705391, 2785876..2785900, 2796650..2796801
MSVVLQDTQTLTIDSNINSLIVALLVTGITGMHHHARLILKLFVSKSSINFAD
FISQSSASPGGVVDYILHGSTVTFQHGQNLFINISIIDNESEFEPIEILLTGATGGAV
LGRHLVSRILAKSDSPFGVIRFLNQSKISIANPNSTMILSLVLERTGGLLGEIQVNWET
40 VGPNSQEALLPQNRDIADPVSGLFYFGEGEGGVRTIILTIYPHEEIEVEETFIKLHLVK
GEAKLDSRAKDVTLTIQEFGDPNGVVQFAPETLSKITYSEPLALEGPLLITFFVRRVK
GTFGEIMVYWELSSEFDITEDFLSTSGFFTADGESEASFDVHLLPDEVPEIEEDYVIQL
VSVEGGAELDLEKSITWFSVYANDDPHGVFALYSDRQSILIGQNLIRSIQINITRLAGT
FGDVAVGLRISSDHKEQPIVTENAERQLVVKDGATYKVDVFGTFYYSFISCTDGAVN
45 LTYIQISKPIFSHYTDAYIFLHYSLLNTFLCDNSHFKISRK (SEQ ID NO: 84)

atgagtggtgtctgcaggatactcagacgttaacaatagactcaaacattaacagcctgctcatagttgcctgctggttaact
gggattacagggcatgcaccaccagcccggttaattttaaattatttgaagtaaaagtagcataaactttgctgattcatctcagag
ctcctctgccagtcctggaggtgtgattacatttgcagtcagtcaccttcagcatgggcaaaacttaagtttataaatatctc
catcattgatgacaatgaaagtgaatttgaggagccattgaaatttactactggagctactggaggagcggtccttggcgccacc

-71 -

tagtgagcagaatcataatagctaagagtgactctcccttggagttataaggtttctcaatcaaaagcaaaatttctattgctaataccaattc
 cacaatgattttatcactgggtgctggagcggactggaggactcttgggagagattcaggtgaactgggagacagtaggaccaactct
 caagaagccttactgccacagaatagagacattgcagaccagtgagcgggtgttctatttggagaaggaggaaggagtgaga
 accataattctgacaatctatctcatgaagaaattgaagttgaagagacattcatttaaaactcattctgtgaaaggagaagctaaatta
 5 gactccagagctaaagatgttacattaaccatacaagagtttggtagcccaaatggagttgtcagtttgcctcgtgaaactttgtc
 gacttattcagagcctctggctctggaaggccctgtctcattaccttcttgcagaagagtcaggccacctttggagagattatggtt
 actgggaattaagtagtgagttgacattactgaagactttcttccaccagtggttttaccattgctgatggagagagtgaaagctagct
 ttgatgttcatcttaccagatgaggtacctgagatagaggaagattatgtgatccagcttcttctgtagaggaggagccgaactgg
 atctggagaagagatcacatggttctctgtttatgcaaatgatgccacatggagatttgcctgtattcggatccagtcataactta
 10 ttgggcagaaccttattagatccatccaaattaacataaccggcttctggaacatttggagatgtggtgttgggttcgaatatcatcg
 gatcataaagaacagccgatgttaccgaaatgcagagaggcagctggtgtcgaagtggtgcccataaaatggacgtgtttg
 gaacctttattacagcttcatctcctgtactgatggagctgtaaatcaacatacatccagatcattcaaaacctatttttctactacaca
 gatgcttatattttcttattacagccttttaatacttttctgtgataattccacctttaaatttcgagaaag (SEQ ID NO: 83)

15 MOOSE01169 ctg13067 1981228..1981248, 1981792..1982139, 1984400..1984592,
 1984626..1984712, 1985489..1985522, 1985564..1985647, 1985892..1985938,
 1986646..1986768, 1988270..1988412, 1988754..1988824, 1989127..1989251,
 1991650..1992536

GGGILFMLFPSKIHLITYKVYFFFRFNFQRFRWMKAMIHMIKEINKRKDILPN
 20 ITLGYQIFDTCFTISKSVEAVLVFLTGQENRPNFRNSTGAFFPAGIVGAGGSFLSVPAS
 RILGLYYLPQVGYTSTCVILSDKYQFPSYLRVIASDKIQSKAVVKRIQHFHFLTLSPRL
 ECSGAILAHGNLCLPVAGITGVCHHARLIFVFLVETGFCHVAQADGVSLCCHAGVYN
 SPASAPLVAGTTGAHHHAQLIFVFLRYVTLLSLQKGQSCPNVFMHYLGEEYFQHREQ
 HLLNPEARVAGTLEEQRKSQCGWKDLSIVYTYFCNVMYHNLAQRLVIFSMLFNSDL
 25 LWKTQHMKILISKINIKGKYFLGFQDDSWNHRSTSRNRPLPHSVCTDVCPPGTRKGI
 RSEGEPICCFDSIPCADGHVSRKPGERECEQCGEDYWSNAQKSECVLKEVEYLAYDE
 ALGFTLVLSVFGAFVVLAVTAVYVIHRHTPLVNASDWQLGFLIQVSLIIMLLSSMLFI
 DKPHNWSCMAGQVTLALGFSCLCLSGKTSSLFLAYRISKSKTQLTSMHPLYRKIIV
 LISVLAIEIGICTAYLILEPPMVYKNMESQNTKIILGCNEISIEFLYSMFGIDAFLLCFL
 30 TTFVARQLPDNYEYEGKCITFGMLVFFIWMFSFVPLSTKGKFKMAVEIFAILASSHG
 LLGCIFAPKCLILLRPERNTSEI VCG (SEQ ID NO: 86)

gggggaggtattttatgtctgttttccctcaaaagatccacctaatacctacaaagtctatttctttcaggttaactttca
 gagattccgctggatgaaagccatgatccacatgatcaaggagattaataaggaaggatatttggccaacatcacttgggtatc
 agatctttgatacctgttttaccatctccaaatcagtggaagcagcttgggtatttcttaccaggcgaggaagaaaacaggcccaattttaga
 35 aacagcactggagcatttccggcaggaattgttggagcaggtggatcattcttaccagttcctgttcaagaattctagggttaattatttg
 cctcaggtgggtatccttaccctgcgtgattcttagtgacaaataccagtttccatcttcttctgttaatagccagcgataagatcca
 gtcgaaggctgtggtaaaacgatccaacactttcacttctcagctgtcggccaggctggagtgagtgagtgccatcctggctcatgg
 caacctctgctcccagtagctgggattacaggtgtgtgccaccatgccagactaattttgtatttttagtagagacaggggtttgccatgt
 tgcccaggctgACGGAGTCTCGCTCTGTTGCCATGCTGGAGTATAcaattctcctgcctcagccccct
 40 agtagctgggactacaggcgacaccacacgctcagctaattttgtattttaagatatgtaacacttctgtcattgcagaaggagcag
 agctgccctaattgtttcatgcatatcagggaagaatatttccagcacagggaacagcaccctttaaaccctgaggcgcgtgtgtgct
 ggcaatttggaggaacagaaaagagtaattgtgtggaagacttatttgtgtatatacattctgtatgttatgtaccataacct
 agctcagagattggttaattttctatgttatttaattcagatttcttggaaaactcaacatatgaaattctgatttcaaaataaataaa
 gggaaaataatttttaggtttcaagatgattcttggatcataggtcttcacaagcaggaacagaccttccccattcagtggtactga
 45 tgtgtctcctcctgggactcggaggggattcgttcaggggagaaccaatgtctgttctgactccatcccatgtgtgtgacacgt
 gtcacggaaacagggtgaaggaggatgtgaacaatgtgtgtgaagactattgtcaaatgcacaaaagagcgagtggtgtgtgaaaga
 ggtggaaatccttcttatgatgaggccctgggattcacacttctcatttcttcttggggcatttgggtctggcagtcacagctgtg
 tatgtgatacacaggcacactcccctggtgaacgccagtgactggcagctgggcttctcattcaggttctctgatcatcatgtctgtc
 gtccatgctttcattgacaagccacacaactggtcctgcatggctggccaggctcacttggcactgggcttttcttggcctgtctgcct

-72 -

tcttggaagactagttcactgttttagcctacagaatttcctcaaaactcaactacatccatgcaccccccttaicggaaaatcatt
gtgctaactctctgttctagcggagattggcatatgtacagcctacttgatattggaacctccatgggtatacaagaacatggaatctcaaaa
tacaagatcattctgggatgcaatgaaattccatagagttttgtactcgtgttggaattgatgccttcttagccttgctatgctttcttac
aacttttgggtcgcaggtaccagataattactatgaaggaaaaatgcatcaccttgggatgctgtcttttcatcattggatgtctttgt
5 cctgtttattttagcaccaaaaggcaagtcaaaatggctgtggaaatatttgaatcttggcatccagccatggctgttgggtgtatatt
tgctcctaagtgccctcattattttgtgaggccagagaggaacaccagtgaattgttggga (SEQ ID NO: 85)

MOOSE00810 ctg13284 7238060..7238539, 7247370..7247453, 7258514..7258731,
7329591..7329682, 7438551..7438609
10 RLVLA AVETTVLV LIFAVSLLGNVCALVLVARRRRRGATA CLVLNLF CADLL
FISA IPLVLA VRWTEAWLLGPVACHLLFYVMTLSGSVTILTLAAVSLERMVCIVHLQ
RGVRGPGRRARAVLLALIWGYSAVAALPLCVFFRVVPQRLPGADQVSAPLCISWDV
SFVTLNFLVPGLVVISYSKILQIRVSQQDFRLFRTLFLLMV SFFIMWSPHITILLILIQNF
KQDLVIWPSLFFWVVAFTFANSALNPILYNMTRLRVFRHRVLEIRDKLWPLTILHKFSS
15 GTSLPLGHTHTQAHTHTHAHTHLHT (SEQ ID NO: 88)

cggctggtgctggccgcgggtggagacaaccgtgctggtgctcatcttgcagtgctgctgctgggcaacgtgtgcgccttg
gtgctggtggcgccgacgacgccggcgccgactgcctgctggtactcaaccttctgcgcggacctgctctcatcagcgcta
tcctctggtgctggcggtgcgctgactgagggcctggctgctgggccccgttgcctgccacctgctctctacgtgatgccctgagc
ggcagcgctaccatcctcagcgtggccgcggcagcctggagcgcatggtgtgcatcgtgcacctgcagcgccgctgctggggctc
20 ctggcgccggggcgccggcgagtgctgctggcgctcatctggggctattcggcgctgccgctctgctctctcgtctcttccgagt
cgctccgcaacggctccccggcgccgaccaggtgagcgccccctgtgtatctcgtgggatgtctctttgtactttgaacttctgttg
ccaggactggtcattgtgatcagttactccaaaatttaccagatccgctgtgccagcaggactccggctctccgacctcttctctct
catggtctctcttctcatctgtggagccccatcatcatcacatcctctcatctgatccagaactcaagcaagacctggtcatctggc
cgctccctcttcttgggtggtggccttcacatttgaattcagccctaaacccatccttacaacatgacactcagagcttcaggcac
25 agggctcctggagattaggagacaaatttggccccgtgacaatttgcataagttcagctctggcacaagctaccattgggacatacacac
acacaggcacacacacacacatgcacacacacactgcacaca (SEQ ID NO: 87)

MOOSE01192 ctg14473 2193277..2193464, 2196762..2196915, 2197105..2197234,
2208484..2208612, 2213869..2213892, 2217011..2217047, 2219508..2219537,
30 2222803..2222949, 2223833..2223862, 2224187..2224215, 2281784..2281826,
2317525..2317642

MGSGISSESKESAKRSKELEKKLQEDAERDARTVKLLLLGAGESGK
STIVKQMKRIQGKHYSSESAAWSLSAWSNIHKSINLIHHINRTKNKNHMISSIEAEK
AFHKIQQLMLKTLNKQERETISNLWSGVNIQNLYSYTEYLIPACTTSYLNLDLDRITA
35 SGYVPNEQDVLHSRVKTTGIIETQFSFKDLHFRMFDVGGQRSEKRWIHC FEGVTCII
FCAALSAYDMVLVEDEEVNRMHESLHLFNSICNHKYFSTTSIVLFLNKKDIFQEKVT
KVHLSICFPEYTGPNTEFAGNYIKNQFLDLNLKKEDKEIYSHMTCATDTQNVKFVF
DAVTDIIKENLKDCLF (SEQ ID NO: 90)

atgggaagtgaattagttcagagagcaaggagtcagccaaaagatcaaaagaactggagaaaaagcttcaggaggatg
40 ctgagcgagatgcaagaaccgtaaagctgctactattaggagcaggagaatctgggaaaagtactattgttaacaaatgaagagaat
atacagggaaaacattatacatcggaggaatctgctgcatggagcttgagtccctggctgaacatacaaaatcaataaacttaatcc
atcacataaacagaaccaagaacaaaaaccacatgattagctcaatagaagcagaaaaaggcctccacaaaattcaacagccttgat
gtaaaaaactctcaataaacaagagagagagacgataagtaattatggtcagggggtaataccaaaaattatattacacacgaatat
ttaataccagcctgcacaacaagctacctaattgattagatagaataacagcatctgggtatgtgccaatgaacaagatgttctcattc
45 tcgagtgaanaacgactggaatcattgaaactcaattctctttaaagacttgcacttcaggatgtttgatgtagggtggacagagatctgag
agaaagaagtggattcactgcttgaaggagttacatgcatatattttgtgctgcacttagtgcttatgacatggctcctcgtggaagacga
agaagtgaatagaatgatgaagccttcacctgttaacagtatctgtaatacagaatttttaacaacctccattgtcctgttctcaa
caaaaaagatatcttaagaaaaggtaaccaagggtcatcttagtatctgcttccagaatacactgggccaatacattgaaagatga
ggaaactacatcaagaaccagtttctagacctgaatttaaaaaagaagataaggaaatttatcccatgacctgtgctactgacacc

SPGSRVILYIVFGFGAVLAVFGNLLVMISILHFKQLHSPTNFLVASLACADFLV
GVTVMPFMSMVRTVESCWYFGRSFCFTHTCCDVAFICYSSLFHLCFISIDRYIAVTDPLV
YPTKFTVSVSGICISVSWILPLMYSGAVFYTGVDGLEDSDALNCIGGCQTVVNQ
10 NWVLTDFLSFFIPTFIMILYGNIFLARRQAKKIENTERKAAKTLGVTVAFMISWLP
YSIDSLIDAFMGFITPACIYEICCWCAYYNSAMNPLIYALFYPWFRKAIKKLRKCKVF
REYENKTTRLGVVGHACNPSTLGGGGWITRSKD (SEQ ID NO: 92)

30 CYNQTLSTVLTCTIISLVGLTGNAVVLWLLGYRMRRNAVSTIYLNLAAADFLF
LSFQIIRLPLRLINISHLIRKILVSVMTFPYFTGLSMLSJASTERCLSVLWPIWYRCRRPT
HLSAVVCVLLWGLSLLFSMLEWRFCDFLFGADSSWCETSDFIPVAWLIFLCVVLVCV
SSLVLLVRILCGSRKMPLTRLYVTILLTVLVFLLCGLPFGILGALIYRMHLNLEVLYCH
VYLVCMSLSSLNSSANPIIYFFVGSFRQRQNRQNLKLVLQRALQDKPEVDKASATRS
RTRTTSTSSASTPPRPT (SEQ ID NO: 94)

45 CGKETLIPVFLILFIALVGLVGNFVLWLLGFRMRNFAFSVYVLSLAGADFLF
LCFQIINCLVYLSNFFCSISINFPSFFTVMTCAYLAGLSMLSTVSTERCLSVLWPIWYR
CRRPRHLSAVVCVLLWALSLLLSILEGKFCGFLFSDGDSGWCQTFDFITAAWLIFLFM
VLCGSSLALLVRILCGSRGLPLTRLYL TILLTVLVFLLCGLPFGIQWFLILWTWKDSDV
LFCHIHVPVSVLSSLNSSANPIYFFVGSFRKOECSLSCLSKOKSP TLLSERDFWIAVIA

-74 -

EVSRRGRRHEGFTLSFLG (SEQ ID NO: 96)

tggtggcaaggagaccctgatcccggctctcctgatcctttcattgccctggcgggctggtaggaaacgggttgctctg
gtccttgggcttccgcatgcgcaggaacgccttctctgtctacgtcctcagcctggccggggccgacttcttctctgtctccagatt
ataaattgcttgggtgacccagtaacttctctgttccatctccatcaatttccctagcttctcaccactgtgatgacctgtgcttacccttg
5 aggcctgagcatgctgagcaccgtcagcaccgagcgctgctgctgctggtgcccacatctggtatcgtgccgcccccagaca
cctgtcagcggctgtgtgtctctgttggccctgtccctactgtcgtgagcatcttgaagggaagtctgtggcttcttattagtgaig
gtgactctgtgtgtgtcagacatttgatttcatcactgcagcggtggctgattttttatcatggttctctgtgggtccagctgtgccctgtg
gtcaggatcctctgtggctccaggggctgtccactgaccaggctgtacctgacctcctgtcacagtgtggtgttctcctctgtcggc
ctgcccttggcattcagtggttctaatattatggatctggaaggattctgatgtcttatttgcataattatccagtttcagttgtcctgtcat
10 ctcttaacagcagtgccaaccccatatttacttctgtgggctcttttaggaagcaggagtgtcactctcctgtttaagcaagcagaag
tctccaccctcttctcagagagagacttctgattgcagttatgtgaagtaagccgaggaagaagacacgaggggttcacacttcc
tttttaggc (SEQ ID NO: 95)

MOOSE05740 ctg3235 274265..275065, 285148..285258

15 CYKQTLSTGLTCIVSLVALTGNAVVLWLLGCRMRRNAVSIYILNLVAADFL
FLSGHIICSPLRLINIRHPISKILSPVMTFPYFIGLSMLSAISTERCLSILWPIWYHCRPR
YLSSVMCVLLWALSLLRSILEWMFCDFLFSGANSVWCETSDFTTIAWLVLFCVVLG
SSLVLLVRILCGSRKMPLRLYVTILLTVLVFLLCGLPFGIQWALFSRIHLDWKVLFC
HVHLVSIFLSALNSSANPIYFFVGSFRQRQNRQNLKLDSMCRRTALYKTIRESYSYL
20 SREQQREDPTHDSILS (SEQ ID NO: 98)

tgctacaagcagaccctgagcttcacggggctgacgtgcacgttccctgtcgcgtgacaggaaacgcggttgctctt
ggctcctgggctgccgcatgcgcaggaacgctgtctccatctacatcctcaacctggctgcggccgacttcttctttagcgccac
attatattgttgcggttacgctcctcaataccgccatcccatctccaaaaactcagctcctgtgatgaccttccctactttaggcctaa
gcatgtgagcgccatcagcaccgagcgctgctgctcctgtggtccatctggtaccactgccgccgcccagatacctgtcatc
25 agtcatgtgtgtctgtctgtggccctgtccctgtcgggagatcctggagtggatgttctgtgacttctgttagtggtgtaattctgtt
tggtgtgaaacgtcagatttcattacaatcgctggctgtttttatgtgtgttctgtgtgggtccagcctgtgctgtgtgacaggattc
tctgtggatcccggaagatgccgctgaccaggctgtacgtgacctcctcctcacagtgtggttctcctcctgtgtgctgtcccttgg
cattcagtgggccctgtttccaggatccacctggattgaaagtcttatttgcattgtgcatctagtttccatttctgtccgctcttaaca
gcagtgccaaaccccatatttacttctgtgggtccttttaggcagcgtcaaaaataggcagaacctgaagctggacagcatgtgcagg
30 agaacggcccttataaaacccatcagatctcgtgagagtattcactatcacgagaacagcagagggaagacccaacctatgattcaat
acttcc (SEQ ID NO: 97)

MOOSE05748 ctg4256 14884996..14885118, 14904164..14905015

35 HSPHTHFLFLVLAIFSVAFMGNSVMVLLIYLDLTLHTPMYFLLSQLFLMDLM
LICSTVPKMAFNYLSGSKSISMAGCATQIFFYVSLLGSECFLLAVMSYDRYIAICHPLR
YTNLMRPKICGLMTAFSWILGSMDAIDAVATFSFSYCGSREIAHFFCDFPSLLILSCN
DTSIFEKVLFICCIVMIVFPVAIIASYARVILAVIHMGSGEGRRAFTTCSHLMVVG
MYYGAGLFMYIRPTSDRSPMQDKLVSVFYTLTPMLNPLIYSLRNKEVTRALRKVRG
40 APLERKHSDSGFSTSSRSTGCATFSLCAHLRATSSAEV (SEQ ID NO: 100)

cacagccccacccacaccttcttcttctgtgctcctggccatctttcagtgcccttcagtggaactctgtcatggttctcct
catctacctggacacccagctccacaccccatgtacttctcctcagtcacactgttctcctcatggacctcatgctcatctgtctaccgtac
ccaagatggccttaactacttgtctggcagcaagtcatttctatggctggtgtgccaacacaaatttcttctatgtatcactgttggctc
cgaatgcttctgttggctgttatgtctatgaccgctataattgccatttggccaccttaagatacacaatctcatgagacccaaa
atttgaggactatgactgccttctcctggatcctgggctctatggatgcaatcattgatgtgtagcgacatttcttcttactgtgggtc
45 tcgggaaatagccacttcttctgtgacttcccttactaactctctcatgcaatgacacatcaatatttgaagggttcttctatctgt
gtatagtaatgattgttttctgttgaatcatatcgttcttctgtcgtgatttctggctgtcattcacatgggatctggagagggtcgt
cgcaagcttttactacctgttctcctcactcatggtgtgggaatgtactatggagcaggttgttcatgtacatagggccacatctga
tcgtcctcctatgcaggacaagctggtgtgtgtattctacaccatctcactcccatgtgaatccctcatctacagcctccgcaacaag

-75-

gagggtgaccagagcactcaggaagtgagaggagccccgctggaaaggaaacattcggactccgggttcagcacctcctccagaa
gcacaggatgtgcgaccttcagccttctgtgccacctccgagccaccagctccgcagaagta (SEQ ID NO: 99)

MOOSE05757 ctg30162 475149..475607, 475650..476006, 490932..491042

5 RWELQIFFVTFSLIYGATVMGNILMVTVTCRSTLHSPLYFLLGNLSFLDMCL
STATTPKMIIDLLTDHKTISVWGCVTQMFFMHFFGGAEMTLIIMAFDRYVAICKPLH
YRTIMSHKLLKGFAILSWIIGFLHSISQIVLTMNLPFCGHNACIETYTLFVIADSG
LSFTCFILLVSYIVILVSVPKSSHGLSKALSTLSAHIVVTLFFGPCIFYVWPFSSLAS
NKT LAVFYTVITPLLNPSTYTLRNKKMQEAIKRLRFQYNSSPSKTFPQTRRRDKDYPR
10 KTRAKEFHYHQIFFIRN (SEQ ID NO: 102)

cgatgggaactcaaatcttcttctgtgacatttcctgtactacgggtgctactgtgatgggaaacattctcattatgggtcaca
gtgacatgtaggtaaccccttacttccctgtacttctccttggaaatctctcttttggacatgtgtcttccactgccacaacacccaa
gatgatcatagattgtcactgaccacaagaccatctctgtgtggggctgctgacccagatgttctcatgcacttcttgggggtgctg
agatgacttctgataatcatggccttgacaggatgtagccatagttaaaccctgcactataggacaatcatgagccacaagctgct
15 aaagggggttgatacttcatggataattggtttttacactcctaagccagatagtttaacaatgaactgccttctgtgccacaat
cttgcctgcatgaaacatacacccctggaattattgtcattgctgacagcgggctgctcttccactgttcatcctctgctgtttctac
attgtcatctggcagtgtaacaaaaaatcatcacatgggctctccaaggcgtgtccacattgtctgccacatcatgtgtgactct
gttcttggaccttgatttttctatgtttggccattcagtagttggcaagcaataaaactcttgcctgattttatacagttatcacacctta
ctgaatccgagattttataccctgagaataaagaaaatgcaagagggccataagaaaattacgggtccaataataatgtcaccagcaaa
20 acttccctcagacacgaagaagagataaagactatccagaaaacaagagctaagggaattcattaccaccaaactttttataagaa
ac (SEQ ID NO: 101)

MOOSE05798 ctg13495 208823..208941, 209823..210141, 210181..210672

25 SQDIQLLVFVLILIFYLILPGNFIIFTIRSDPGLTAPLYLFLGNLAFLDASYSFIV
APRMLVDLSEKKVISYRGCTQLFFLHFLGGGEGLLLVMMAFDRIAICRPLHCSTV
MNPRACYAMMLALWLGGFVHSIIQVVLILRLPFCGPNQLDNFFCDVRQLLMVFNSG
LMTLLCFLGLLASYAVILCHVRAASEGKNKAMSTCTTRVIIIIMFGPAIFTYMCPRF
ALPADKMVSLFHTVIFPLMNPMTYTLRNQEVKTSMKRLLIRCLVLCRLMTQTHTRSG
LRNRKFIRQEGREELPHTEGEA (SEQ ID NO: 104)

30 tctcaagatattcagctcttggcttctgtgctgacttaattttctaccttatcatcctccctggaaatttctcattattttaccataa
ggctcagacctgggctcacagccccctctattttcttgggcaacttggccttctggatgcactcactccttattgtggttccagg
atgttgggtgacttctctctgagaaaaagtaatctcctacagaggtgcatcactcagctcttttcttgcactccttggaggaggga
gggattactccttgtgtgatggccttgaccgctacatgccatctgccggcctctgcactgttcaactgtcatgaaccctagagcctgct
atgcaatgatgttggctctgtggcttgggggttttccactcattatccagggtgctcctcatcctccgttgccttttggggccaaacc
35 agctggacaacttcttctgtgatgtccgacagcttctaattggtctcaacagtggcctgatgacactcctgtgcttctggggcttctggtt
cctatgcagtcactccttgcctatgttcgttagggcagcttctgaagggaagaacaaggccatgtccacgtgcaccactgtgtcattattat
acttcttatgttggacctgtatcttcatctacatgtgccctttagggccttaccagtgacaagatggttctcttcttccacagtgatctt
tccattgatgaatcctatgattatacccttgcacaccgaagtgaaaacttccatgaagagggtattgattcgttctgtgtgtgtgccg
attaatgacacagactcacacacggagtgggttaagggaacagaaggttatttaggcaagaaggagaagagcctccccatacaga
40 gggagaagca (SEQ ID NO: 103)

MOOSE05802 ctg832 2973509..2973633, 2988359..2988723, 2988742..2989221

45 LEAAHIWISIPFCVVYLLALLNGSLLFIKTEPSLHEPMYFLCMLAVVDLVV
CSTAVPKLLSLFWFHDGEIRFETCLSLVFLIHSCSTMESGFFLAMAFDRYVAICNPLRH
SAILTRAVIGRVGLAIVLRGIALSPHSFLLRWLPYCRTHIISHTYCEIACAETKFRRAY
SLIVAFLTGVVDFILIYSYVLILHTVFQLPSKDARLKSGLTCGSHVCVILVSYTPAFFS
FLTHRFGHHVAPHFHFVANYLLVPPMVNPIYGVRTKRIWDRFLKVFRLNFQCHIFV
ITDHKRLSISSFPIKEAACC KQRFCMKLCRR (SEQ ID NO: 106)

ttggaagctgctcacatctggatctccatcccttctgtgtggtctacgttggcctactgggaaacggctctcttctgtttatc

-76-

atcaagacagagcccagcctccatgagccaatgtacctcttctatgcatgctggctgtagttgattgtgtgtgttacagctgtgcc
caaacttctcagttcttctggtccatgatggagagattcgcttgaaacctgcctctcactcgtgttctgattcacttctgtccaccatg
gaatctggccttcttctggccatggcctttgaccgatagtggccattgcaatccattaagacattcagctattctgacacgcgctgaatt
gggagagtgggcctagctattgtctcaggggcatagcacttctcagttcctcacttcttctactacgctggcttccctactgcagaaccc
5 atatcatttctcacacctactgtgagattgcctgtgctgagacaaaattccgcagagcctacagcctcattgttgccttctactggggtg
gtagactttatattgatcatttattctatgtcctcatactccacactgttccagctcccatccaaagatgcccgctcaaatctttgggcac
ctgtggctcccatgtctgtcatcttagtatcctatactccagccttctctgtttctacccacaggttgggcacccatgtggctcccat
ttcacataattgtggccaacatctatcttctgtcccacccatgggtaacccattatctatgggtaagaacaaaaggatttgggacag
gttccctaaagtgttcagggttaaattccagtgccacataattgtaactcagtgatcataaaagactcagtataatcttcttccccataaaaga
10 agcagcctgtcgaacaaaagggttcgcatgaagttatgcaggcga (SEQ ID NO: 105)

MOOSE05811 ctg15944 2627738..2628080, 2633616..2633643, 2638652..2639093,
2664854..2664991

NPENNVVLSVLFLLIYLITVLGNFWIIIIILASAQLHSPMYFFLSQLAFLDFCYSS
15 VLIPKMLVNYIAGQKVVISYHGCLLQYSFVSLFLTTECFLLAAMACDRYLA VCHPLHY
KEHRVQEPICSLISVWVISSLAFCDDSSINHFFCDTTALLALSCVDTFGTEMVSFVLG
FTLLSSLLIITVTYIIISAILRIQSAAGRQKAFSTCASHLMAVTIFYGSLIFTYLQPDNTS
SLTQAQVASVFYTTIVPMLNPLIYSLRNKDVKNALLRCSGAVSAHCKLCLLNSRHSPA
SASQVAGTTGARHHARLFFLFLVET (SEQ ID NO: 108)

20 aacctgaaatgaatgttcttctgtgctcttcttattaatctatctcattactgtcttgggcaacttttgattatcataataattc
tggttagtgcccaactccattcaccatgtacttttcttagccagttggcttcttagatttctgctatttctcagtttgattcctaaaatgtt
gggtgaattacatagcaggacagaaagtcattctctacacgggtgcctcctcagttatcttctgagctgttcttactactgaatgcttc
ctctggctgccatggcatgtatcgtggttctgctgtttgccaccacttactacaaagaacatagagtcaggagccaattagatgc
tcgctgatatctgtctgggtgataagcagtttggcgttctgtgattccagcatcaatcttttttgtgacaccacagctcttttagcactctc
25 ctgtgtagatacatcggcacagaaatgtgagcttctgttagctggattcactcttcttagctctctccttatcatcacagtcacttatca
tcattctcagccatctgaggtccagtcagcagcaggcaggcagaaggccttctccactgcgcacccacccatggctgtaact
atctttatgggtctctgattttacatttgaacctgataacacatcatcgtgaccaggcgcaggtggcatctgtattctatcagattg
tcattccatgtgaattcactcatctacagctgaggaaacaaagatgtaaaatgctcttctgagatgcagtggtgctgtcggctca
ctgcaagctctgctcctgaattcagccattctcctgctcagcctcccaagtcgtgggactacaggcggccgccaccacgcaagg
30 ctatttttttttttagtagagacg (SEQ ID NO: 107)

MOOSE05812 ctg4256 14956033..14956176, 14958553..14958878,
14958906..14959383

QSRIGLFVFTLIFLIFLMALIGNLSMILLIFLDIHLHTPMYFLLSQLSLIDLNYISTI
35 VPKMVYDFLYGNKSISFTGCGIQSFFFLTLAVAEGLLLTSMAYDRYVAICFPLHYPIRI
SKRVCVMMITGSWMISSINCAHTVYALCIPYCKSRANHFFSCTDTWVYESTVFLSS
TIFLVLPFTGIACSYGRVLLAVYRMHSAKGRNKVYSTCSTHLTVVYFYYAPFAYTYV
RARSLRSPTEDKILAVFYTLTPMLNPIIYSLRNKESFCTAKETTIRVNRQPTEWEKIFA
TYSSDKGLISRIYNELKQTYKKKT (SEQ ID NO: 110)

40 caatcaagaattggcctttctgtattcaccctcattttctcattttcctaattggctctaattggaatctatccatgattcttctatct
ttttggacatccatctccacacacctatgtatttctacttagtcagctctccctcattgacctaaattacatctccaccattgttccaaagatg
gtttatgatttctgtatggaaacagtcattctccttctcactggatgtgggattcagagtttcttctttagcttttagcagttgcagaagggt
gctcctgacatcaatggcctatgctgttatgtggccattgttcttctcctactatcccatccgataagcaaaaagagtggtgtgtgatgat
gataacaggatcttggatgataagctctatcaactctgtgtctacacagtatatgcactctgtatcccatattgcaagtcagagccatca
45 atcatttttctcctgcacagacacttgggtctatgagagcacagtggtttttagcagcaccatcttctgtgtcttcttactgggtattgcat
gttccataggccgggttctcttctgtctacccgcatgcactctgcaaaaggaggagaataaggcttattcaacctgtagcaccacaccca
ctgtgtgtacttctactatgcacccttggcttatacctatgtacgtgcaagatccctgcgacttccaaccaggagacaagattctggctgtt
tctacaccatctctaccccaatgtcaaccccatcatctacagcctgagaacaaggagagcttctgcacagcaaaagaaactacat

-77 -

cagagtgaacaggcaacctacagaatgggagaaaattttgcaacctactcatctgacaaagggtaatatccagaatctacaatgaac
tcaaacaaacttacaagaaaaaaca (SEQ ID NO: 109)

MOOSE05827 ctg4256 15055783..15055926, 15062025..15062324,
5 15062361..15062855

PSRIDLFFFLIVFIFLMALIGNLSMILLIFLDTHLHTPMYFLLSQLSLIDLNYISTI
VPKMASDFLHGNKSISFTGCGIQSFFFLALGGAEALLASMA YDRYIAICFPLHYLR
MSKRVCVLMITGWSWIGSINACAH TVVYLHIPYCRSRINHHFCDVPAMGT VFLSATI
FLVFPFIGISCSYGQVLFVYHMKSAEGRKKAYLTCSTHLTVVTFYYAPFVYTYLRP
10 RSLRSPTE DKVLA VFY TIL TPMLNPIYSLRNKESKRKKRKRKRKRKRKKERERKR
EREKEKERKERKERERKERKERKE (SEQ ID NO: 112)

ccatcaagaattgacctttcttctcattctcattgtttcatttctctgatggctctaattggaaacctgtccatgattcttctcatctt
cttggacacccatctccacacacccatgtatttcttactgagtcagctctccctcattgacctaaattacatctccaccattgttcttaagat
ggcatctgatttctgcatggaaacaagtctatctcttctactgggtgtgggattcagagtttcttcttctggcattaggagggtgcagaagc
15 actattttggcatctatggcctatgatcgttactgtatttcttcttctccactatctcatccgcatgagcaaaagagtggtgtgtctga
tgataacagggtcttgatcataggctgatcaatgcttggctcacactgtatatgtactccatattccttattgccgatccagggccatca
atcatttctctgtgatgtccagcaatgggcacagtggttttgatgtccaccatcttctcgtgttccctcattgttattcatgttctatgg
ccagggttcttctgtgtctaccacatgaaatctgcagaaggagggaagaaagcctatttgacctgcagcaccacccactactgtatgaac
ttctactatgacaccttttcttactatctacgtccaagatccctgcgatctcaacagaggacaaggttctggctgttcttaccaccatc
20 ctaccccaatgctcaacccatcatctatagcctgaggacaaggagagcaagagaaaagaaaagaaagaaagagaaaa
gaaagaaaagaaaagaaaagaaaagagagaaaagagaaaagagaaaagaaaagaaaagagaaa
aagaaaagaaaagaaaagaaaagag (SEQ ID NO: 111)

MOOSE05861 ctg15944 6729088..6729914, 6731331..6731469
25 SRELSQVLF TFLFLVYMTTLMGNFLIMVTVTCESHLHTPMYFLLRNLSILDICF
SSITAPKVLIDLLSETKTISFSGCVTQMFFHLLGGADVFSLSVMAFDYRIAISKPLHY
MTIMSRGRCTGLIVGFLGGGLVHSIAQISLLLPLPVC GPNVLDTFYCDVPQVLKLACT
DTFTLELLMISNNGLVSWFVFFLLISYTVILMMLRSHTGEGRRKAISTCTSHITVVTL
HFVPCIYVYARPFTALPTDTAISVTFTVISPLNPIYTLRNQEMNRSRHL SKKKKKR
30 KDKKKPACAKKENEVRLCHICVTVNSVQPWRNT (SEQ ID NO: 114)

tcccgagaactgagccaggctctatttaccttctgttttgggtgtacatgacaactctaattgggaaaccttctcatcatggttac
agttacctgtgaatctcaccttcatacgcccatgtacttctgtctcgcaacctgtctattcttgacatctgttcttctccatcacagctcta
aggtctctgatagatcttctatcagagacaaaaaccatctcttctcagtggtgtgtcactcaaatgttcttctccaccttctggggggagca
gacgttttcttctctctgtgatggcgtttgaccgtatagccatctccaagccctgcactatagccatcatgagtagggggcgatg
35 cacaggcctcatcgtgggttcttgggtggggggtgtcactccatagcgcagatttcttattgtccactccctgtctgtggaccc
aatgttctgacacttctactgcatgtccccaggctcctaaacttgctgcactgacaccttactctggagctcctgatgattcaaat
aatgggttagtcagttggttatttcttcttctcctatcttacacgggtcatcttgatgatgctgaggtctcacactggggaaggcaggga
ggaaagccatctccactgcacctcccatcacctgggtgacctgcatcttgccctgcactatgtctatgccggcccttactg
ccctcccccagacactgcatctctgtcaccttactgtcatctcccttctgctcaatctataatttacacgctgaggaatcaggaaatg
40 aacaacagatcaagacacttgcataaaaaaaaagaaaagaaaagacaaaaagaaaccagcatgcgcaaaagaaaagaaatgagg
tgagattgtgccacattgtgtaacagtgaactcagtcagccatggcgtaataca (SEQ ID NO: 113)

MOOSE05863 ctg15907 31055206..31056122, 31068740..31068797
45 WQQQQVLLFALFLCLYL TGLFGNLLILLAIGSDHCLHTPMYFFLANLSLVDLC
LPSATVPKMLLNQQTQTISYPGCLAQM YFCMMFANMDNFLTVMA YDRYVAICH
PLHYSTIMALRLCASLVAAPWVIAILNPLLHTLMM AHLHFCSDNVIHHFCDINSLLP
LSCSDTSLNQLSVLATVGLIFVPSVCILVSYILIVSAVMKVPSAQGKLKAFSTCGSHL
ALVILFYGAITGVYMSPLSNHSTEKDSAASVIFMVVAPVLNPFYSLRNNE LKGT LKK
TLSRPGAVAHACNPSTLGGRGGNTWTEAKYVHRE VHMIMKR (SEQ ID NO: 116)

-78 -

tggaacaacagcaggtgctactctttgcacttttctgtgtctctatttaacagggtgtttggaaacttactcatcttgctggc
cattggctcggatcactgccttcacacacccatgtatttcttcttgcgaatctgcttggtagaccttgccttccctcagccacagtccc
caagatgctactgaacatccaaacccaaacccaaacccatctctatcccggctgcttggctcagatgtatttctgtatgatgtttgccaat
atggacaattttctctacagtgatggcatatgaccgttacgtggccatctgtcaccctttacattactccaccattatggccctgcgcctc
5 tgtgctctcttggtagctgcaccttgggtcattgccatttgaacccctcttgcacactcttatgatggccatctgcacttctgctctgata
atgttatccaccatttctctgtgatatcaactctctcctcctctgtcttgcgacaccagctttaatcagttgagtggtctg
gctacgggtggggctgacttcttgggtaccttcagtggtatcttgcgtatctatactctcatgtttctgctgtgatgaaagtccttctgcc
aaggaaaactcaaggcttctctaccttggatctcacccttgccttggctcatttcttatggagcaatcacaggggtctatatgagccct
tatccaatcacttactgaaaaagactcagccgcacagtcattttatggttgtagcaccgtgttgatccattcattacagtttaagaaa
10 caatgaactgaagggtacttataaaaagaccctaagccgaccggcgcggtggctcagcctgtaatcccagcactttgggaggcc
gaggcggaatacatgacagaagcaaatatgtcatagagaagtacataatgatcaagaga (SEQ ID NO: 115)

MOOSE05908 ctg15944 2316216..2316693, 2331854..2331911, 2333360..2333372,
2338898..2339200, 2350975..2351085
15 YPEIQVPLFLVFLFVYTVTVVGNLGMIIIRLNSKLHTIMCFFLSHLSLTDFCFST
VVTPKLLENLVVEYRTISFSGCIMQFCFACIFGVTTETFMLAAMAYDRFVAVCKPLLY
TTIMSQKLCALLVAGSYTWGIVCSLILTYFLLDLSFCESTFINNFISFNSTLYYKIYHQT
FSCICEHFLPMCTLLILTSYVFIFVTVLKIRSVSGRHKAFTSWASHLTSITIFHGTLFLY
CVPNSKNSRQTVKVASVFYTVVNPMLNPLIYSLRNKDVKDAFWKLIHTQSRRRQSL
20 RRLSLRNSHLMTTISIEGVTHSTILELCSS (SEQ ID NO: 118)

taccagaaatccaggttccactcttctggtttcttctgctctacacagtcactgtagtggggaactgggcatgataataat
catcagactcaattcaaaactccatacaatcatgtgcttttctttagtcactgtccttgacagacttctgttttccactgtagtacacctaa
actgttggagaacttgggtgtggaatacagaaccatctcttcttctggttgcacatgcaattttgttttgccttgcattttggagtacagaaa
ctttcatgttagcagcgatggcttatgaccgttttggcgagtttgaaccccttgcgtataccactattatgtctcagaagctctgtgctctt
25 ctgttggctgggtcctatatacatgggggatagtgtgctcctgatactacataatttcttctgacttatcgttttgaatctaccctcataaat
aattttatctcttcaactccaccctataactataaaatataccacaaaccccttctctgtatatgtgagcacttctgccaatgtgtacactactg
atcatcctcacttctctatgttttcattttgtgactgtactaaaaatccgttctgttagtgggcgccacaaagccttctccacctgggctccc
acctgacttctatccactcttccatgggaccatccttttcttactgtgtacccaactccaaaaactctggcaaacagtcaaaagtggcc
tctgtatttatacagttgtcaaccccatgtgaacctctgactacagcctaaggaataaagacgtgaaggatgcttcttggaaagtaaat
30 acatacacaatacaaggaggcagagcttgaggaggtccttgagaaattccatttaataaccaccagcattgaagaaggagtcacc
cacaccagtaccattctggagctctgctcatcc (SEQ ID NO: 117)

MOOSE05917 ctg30162 1982852..1982944, 1985177..1985529, 1985575..1986055
PLRLRTLFFVFFFLIYILTQLGNLLILITVWADPRLHARPMYIFLGVLVIDMSIS
35 SIIVPRLMMNFTLGVKPIPFGGCVAQLYFYHFLGSTQCFLYTLMA YDRYLAICQPLRY
PVLMTAKLSALLVAGAWMAGSIHGALQAILTFRLPYCGPNQVDYFFFNELVT FVDIG
VVVASCFSLLLSYIQIIQAILRIHTADGRRRAFSTCGAHVTVVTVVYVPCAFIYLRPET
NSPLDGAAALVPTAITPFLNPLIYTLRNQEVKLALKRMLRSPRTPSEHFGRPRRVDHL
RSGVRDQPNQHGETASLPKI (SEQ ID NO: 120)

ccactcaggctaaggacactcttttctgttcttttctaatctacatcctgactcagctgggaaacctgcttatttaactctgt
ctgggcagaccgaaggctccatgcccgcctcatgacatcttcttgggttctctcagtcattgatagacatctctccatcatgtgcc
tcgcctcatgatgaacttactttaggtgtcaaacccatccatttgggtgctgtgtcacttatttctatcacttctgggcagcacc
cagtgcttctctacacccatgaatggcctatgacaggtacctggcaatatgtcagccctgcgctaccctgtgctcatgactgctaagctg
agcgcttctgttggctggagcctggatggcaggtacatccatggggctctccaggccatcctaaccttccgctgcctactgtgg
45 gcccaatcaggtggattacttcttcaacgagctgtgtgacgttttagacattgggggtgtgttgcaggtgtcttctcctgatctctc
ctctacatacagatcattcaggccatcttgagaatcacacagctgatggcgggcgccgggcttttcaacttggagcccatgtaa
ccgtgtcaccgtgtactatgtgcccgtgtccttactctgagggcctgaaaccaacagccccctggatggggcagctgccttagtc
cccacggccatcactcttctcaaccccttatctacactctcggaaccaagggtgaagctggccctgaaaagaatgctcagaa

gcccagaactccgagtgagcactttgggaggccaaggcgggtggatcacctgaggtcgggaggttcgagaccagcctaaccaacat
ggagaaactgcatctttacaaaaata (SEQ ID NO: 119)

MOOSE06051 ctg15064 38069881..38070569, 38071866..38071965,
5 38089519..38089577, 38100385..38100508

DPIVTPHLISLYFIVLIGGLVGVISILFLLVKMNTRSVTTMAVINLVVHVSFLL
TVPFRLTYLIKKTWMFGLPFCKFVSAMLIHMYLTFLFYVVLVTRYLIFFKCKDKVE
FYRKLHAVAASAGMWTLVIVVPLVVSRYGIHEEYNEEHCFKFHKELAYTYVKIIN
YMIVIFVIAVAVILLVFQVFIIMLMVQKLHSLLSHQEFWAQLKNLFFIGVILVCFLPY
10 QPHCVMFPSLPCPCVFIVQLPLLSENMRCLVFCSLIHFLLYIFIVHNMRYSYMNFVS
CPLPACNAV MQCSGSNLEQSRKQYSQCSRPGTARGKL (SEQ ID NO: 122)

gacccctatagtgacaccccacttaacagcctctacttcacatgcttattggcgggctggtgggtgtcatttcattctttcctc
ctggtgaaaatgaacacccggctcagtgaccaccatggcggctattaacttggtggtggtccacagcgttttctgctgacagtgccatttc
gcttgacctacatcatcaagaagacttggatgtttgggctgcccttctgcaaatttgtagtgccatgctgcacatccacatgtacctcac
15 gttcctattctatgtggtgatcctggtcaccagatacctcatcttctcaagtgcagaaagacaaagtggaaattctacagaaaactgcatgctg
tggctgccagtgctggcatgtggacgctggtgattgtcattgtggtacccctggtgtctcccggtatggaatccatgaggaatataatg
aggagcactgttttaattcacaaagagcttgctacacatatgtgaaatcatcaactatatgatagtcattttgtcatagccgttgctgt
gattctgttggtctccaggcttcatcattatgttgatggtgcagaagctacgccactcttactatcccaccaggagttctgggctcagct
gaaaaactattttataggggctacccctgtttgttcttccctaccagccccattgtgtgatttccctccctgtgcatgtgttttcatt
20 gttaactcccacttctaagtgaacatgcgggtgtttgttctgtcctgtttgattcatttttattgtatatattatagtgacacatgag
gtattcatacatgtataacttcgctcagctgtccttggcagcatgtaatgcagtgatgcaatgctctggtagtaattggaacaatccaggaa
gcaatatctcagtggtcaaggcccggcactgcccgggggaaatta (SEQ ID NO: 121)

MOOSE07369 ctg15361 27381078..27381945, 27422885..27422949
25 HVLNFQELFFLVFGVSTLIVVFLMVLILTLVGNLIVIVSISHFKQLHTPTNWLI
HSMATVDFLLGCLVMPYSMVRS AEHCWYFGEVFCKIHTSTDIMLSSASIFHLSFISID
RYYA VCDPLRYKAKMNILVICVMIFISWSVPAVFAFGMIFLELNFKGAEEIYYKHVH
CRGGCSVFFSKISGVLTFMTSFYIPGSIMLCVYYRIYLIAKEQARLISDANQKLQIGLE
MKNGISQSKERKAVKTLGIVMGVFLICWCPFFICTVMDPFLHYIIPPTLNDVLIWFGY
30 LNSTFNPMVYAFFYPWFRKALKM (SEQ ID NO: 124)

catgttcttaattccaagaactcttttcttcttctcggagtccaactattgtgttttttaattggtgctcataattctgaccac
actcgttggcaatctgatagttattgtttctatatcacacticaaacaacttcataccccaacaaattggctcattcattccatggccactgtg
gactttcttctggggtgtctggtcatgccttacagtatggtgagatctgctgagcactgttggtatttggagaagcttctgtaaaattcaca
caagcacccgacattatgctgagctcagcctcatttccattgtcttcatctccattgaccgctactatgctgtgtgtgatccactgagata
35 taagccaagatgaatatcttggttattgtgtgatgacttcattagttggagtgctcctgctgttttgcatttgaatgatcttctggagct
aaacttcaaaggcgtgaagagatatattacaacatgttcactgcagaggaggtgctctgtcttcttagcaaaatatctgggtactg
accttatgacttcttttatatacctggatctattatgttatgtgtctattacagaatatattctatcgttaagaacaggcaagattaattagtg
atgccaatcagaagctccaaattggattggaaatgaaaaatggaattcacaaagcaaaagaaaggaaagctgtgaagacattggggat
tgtgatgggagtttcttaatatgctggtgcccttcttctgtacagtcattggacctttcttactacatttccaccttgaatgat
40 gtattgatttggttgctacttgaactctacatttaacaaatggttatgcattttctatccttggtttagaaaagcactgaagatg (SEQ
ID NO: 123)

Table III

	ctg14797_MOOSE00162.xml	Angiotensin
	ctg16465_MOOSE00638.xml	Class A Orphan
5	ctg16008_MOOSE00693.xml	Class A Orphan
	ctg16282_MOOSE00717.xml	Class A Orphan
	ctg16228_MOOSE00721.xml	Class A Orphan
	ctg877_MOOSE00741.xml	Class A Orphan
	ctg15378_MOOSE00766.xml	Class A Orphan
10	ctg78_MOOSE00772.xml	Class A Orphan
	ctg15540_MOOSE00775.xml	Class A Orphan
	ctg16537_MOOSE00779.xml	Class A Orphan
	ctg30162_MOOSE00804.xml	Class A Orphan
	ctg15378_MOOSE00814.xml	Class A Orphan
15	ctg15907_MOOSE00818.xml	Class A Orphan
	ctg14294_MOOSE00822.xml	Class A Orphan
	ctg15968_MOOSE00826.xml	Class A Orphan
	ctg14145_MOOSE00829.xml	Class A Orphan
	ctg14667_MOOSE00838.xml	Class A Orphan
20	ctg14333_MOOSE00841.xml	Class A Orphan
	ctg15064_MOOSE00843.xml	Class A Orphan
	ctg15944_MOOSE00846.xml	Class A Orphan
	ctg14333_MOOSE00855.xml	Class A Orphan
	ctg16279_MOOSE00861.xml	Class A Orphan
25	ctg18147_MOOSE00872.xml	Class A Orphan
	ctg15944_MOOSE00880.xml	Class A Orphan
	ctg15944_MOOSE00882.xml	Class A Orphan
	ctg15296_MOOSE00886.xml	Class A Orphan
	ctg17659_MOOSE00899.xml	Class A Orphan
30	ctg18867_MOOSE00930.xml	Class A Orphan
	ctg3235_MOOSE00941.xml	Class A Orphan
	ctg15907_MOOSE00981.xml	Class A Orphan
	ctg17802_MOOSE00994.xml	Class A Orphan
	ctg12634_MOOSE01139.xml	Class B Secretin Receptor
35	ctg15998_MOOSE01146.xml	Class B Secretin Receptor
	ctg12559_MOOSE01148.xml	Class B Secretin Receptor
	ctg15361_MOOSE01165.xml	Class C Metabotropic Glutamate Receptor
	ctg14779_MOOSE01172.xml	Class C Metabotropic Glutamate Receptor
	ctg17658_MOOSE01176.xml	Class C Metabotropic Glutamate Receptor
40	ctg13655_MOOSE01371.xml	Frizzled related GPCR
	ctg17341_MOOSE01451.xml	Gonadotropin receptor
	ctg37_MOOSE01609.xml	Lysosphingolipid Receptor
	ctg15037_MOOSE02359.xml	Mollusc Rhodopsine-like GPCR
45	ctg15907_MOOSE02360.xml	Mollusc Rhodopsine-like GPCR
	ctg12376_MOOSE02352.xml	unclassified GPCRs
	ctg13067_MOOSE01169.xml	Class C Metabotropic glutamate pheromone
	ctg13284_MOOSE00810.xml	Class A Orphan other
50	ctg14473_MOOSE01192.xml	Class Y G proteins

5	ctg15361_MOOSE05621.xml	Class A Orphan GPCRs
	ctg3235_MOOSE05712.xml	Class A Orphan GPCRs
	ctg3235_MOOSE05732.xml	Class A Orphan GPCRs
	ctg3235_MOOSE05740.xml	Class A Orphan GPCRs
	ctg4256_MOOSE05748.xml	Class A Orphan GPCRs
	ctg30162_MOOSE05757.xml	Class A Orphan GPCRs
	ctg13495_MOOSE05798.xml	Class A Orphan GPCRs
	ctg832_MOOSE05802.xml	Class A Orphan GPCRs
10	ctg15944_MOOSE05811.xml	Class A Orphan GPCRs
	ctg4256_MOOSE05812.xml	Class A Orphan GPCRs
	ctg4256_MOOSE05827.xml	Class A Orphan GPCRs
	ctg15944_MOOSE05861.xml	Class A Orphan GPCRs
	ctg15907_MOOSE05863.xml	Class A Orphan GPCRs
15	ctg15944_MOOSE05908.xml	Class A Orphan GPCRs
	ctg30162_MOOSE05917.xml	Class A Orphan GPCRs
	ctg15064_MOOSE06051.xml	Class A Orphan GPCRs
	ctg15361_MOOSE07369.xml	Serotonin Gated Ion Channel Receptor

Table IV

OTHER GPCRs

RA (Rheumatoid Arthritis)

Locus2	Marker:D6S265	Lod:3	CM RANGE of one LOD drop: 6
30	MOOSE05863	Class A Orphan other	DISTANCE: -1.97 Mb
	MOOSE06011	Class A Orphan other	DISTANCE: 8.000 Mb

COPD (Chronic Obstructive Pulmonary Disease)

Locus4	Marker:D19S884	Lod:2.9	CM RANGE of one LOD drop: 20
40	MOOSE05784	Class A Orphan other	DISTANCE: 0.959 Mb

Asthma

45	Locus1	Marker:D3S3698	Lod:3.8	CM RANGE of one LOD drop: 15
		MOOSE06049	Class A Orphan other	

-82 -

DISTANCE: -12.8 Mb

#####

NIDDM (Non-insulin dep. Diabetes)

5 Locus4 Marker:D17S785 Lod:3.2 CM RANGE of one LOD drop: 10

MOOSE05814 Class A Orphan other
10 DISTANCE: -2.47 Mb

#####

Obesity

15 Locus4 Marker:D14S283 Lod:3.2 CM RANGE of one LOD drop: 12

MOOSE05757 Class A Orphan other
DISTANCE: -2.15 MbMOOSE05917 Class A Orphan other
20 DISTANCE: -0.65 Mb

Locus5 Marker:SHGC-1089 Lod:4.6 CM RANGE of one LOD drop: 20

MOOSE05798 Class A Orphan other
25 DISTANCE: -9.98 Mb

#####

Bipolar (Genomewide scan only)

30 Locus1 Marker:D1S434 Lod:3.3 CM RANGE of one LOD drop: 5

MOOSE06105 Class C Metabotropic glutamate pheromone
DISTANCE: -10.6 MbMOOSE06101 Class C Metabotropic glutamate pheromone
35 DISTANCE: -6.55 Mb

Locus3 Marker:D16S3041 Lod:2.5 CM RANGE of one LOD drop:25

MOOSE05745 Class A Orphan other
40 DISTANCE: 0.725 Mb

#####

OP (Osteoporosis)

Locus5 Marker:D20S194 Lod:5.05 CM RANGE of one LOD drop: 5

45 MOOSE05705 Class A Orphan other
DISTANCE: -0.86 Mb

#####

Alzheimer's Disease

5 Locus1 Marker:D13S785 Lod:4.06 CM RANGE of one LOD drop: 7
 MOOSE05635 Class A Orphan other
 DISTANCE: 4.447 Mb

#####

10 **AMD (Age-related Macular Degeneration)**

15 Locus2 Marker:D3S3631 Lod:2.91 CM RANGE of one LOD drop:20
 MOOSE06049 Class A Orphan other
 DISTANCE: -10.5 Mb

#####

MI (Myocardial Infarction)

20 Locus1 Marker:D6S282 Lod:1.99 CM RANGE of one LOD drop:19
 MOOSE06011 Class A Orphan other
 DISTANCE: -7.07 Mb
 25 MOOSE07334 Rhodopsin Other
 DISTANCE: 5.065 Mb
 Locus5 Marker:D13S167 Lod:2.38 CM RANGE of one LOD drop:25
 30 MOOSE05635 Class A Orphan other
 DISTANCE: 2.102 Mb

#####

Schizophrenia

35 Locus1 Marker:D3S1315 Lod:2.73 CM RANGE of one LOD drop:21
 MOOSE06103 Class C Metabotropic glutamate pheromone
 DISTANCE: 5.243 Mb

#####

Osteoarthritis

45 Locus3 Marker:D16S401 Lod:2.7 CM RANGE of one LOD drop: 6
 MOOSE05745 Class A Orphan other
 DISTANCE: -4.43 Mb

#####

Longevity

5	Locus1	Marker:D9S1826	Lod:2.30	CM RANGE of one LOD drop:15
		MOOSE06089	Class B Secretin like DISTANCE: -12.5 Mb	
10	Locus2	Marker:D11S987	Lod:2.07	CM RANGE of one LOD drop:12
		MOOSE05934	Class A Orphan other DISTANCE: -14.1 Mb	
15		MOOSE05861	Class A Orphan other DISTANCE: -12.4 Mb	
		MOOSE05761	Class A Orphan other DISTANCE: -0.76 Mb	
		MOOSE05781	Class A Orphan other DISTANCE: 0.884 Mb	
		MOOSE05938	Class A Orphan other DISTANCE: 1.364 Mb	
20				

#####

Psoriasis

25	Locus1	Marker:GDB:182383	Lod:10.61	CM RANGE of one LOD drop: 2
		MOOSE05863	Class A Orphan other	
			DISTANCE: -3.49 Mb	
		MOOSE06011	Class A Orphan other	
30			DISTANCE: 6.481 Mb	
	Locus2	Marker:D7S669	Lod:1.81	CM RANGE of one LOD drop:20
		MOOSE06127	Class Y G proteins	
35			DISTANCE: 2.208 Mb	

CLAIMS

What is claimed is:

- 5 1. An isolated nucleic acid molecule comprising a G protein-coupled receptor (GPCR) gene, wherein the GPCR gene has a nucleotide sequence selected from the group of nucleic acid sequences as shown in Tables I and II, or the complements of the group of nucleic acid sequences as shown in Tables I and II.
- 10 2. A nucleic acid encoding a polypeptide, wherein the polypeptide has an amino acid sequence selected from the group consisting of the group of amino acid sequences as shown in Tables I and II.
- 15 3. An isolated nucleic acid molecule which hybridizes under high stringency conditions to a nucleotide sequence selected from the group of nucleic acid sequences as shown in Tables I and II, or the complements of the group of nucleic acid sequences as shown in Tables I and II.
- 20 4. An isolated nucleic molecule that hybridizes under high stringency conditions to a nucleotide sequence encoding an amino acid sequence selected from the group consisting of the group of amino acid sequences as shown in Tables I and II.
- 25 5. A method for assaying for the presence of a first nucleic acid molecule in a sample, comprising contacting said sample with a second nucleic acid molecule, where the second nucleic acid molecule comprises a nucleotide sequence selected from the group of nucleic acid sequences as shown in Tables I and II, and hybridizes to the first nucleic acid under high stringency
30 conditions.
6. A vector comprising an isolated nucleic acid molecule selected from the group consisting of:
 - 35 (a) the nucleic acid sequences as shown in Tables I and II;
 - (b) the complement of one of the nucleic acid sequences are shown in Tables I and II; or
 - (c) a nucleic acid encoding an amino acid molecule as shown in Tables I and II;

wherein the nucleic acid molecule is operably linked to a regulatory sequence.

- 5 7. A recombinant host cell comprising the vector of Claim 6.
8. A method for producing a polypeptide encoded by an isolated nucleic acid molecule, comprising culturing the recombinant host cell of Claim 7 under conditions suitable for expression of the nucleic acid molecule.
- 10 9. An isolated polypeptide encoded by the nucleotide sequence of the group of nucleic acid sequences as shown in Tables I and II, or the complements thereof.
- 15 10. The isolated polypeptide of Claim 9, wherein the polypeptide has an amino acid sequence selected from the group consisting of the group of amino acid sequences as shown in Tables I and II.
- 20 11. An isolated polypeptide comprising an amino acid sequence, wherein the amino acid sequence is greater than about 95% identical to an amino acid sequence selected from the group consisting of the group of amino acid sequences as shown in Tables I and II.
- 25 12. A fusion protein comprising an isolated polypeptide of Claim 2.
- 30 13. A fusion protein comprising an isolated polypeptide of Claim 11.
14. An antibody, or an antigen-binding fragment thereof, which selectively binds to a polypeptide of Claim 2, or to a fragment or variant of said amino acid sequence.
- 35 15. An antibody, or an antigen-binding fragment thereof, which selectively binds to a polypeptide of Claim 11, or to a fragment or variant of said amino acid sequence.
16. A method of assaying for the presence of a polypeptide encoded by an isolated nucleic acid molecule according to Claim 1 in a sample, the method comprising contacting the sample with an antibody which specifically binds to the encoded polypeptide.

17. A method of identifying an agent which alters the activity of a GPCR, the method comprising:
- (a) contacting a polypeptide of Claim 9, or a derivative or fragment thereof, with an agent to be tested;
 - (b) assessing the level of activity of the polypeptide or derivative or fragment thereof; and
 - (c) comparing the level of activity with a level of activity of the polypeptide or active derivative or fragment thereof in the absence of the agent;
- wherein if the level of activity of the polypeptide or derivative or fragment thereof in the presence of the agent differs, by an amount that is statistically significant, from the level in the absence of the agent, then the agent is an agent that alters activity of a GPCR.
18. An agent that alters the activity of a GPCR, identifiable according to the method of Claim 17.
19. The agent of Claim 18, where the agent is selected from the group consisting of: a GPCR gene binding agent; a G-protein; a peptidomimetic; a fusion protein; a prodrug; an antibody; and a ribozyme.
20. A method of altering activity of a polypeptide encoded by a GPCR gene, comprising contacting the polypeptide with an agent of Claim 19.
21. A method of identifying an agent which alters interaction of the polypeptide of Claim 9 with a GPCR gene binding agent, comprising:
- a) contacting the polypeptide or a derivative or fragment thereof, and the binding agent, with an agent to be tested;
 - b) assessing the interaction of the polypeptide or derivative or fragment thereof with the binding agent; and
 - c) comparing the level of interaction with a level of interaction of the polypeptide or derivative or fragment thereof with the binding agent in the absence of the agent,
- wherein if the level of interaction of the polypeptide or derivative or fragment thereof in the presence of the agent differs by an amount that is statistically significant, from the level of interaction in the absence of the

agent, then the agent is an agent that alters interaction of the polypeptide with the binding agent.

- 5 22. An agent that alters interaction of a GPCR polypeptide with a GPCR binding agent, identifiable according to the method of Claim 21.
- 10 23. An agent that alters interaction of a GPCR polypeptide with a GPCR binding agent, selected from the group consisting of: a second GPCR binding agent; a G-protein; a peptidomimetic; a fusion protein; a prodrug; an antibody; and a ribozyme.
- 15 24. A method of altering interaction of a GPCR polypeptide with a GPCR binding agent, comprising contacting the GPCR gene polypeptide and/or the GPCR gene binding agent with an agent of Claim 23.
- 20 25. A method of identifying an agent that alters expression of a GPCR gene, comprising the steps of:
a) contacting a solution containing a nucleic acid comprising the promoter region of the GPCR gene operably linked to a reporter gene with an agent to be tested;
b) assessing the level of expression of the reporter gene; and
c) comparing the level of expression with a level of expression of the reporter gene in the absence of the agent,
25 wherein if the level of expression of the reporter gene in the presence of the agent differs, by an amount that is statistically significant, from the level of expression in the absence of the agent, then the agent is an agent that alters expression of the GPCR gene.
- 30 26. An agent that alters expression of the GPCR gene, identifiable according to the method of Claim 25.
- 35 27. A method of identifying an agent that alters expression of a GPCR gene, comprising the steps of:
a) contacting a solution containing a nucleic acid of Claim 1 or a derivative or fragment thereof with an agent to be tested;
b) assessing expression of the nucleic acid, derivative or fragment; and
c) comparing expression with expression of the nucleic acid, derivative or fragment in the absence of the agent,

wherein if expression of the nucleotide, derivative or fragment in the presence of the agent differs, by an amount that is statistically significant, from the expression in the absence of the agent, then the agent is an agent that alters expression of the GPCR gene.

5

28. The method of Claim 27, wherein the expression of the nucleotide, derivative or fragment in the presence of the agent comprises expression of one or more splicing variant(s) that differ in kind or in quantity from the expression of one or more splicing variant(s) the absence of the agent.

10

29. An agent that alters expression of a GPCR gene, identifiable according to the method of Claim 27.

15

30. An agent that alters expression of a GPCR gene, selected from the group consisting of: antisense nucleic acid to a GPCR gene; a GPCR gene polypeptide; a GPCR gene receptor; a GPCR gene binding agent; a peptidomimetic; a fusion protein; a prodrug thereof; an antibody; and a ribozyme.

20

31. A method of altering expression of a GPCR gene, comprising contacting a cell containing a GPCR gene with an agent of Claim 30.

25

32. A method of identifying a polypeptide which interacts with a GPCR gene polypeptide, comprising employing a yeast two-hybrid system using a first vector which comprises a nucleic acid encoding a DNA binding domain and a GPCR gene polypeptide, splicing variant, or a fragment or derivative thereof, and a second vector which comprises a nucleic acid encoding a transcription activation domain and a nucleic acid encoding a test polypeptide, wherein if transcriptional activation occurs in the yeast two-hybrid system, the test polypeptide is a polypeptide which interacts with a GPCR polypeptide.

30

35

33. A GPCR gene therapeutic agent selected from the group consisting of: a GPCR gene or fragment or derivative thereof; a polypeptide encoded by a GPCR gene; a G-protein; a GPCR gene binding agent; a peptidomimetic; a fusion protein; a prodrug; an antibody; an agent that alters GPCR gene expression; an agent that alters activity of a polypeptide encoded by a GPCR gene; an agent that alters posttranscriptional processing of a polypeptide

encoded by a GPCR gene; an agent that alters interaction of a GPCR gene with a GPCR gene binding agent; an agent that alters transcription of splicing variants encoded by a GPCR gene; and a ribozyme.

- 5 34. A pharmaceutical composition comprising a GPCR gene therapeutic agent of Claim 33.
35. The pharmaceutical composition of Claim 34, wherein the GPCR gene
10 therapeutic agent is an isolated nucleic acid molecule comprising a GPCR gene or fragment or derivative thereof.
36. The pharmaceutical composition of Claim 34, wherein the GPCR gene therapeutic agent is a polypeptide encoded by the GPCR gene.
- 15 37. A method of treating a disease or condition associated with a GPCR in an individual, comprising administering a GPCR gene therapeutic agent to the individual, in a therapeutically effective amount.
38. The method of Claim 37, wherein the GPCR gene therapeutic agent is a
20 GPCR gene agonist.
39. The method of Claim 38 wherein the GPCR gene therapeutic agent is a GPCR gene antagonist.
- 25 40. A transgenic animal comprising a nucleic acid selected from the group consisting of: an exogenous GPCR gene and a nucleic acid encoding a GPCR gene polypeptide.
41. A method for assaying a sample for the presence of a GPCR gene nucleic acid,
30 comprising:
- a) contacting said sample with a nucleic acid comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the sequence of said GPCR gene nucleic acid under conditions appropriate for hybridization, and
- 35 b) assessing whether hybridization has occurred between a GPCR gene nucleic acid and said nucleic acid comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the sequence of said GPCR gene nucleic acid;

wherein if hybridization has occurred, a GPCR gene is present in the nucleic acid.

- 5 42. The method of Claim 41, wherein said nucleic acid comprising a contiguous nucleotide sequence is completely complementary to a part of the sequence of said GPCR gene nucleic acid.
- 10 43. The method of Claim 41, comprising amplification of at least part of said GPCR gene nucleic acid.
- 15 44. The method of Claim 41, wherein said contiguous nucleotide sequence is 100 or fewer nucleotides in length and is either: a) at least 80% identical to a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II; b) at least 80% identical to the complement of a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II; or c) capable of selectively hybridizing to said GPCR gene nucleic acid.
- 20 45. A reagent for assaying a sample for the presence of a GPCR gene nucleic acid, said reagent comprising a nucleic acid comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the nucleotide sequence of said GPCR gene nucleic acid.
- 25 46. The reagent of Claim 45, wherein the nucleic acid comprises a contiguous nucleotide sequence that is completely complementary to a part of the nucleotide sequence of said GPCR gene nucleic acid.
- 30 47. A reagent kit for assaying a sample for the presence of a GPCR gene nucleic acid, comprising in separate containers:
- a) one or more labeled nucleic acids comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the nucleotide sequence of said GPCR gene nucleic acid, and
- b) reagents for detection of said label.
- 35 48. The reagent kit of Claim 47, wherein the labeled nucleic acid comprises a contiguous nucleotide sequences which is completely complementary to a part of the nucleotide sequence of said GPCR gene nucleic acid.

49. A reagent kit for assaying a sample for the presence of a GPCR gene nucleic acid, comprising one or more nucleic acids comprising a contiguous nucleotide sequence which is at least partially complementary to a part of the nucleotide sequence of said GPCR gene nucleic acid, and which is capable of acting as a primer for said GPCR gene nucleic acid when maintained under conditions for primer extension.
50. The use of a nucleic acid which is 100 or fewer nucleotides in length and which is either: a) at least 80% identical to a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II; b) at least 80% identical to the complement of a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II; or c) capable of selectively hybridizing to said GPCR gene nucleic acid, for assaying a sample for the presence of a GPCR gene nucleic acid.
51. The use of a first nucleic acid which is 100 or fewer nucleotides in length and which is either:
- a) at least 80% identical to a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II;
 - b) at least 80% identical to the complement of a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II; or
 - c) capable of selectively hybridizing to said GPCR gene nucleic acid; for assaying a sample for the presence of a GPCR gene nucleic acid that has at least one nucleotide difference from the first nucleic acid.

52. The use of a nucleic acid which is 100 or fewer nucleotides in length and which is either:

 - a) at least 80% identical to a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II;
 - b) at least 80% identical to the complement of a contiguous sequence of nucleotides in one of the nucleic acid sequences as shown in Tables I and II; or
 - c) capable of selectively hybridizing to said GPCR gene nucleic acid; for diagnosing a susceptibility to a disease or condition associated with a GPCR.

1/160

SEQUENCE LISTING

<110> deCODE genetics ehf.
Martinez, Roger Alfonso Moraga
Sigurdsson, Gunnar Thor

<120> Nucleic Acids Encoding G Protein-Coupled
Receptors

<130> 2345.2028003 PCT

<150> US 60/301,095
<151> 2001-06-26

<150> US 60/333,185
<151> 2001-11-06

<160> 124

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 1080
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(1080)

<400> 1

atg att cag aca atc agt aat gtt agt gaa gca gta gtc caa atc ata	48
Met Ile Gln Thr Ile Ser Asn Val Ser Glu Ala Val Val Gln Ile Ile	
1 5 10 15	
gct tct caa atg cca gat gga gac aat aca gat ttt cga tac ttt att	96
Ala Ser Gln Met Pro Asp Gly Asp Asn Thr Asp Phe Arg Tyr Phe Ile	
20 25 30	
tat gca gtg aca tac act gtc att ctt gtg cca ggt ctc ata ggg aat	144
Tyr Ala Val Thr Tyr Thr Val Ile Leu Val Pro Gly Leu Ile Gly Asn	
35 40 45	
ata tta gcc ctg tgg gta ttc tat ggt tat atg aaa gaa aca aaa cga	192
Ile Leu Ala Leu Trp Val Phe Tyr Gly Tyr Met Lys Glu Thr Lys Arg	
50 55 60	
gct gtg ata ttt atg ata aac tta gcc att gct gac tta cta caa gtt	240
Ala Val Ile Phe Met Ile Asn Leu Ala Ile Ala Asp Leu Leu Gln Val	
65 70 75 80	
ctt tcc ttg cca ctg agg atc ttc tac tac ttg aat cat gac tgg cca	288
Leu Ser Leu Pro Leu Arg Ile Phe Tyr Tyr Leu Asn His Asp Trp Pro	
85 90 95	
ttt ggg cct ggt ctc tgc atg ttc tgt ttc tac ctg aag tat gtc aac	336
Phe Gly Pro Gly Leu Cys Met Phe Cys Phe Tyr Leu Lys Tyr Val Asn	
100 105 110	
atg tat gca agc atc tac ttc ttg gtc tgc atc agt gtg cga cga ttt	384
Met Tyr Ala Ser Ile Tyr Phe Leu Val Cys Ile Ser Val Arg Arg Phe	
115 120 125	

2/160

tgg ttt ctc atg tac ccc ttt cgc ttc cat gac tgc aaa cag aaa tat	432
Trp Phe Leu Met Tyr Pro Phe Arg Phe His Asp Cys Lys Gln Lys Tyr	
130 135 140	
gac ctg tac atc agc att gct ggc tgg ctg atc atc tgc ctt gcc tgt	480
Asp Leu Tyr Ile Ser Ile Ala Gly Trp Leu Ile Ile Cys Leu Ala Cys	
145 150 155 160	
gta ctc ttt cca ctc ctc aga acc agt gat gat acc tct ggc aat agg	528
Val Leu Phe Pro Leu Leu Arg Thr Ser Asp Asp Thr Ser Gly Asn Arg	
165 170 175	
acc aaa tgc ttt gtg gat ctt cct acc agg aat gtc aac ctg gcc cag	576
Thr Lys Cys Phe Val Asp Leu Pro Thr Arg Asn Val Asn Leu Ala Gln	
180 185 190	
tcc gtt gtt atg atg acc att ggc gag ttg att ggg ttt gta act ccg	624
Ser Val Val Met Met Thr Ile Gly Glu Leu Ile Gly Phe Val Thr Pro	
195 200 205	
ctt ctg att gtc cta tat tgt acc tgg aag acg gtt tta tca ctg caa	672
Leu Leu Ile Val Leu Tyr Cys Thr Trp Lys Thr Val Leu Ser Leu Gln	
210 215 220	
gat aaa tat ccc atg gcc caa gat ctt gga gag aaa cag aaa gcc ttg	720
Asp Lys Tyr Pro Met Ala Gln Asp Leu Gly Glu Lys Gln Lys Ala Leu	
225 230 235 240	
aag atg att cta acc tgt gca ggg gta ttc cta att tgc ttt gca cct	768
Lys Met Ile Leu Thr Cys Ala Gly Val Phe Leu Ile Cys Phe Ala Pro	
245 250 255	
tat cat ttc agt ttt cct tta gat ttc ctg gtg aag tcc aat gaa att	816
Tyr His Phe Ser Phe Pro Leu Asp Phe Leu Val Lys Ser Asn Glu Ile	
260 265 270	
aaa agc tgc cta gcc aga agg gtg att cta ata ttt cat tct gtg gca	864
Lys Ser Cys Leu Ala Arg Arg Val Ile Leu Ile Phe His Ser Val Ala	
275 280 285	
ttg tgt ctt gct agt ctg aat tca tgt ctt gac cca gtc ata tac tac	912
Leu Cys Leu Ala Ser Leu Asn Ser Cys Leu Asp Pro Val Ile Tyr Tyr	
290 295 300	
ttt tcc act aat gaa ttt aaa aag tcc ttc ctg gaa caa ttc agg gtg	960
Phe Ser Thr Asn Glu Phe Lys Lys Ser Phe Leu Glu Gln Phe Arg Val	
305 310 315 320	
att gca tcc aca caa gag gat cac tcc tca gca gaa gaa aga att agt	1008
Ile Ala Ser Thr Gln Glu Asp His Ser Ser Ala Glu Glu Arg Ile Ser	
325 330 335	
gag ctt gaa gac agg cta ctt gaa aat ata cag tca gag gag aca aaa	1056
Glu Leu Glu Asp Arg Leu Leu Glu Asn Ile Gln Ser Glu Glu Thr Lys	
340 345 350	
gaa aaa aga ata aaa aac aat gaa	1080
Glu Lys Arg Ile Lys Asn Asn Glu	
355 360	

3/160

<211> 360

<212> PRT

<213> Homo sapiens

<400> 2

```

Met Ile Gln Thr Ile Ser Asn Val Ser Glu Ala Val Val Gln Ile Ile
 1           5           10           15
Ala Ser Gln Met Pro Asp Gly Asp Asn Thr Asp Phe Arg Tyr Phe Ile
      20           25           30
Tyr Ala Val Thr Tyr Thr Val Ile Leu Val Pro Gly Leu Ile Gly Asn
      35           40           45
Ile Leu Ala Leu Trp Val Phe Tyr Gly Tyr Met Lys Glu Thr Lys Arg
      50           55           60
Ala Val Ile Phe Met Ile Asn Leu Ala Ile Ala Asp Leu Leu Gln Val
65           70           75           80
Leu Ser Leu Pro Leu Arg Ile Phe Tyr Tyr Leu Asn His Asp Trp Pro
      85           90           95
Phe Gly Pro Gly Leu Cys Met Phe Cys Phe Tyr Leu Lys Tyr Val Asn
      100          105          110
Met Tyr Ala Ser Ile Tyr Phe Leu Val Cys Ile Ser Val Arg Arg Phe
      115          120          125
Trp Phe Leu Met Tyr Pro Phe Arg Phe His Asp Cys Lys Gln Lys Tyr
      130          135          140
Asp Leu Tyr Ile Ser Ile Ala Gly Trp Leu Ile Ile Cys Leu Ala Cys
145          150          155          160
Val Leu Phe Pro Leu Leu Arg Thr Ser Asp Asp Thr Ser Gly Asn Arg
      165          170          175
Thr Lys Cys Phe Val Asp Leu Pro Thr Arg Asn Val Asn Leu Ala Gln
      180          185          190
Ser Val Val Met Met Thr Ile Gly Glu Leu Ile Gly Phe Val Thr Pro
      195          200          205
Leu Leu Ile Val Leu Tyr Cys Thr Trp Lys Thr Val Leu Ser Leu Gln
      210          215          220
Asp Lys Tyr Pro Met Ala Gln Asp Leu Gly Glu Lys Gln Lys Ala Leu
225          230          235          240
Lys Met Ile Leu Thr Cys Ala Gly Val Phe Leu Ile Cys Phe Ala Pro
      245          250          255
Tyr His Phe Ser Phe Pro Leu Asp Phe Leu Val Lys Ser Asn Glu Ile
      260          265          270
Lys Ser Cys Leu Ala Arg Arg Val Ile Leu Ile Phe His Ser Val Ala
      275          280          285
Leu Cys Leu Ala Ser Leu Asn Ser Cys Leu Asp Pro Val Ile Tyr Tyr
      290          295          300
Phe Ser Thr Asn Glu Phe Lys Lys Ser Phe Leu Glu Gln Phe Arg Val
305          310          315          320
Ile Ala Ser Thr Gln Glu Asp His Ser Ser Ala Glu Glu Arg Ile Ser
      325          330          335
Glu Leu Glu Asp Arg Leu Leu Glu Asn Ile Gln Ser Glu Glu Thr Lys
      340          345          350
Glu Lys Arg Ile Lys Asn Asn Glu
      355          360

```

<210> 3

<211> 990

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(990)

<400> 3

4/160

aaa agc gtc ctg ctc tac acg ctc tcc ttc att tac att ttc atc ttc	48
Lys Ser Val Leu Leu Tyr Thr Leu Ser Phe Ile Tyr Ile Phe Ile Phe	
1 5 10 15	
gtc atc ggc atg att gcc aac tcc gtg gtg gtc tgg gtg aat atc cag	96
Val Ile Gly Met Ile Ala Asn Ser Val Val Val Trp Val Asn Ile Gln	
20 25 30	
gcc aag acc aca ggc tat gac acg cac tgc tac atc ttg aac ctg gcc	144
Ala Lys Thr Thr Gly Tyr Asp Thr His Cys Tyr Ile Leu Asn Leu Ala	
35 40 45	
att gcc gac ctg tgg gtt gtc ctc acc atc cca gtc tgg gtg gtc agt	192
Ile Ala Asp Leu Trp Val Val Leu Thr Ile Pro Val Trp Val Val Ser	
50 55 60	
ctc gtg cag cac aac cag tgg ccc atg ggc gag ctc acg tgc aaa gtc	240
Leu Val Gln His Asn Gln Trp Pro Met Gly Glu Leu Thr Cys Lys Val	
65 70 75 80	
aca cac ctc atc ttc tcc atc aac ctc ttc ggc agc att ttc ttc ctc	288
Thr His Leu Ile Phe Ser Ile Asn Leu Phe Gly Ser Ile Phe Phe Leu	
85 90 95	
acg tgc atg agc gtg gac cgc tac ctc tcc atc acc tac ttc acc aac	336
Thr Cys Met Ser Val Asp Arg Tyr Leu Ser Ile Thr Tyr Phe Thr Asn	
100 105 110	
acc ccc agc agc agg aag aag atg gta cgc cgt gtc gtc tgc atc ctg	384
Thr Pro Ser Ser Arg Lys Lys Met Val Arg Arg Val Val Cys Ile Leu	
115 120 125	
gtg tgg ctg ctg gcc ttc tgc gtg tct ctg cct gac acc tac tac ctg	432
Val Trp Leu Leu Ala Phe Cys Val Ser Leu Pro Asp Thr Tyr Tyr Leu	
130 135 140	
aag acc gtc acg tct gcg tcc aac aat gag acc tac tgc cgg tcc ttc	480
Lys Thr Val Thr Ser Ala Ser Asn Asn Glu Thr Tyr Cys Arg Ser Phe	
145 150 155 160	
tac ccc gag cac agc atc aag gag tgg ctg atc ggc atg gag ctg gtc	528
Tyr Pro Glu His Ser Ile Lys Glu Trp Leu Ile Gly Met Glu Leu Val	
165 170 175	
tcc gtt gtc ttg ggc ttt gcc gtt ccc ttc tcc att atc gct gtc ttc	576
Ser Val Val Leu Gly Phe Ala Val Pro Phe Ser Ile Ala Val Phe	
180 185 190	
tac ttc ctg ctg gcc aga gcc atc tgc gcg tcc agt gac cag gag aag	624
Tyr Phe Leu Leu Ala Arg Ala Ile Ser Ala Ser Ser Asp Gln Glu Lys	
195 200 205	
cac agc agc cgg aag atc atc ttc tcc tac gtg gtg gtc ttc ctt gtc	672
His Ser Ser Arg Lys Ile Ile Phe Ser Tyr Val Val Val Phe Leu Val	
210 215 220	
tgc tgg ctg ccc tac cac gtg gcg gtg ctg ctg gac atc ttc tcc atc	720
Cys Trp Leu Pro Tyr His Val Ala Val Leu Leu Asp Ile Phe Ser Ile	
225 230 235 240	
ctg cac tac atc cct ttc acc tgc cgg ctg gag cac gcc ctc ttc acg	768
Leu His Tyr Ile Pro Phe Thr Cys Arg Leu Glu His Ala Leu Phe Thr	

5/160

245										250					255					
gcc	ctg	cat	gtc	aca	cag	tgc	ctg	tcg	ctg	gtg	cac	tgc	tgc	gtc	aac	816				
Ala	Leu	His	Val	Thr	Gln	Cys	Leu	Ser	Leu	Val	His	Cys	Cys	Val	Asn					
			260					265					270							
cct	gtc	ctc	tac	agc	ttc	atc	aat	cgc	aac	tac	agg	tac	gag	ctg	atg	864				
Pro	Val	Leu	Tyr	Ser	Phe	Ile	Asn	Arg	Asn	Tyr	Arg	Tyr	Glu	Leu	Met					
		275					280				285									
aag	gcc	ttc	atc	ttc	aag	tac	tcg	gcc	aaa	aca	ggg	ctc	acc	aag	ctc	912				
Lys	Ala	Phe	Ile	Phe	Lys	Tyr	Ser	Ala	Lys	Thr	Gly	Leu	Thr	Lys	Leu					
	290					295					300									
atc	gat	gcc	tcc	aga	gca	cac	acg	cgc	atg	cac	aca	cac	aca	cat	gca	960				
Ile	Asp	Ala	Ser	Arg	Ala	His	Thr	Arg	Met	His	Thr	His	Thr	His	Ala					
305					310					315					320					
cac	atg	cac	aca	cac	ata	cat	tct	ctt	tct							990				
His	Met	His	Thr	His	Ile	His	Ser	Leu	Ser											
				325				330												

<210> 4

<211> 330

<212> PRT

<213> Homo sapiens

<400> 4

Lys	Ser	Val	Leu	Leu	Tyr	Thr	Leu	Ser	Phe	Ile	Tyr	Ile	Phe	Ile	Phe	
1				5					10					15		
Val	Ile	Gly	Met	Ile	Ala	Asn	Ser	Val	Val	Val	Trp	Val	Asn	Ile	Gln	
			20					25					30			
Ala	Lys	Thr	Thr	Gly	Tyr	Asp	Thr	His	Cys	Tyr	Ile	Leu	Asn	Leu	Ala	
		35					40					45				
Ile	Ala	Asp	Leu	Trp	Val	Val	Leu	Thr	Ile	Pro	Val	Trp	Val	Val	Ser	
	50					55				60						
Leu	Val	Gln	His	Asn	Gln	Trp	Pro	Met	Gly	Glu	Leu	Thr	Cys	Lys	Val	
65					70					75					80	
Thr	His	Leu	Ile	Phe	Ser	Ile	Asn	Leu	Phe	Gly	Ser	Ile	Phe	Phe	Leu	
				85					90					95		
Thr	Cys	Met	Ser	Val	Asp	Arg	Tyr	Leu	Ser	Ile	Thr	Tyr	Phe	Thr	Asn	
		100						105					110			
Thr	Pro	Ser	Ser	Arg	Lys	Lys	Met	Val	Arg	Arg	Val	Val	Cys	Ile	Leu	
		115					120					125				
Val	Trp	Leu	Leu	Ala	Phe	Cys	Val	Ser	Leu	Pro	Asp	Thr	Tyr	Tyr	Leu	
	130					135					140					
Lys	Thr	Val	Thr	Ser	Ala	Ser	Asn	Asn	Glu	Thr	Tyr	Cys	Arg	Ser	Phe	
145					150					155					160	
Tyr	Pro	Glu	His	Ser	Ile	Lys	Glu	Trp	Leu	Ile	Gly	Met	Glu	Leu	Val	
			165						170					175		
Ser	Val	Val	Leu	Gly	Phe	Ala	Val	Pro	Phe	Ser	Ile	Ile	Ala	Val	Phe	
		180						185					190			
Tyr	Phe	Leu	Leu	Ala	Arg	Ala	Ile	Ser	Ala	Ser	Ser	Asp	Gln	Glu	Lys	
		195					200					205				
His	Ser	Ser	Arg	Lys	Ile	Ile	Phe	Ser	Tyr	Val	Val	Val	Phe	Leu	Val	
	210					215					220					
Cys	Trp	Leu	Pro	Tyr	His	Val	Ala	Val	Leu	Leu	Asp	Ile	Phe	Ser	Ile	
225					230					235					240	
Leu	His	Tyr	Ile	Pro	Phe	Thr	Cys	Arg	Leu	Glu	His	Ala	Leu	Phe	Thr	
				245					250				255			
Ala	Leu	His	Val	Thr	Gln	Cys	Leu	Ser	Leu	Val	His	Cys	Cys	Val	Asn	

6/160

```

      260      265      270
Pro Val Leu Tyr Ser Phe Ile Asn Arg Asn Tyr Arg Tyr Glu Leu Met
      275      280      285
Lys Ala Phe Ile Phe Lys Tyr Ser Ala Lys Thr Gly Leu Thr Lys Leu
      290      295      300
Ile Asp Ala Ser Arg Ala His Thr Arg Met His Thr His Thr His Ala
      305      310      315      320
His Met His Thr His Ile His Ser Leu Ser
      325      330

```

<210> 5
 <211> 990
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(990)

```

<400> 5
atc cca ctc aag atg cac tac ctc cct gtt att tat ggc att atc ttc 48
Ile Pro Leu Lys Met His Tyr Leu Pro Val Ile Tyr Gly Ile Ile Phe
  1          5          10          15

ctc gtg gga ttt cca ggc aat gca gta gtg ata tcc act tac att ttc 96
Leu Val Gly Phe Pro Gly Asn Ala Val Val Ile Ser Thr Tyr Ile Phe
      20          25          30

aaa atg aga cct tgg aag agc agc acc atc att atg ctg aac ctg gcc 144
Lys Met Arg Pro Trp Lys Ser Ser Thr Ile Ile Met Leu Asn Leu Ala
      35          40          45

tgc aca gat ctg ctg tat ctg acc agc ctc ccc ttc ctg att cac tac 192
Cys Thr Asp Leu Leu Tyr Leu Thr Ser Leu Pro Phe Leu Ile His Tyr
      50          55          60

tat gcc agt ggc gaa aac tgg atc ttt gga gat ttc atg tgt aag ttt 240
Tyr Ala Ser Gly Glu Asn Trp Ile Phe Gly Asp Phe Met Cys Lys Phe
      65          70          75          80

atc cgc ttc agc ttc cat ttc aac ctg tat agc agc atc ctc ttc ctc 288
Ile Arg Phe Ser Phe His Phe Asn Leu Tyr Ser Ser Ile Leu Phe Leu
      85          90          95

acc tgt ttc agc atc ttc cgc tac tgt gtg atc att cac cca atg agc 336
Thr Cys Phe Ser Ile Phe Arg Tyr Cys Val Ile Ile His Pro Met Ser
      100          105          110

tgc ttt tcc att cac aaa act cga tgt gca gtt gta gcc tgt gct gtg 384
Cys Phe Ser Ile His Lys Thr Arg Cys Ala Val Val Ala Cys Ala Val
      115          120          125

gtg tgg atc att tca ctg gta gct gtc att ccg atg acc ttc ttg atc 432
Val Trp Ile Ile Ser Leu Val Ala Val Ile Pro Met Thr Phe Leu Ile
      130          135          140

aca tca acc aac agg acc aac aga tca gcc tgt ctc gac ctc acc agt 480
Thr Ser Thr Asn Arg Thr Asn Arg Ser Ala Cys Leu Asp Leu Thr Ser
      145          150          155          160

```

7/160

tcg gat gaa ctc aat act att aag tgg tac aac ctg att ttg act gca 528
 Ser Asp Glu Leu Asn Thr Ile Lys Trp Tyr Asn Leu Ile Leu Thr Ala
 165 170 175

act act ttc tgc ctc ccc ttg gtg ata gtg aca ctt tgc tat acc acg 576
 Thr Thr Phe Cys Leu Pro Leu Val Ile Val Thr Leu Cys Tyr Thr Thr
 180 185 190

att atc cac act ctg acc cat gga ctg caa act gac agc tgc ctt aag 624
 Ile Ile His Thr Leu Thr His Gly Leu Gln Thr Asp Ser Cys Leu Lys
 195 200 205

cag aaa gca cga agg cta acc att ctg cta ctc ctt gca ttt tac gta 672
 Gln Lys Ala Arg Arg Leu Thr Ile Leu Leu Leu Ala Phe Tyr Val
 210 215 220

tgt ttt tta ccc ttc cat atc ttg agg gtc att cgg atc gaa tct cgc 720
 Cys Phe Leu Pro Phe His Ile Leu Arg Val Ile Arg Ile Glu Ser Arg
 225 230 235 240

ctg ctt tca atc agt tgt tcc att gag aat cag atc cat gaa gct tac 768
 Leu Leu Ser Ile Ser Cys Ser Ile Glu Asn Gln Ile His Glu Ala Tyr
 245 250 255

atc gtt tct aga cca tta gct gct ctg aac acc ttt ggt aac ctg tta 816
 Ile Val Ser Arg Pro Leu Ala Ala Leu Asn Thr Phe Gly Asn Leu Leu
 260 265 270

cta tat gtg gtg gtc agc gac aac ttt cag cag gct gtc tgc tca aca 864
 Leu Tyr Val Val Val Ser Asp Asn Phe Gln Gln Ala Val Cys Ser Thr
 275 280 285

gtg aga tgc aaa gta agc ggg aac ctt gag caa gca aag aaa att atg 912
 Val Arg Cys Lys Val Ser Gly Asn Leu Glu Gln Ala Lys Lys Ile Met
 290 295 300

gta tca tct tca tca tca tca cat tat cat cat cat cat cat cat 960
 Val Ser Ser Ser Ser Ser Ser His Tyr His His His His His His
 305 310 315 320

cac cat tta cat cca gac agc cag aaa ata 990
 His His Leu His Pro Asp Ser Gln Lys Ile
 325 330

<210> 6

<211> 330

<212> PRT

<213> Homo sapiens

<400> 6

Ile Pro Leu Lys Met His Tyr Leu Pro Val Ile Tyr Gly Ile Ile Phe
 1 5 10 15
 Leu Val Gly Phe Pro Gly Asn Ala Val Val Ile Ser Thr Tyr Ile Phe
 20 25 30
 Lys Met Arg Pro Trp Lys Ser Ser Thr Ile Ile Met Leu Asn Leu Ala
 35 40 45

Cys Thr Asp Leu Leu Tyr Leu Thr Ser Leu Pro Phe Leu Ile His Tyr
 50 55 60
 Tyr Ala Ser Gly Glu Asn Trp Ile Phe Gly Asp Phe Met Cys Lys Phe
 65 70 75 80
 Ile Arg Phe Ser Phe His Phe Asn Leu Tyr Ser Ser Ile Leu Phe Leu

8/160

				85					90					95		
Thr	Cys	Phe	Ser	Ile	Phe	Arg	Tyr	Cys	Val	Ile	Ile	His	Pro	Met	Ser	
			100					105					110			
Cys	Phe	Ser	Ile	His	Lys	Thr	Arg	Cys	Ala	Val	Val	Ala	Cys	Ala	Val	
		115					120					125				
Val	Trp	Ile	Ile	Ser	Leu	Val	Ala	Val	Ile	Pro	Met	Thr	Phe	Leu	Ile	
	130					135					140					
Thr	Ser	Thr	Asn	Arg	Thr	Asn	Arg	Ser	Ala	Cys	Leu	Asp	Leu	Thr	Ser	
145					150					155					160	
Ser	Asp	Glu	Leu	Asn	Thr	Ile	Lys	Trp	Tyr	Asn	Leu	Ile	Leu	Thr	Ala	
			165						170						175	
Thr	Thr	Phe	Cys	Leu	Pro	Leu	Val	Ile	Val	Thr	Leu	Cys	Tyr	Thr	Thr	
		180						185					190			
Ile	Ile	His	Thr	Leu	Thr	His	Gly	Leu	Gln	Thr	Asp	Ser	Cys	Leu	Lys	
	195						200					205				
Gln	Lys	Ala	Arg	Arg	Leu	Thr	Ile	Leu	Leu	Leu	Leu	Ala	Phe	Tyr	Val	
	210					215					220					
Cys	Phe	Leu	Pro	Phe	His	Ile	Leu	Arg	Val	Ile	Arg	Ile	Glu	Ser	Arg	
225				230						235					240	
Leu	Leu	Ser	Ile	Ser	Cys	Ser	Ile	Glu	Asn	Gln	Ile	His	Glu	Ala	Tyr	
			245						250					255		
Ile	Val	Ser	Arg	Pro	Leu	Ala	Ala	Leu	Asn	Thr	Phe	Gly	Asn	Leu	Leu	
		260						265					270			
Leu	Tyr	Val	Val	Val	Ser	Asp	Asn	Phe	Gln	Gln	Ala	Val	Cys	Ser	Thr	
	275					280						285				
Val	Arg	Cys	Lys	Val	Ser	Gly	Asn	Leu	Glu	Gln	Ala	Lys	Lys	Ile	Met	
	290					295					300					
Val	Ser	Ser	Ser	Ser	Ser	Ser	His	Tyr	His	His	His	His	His	His	His	
305				310						315					320	
His	His	Leu	His	Pro	Asp	Ser	Gln	Lys	Ile							
			325						330							

```
<210> 7
<211> 990
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> CDS
<222> (1) ... (990)
```

<400> 7																	
ttc	cta	gcc	ctg	agg	ctc	atg	gtt	gcc	ctg	gcc	tat	ggg	ctt	gtg	ggg	48	
Phe	Leu	Ala	Leu	Arg	Leu	Met	Val	Ala	Leu	Ala	Tyr	Gly	Leu	Val	Gly		
1				5					10					15			
gcc	att	ggc	ttg	ctg	gga	aat	ttg	gcg	gtg	ctg	tgg	gta	ctg	agt	aac	96	
Ala	Ile	Gly	Leu	Leu	Gly	Asn	Leu	Ala	Val	Leu	Trp	Val	Leu	Ser	Asn		
			20					25					30				
tgt	gcc	cgg	aga	gcc	cct	ggc	cca	cct	tca	gac	acc	ttc	gtc	ttc	aac	144	
Cys	Ala	Arg	Arg	Ala	Pro	Gly	Pro	Pro	Ser	Asp	Thr	Phe	Val	Phe	Asn		
		35					40					45					
ctg	gct	ctg	gcg	gac	ctg	gga	ctg	gca	ctc	act	ctc	ccc	ttt	tgg	gca	192	
Leu	Ala	Leu	Ala	Asp	Leu	Gly	Leu	Ala	Leu	Thr	Leu	Pro	Phe	Trp	Ala		
	50					55					60						
gcc	gag	tgc	gca	ctg	gac	ttt	cac	tgg	ccc	ttc	gga	ggg	gcc	ctc	tgc	240	
Ala	Glu	Ser	Ala	Leu	Asp	Phe	His	Trp	Pro	Phe	Gly	Gly	Ala	Leu	Cys		

9/160

65	70	75	80	
aag atg gtt ctg acg gcc act gtc ctc aac gtc tat gcc agc atc ttc				288
Lys Met Val Leu Thr 85	Ala Thr Val Leu 90	Tyr Ala Ser Ile 95	Phe	
ctc atc aca gcg ctg agc gtt gct cgc tac tgg gtg gtg gcc atg gct				336
Leu Ile Thr Ala Leu Ser Val Ala Arg Tyr Trp Val Val Ala Met Ala	100	105	110	
gcg ggg cca ggc acc cac ctc tca ctc ttc tgg gcc cga ata gcc acc				384
Ala Gly Pro Gly Thr His Leu Ser Leu Phe Trp Ala Arg Ile Ala Thr	115	120	125	
ctg gca gtg tgg gcg gcg gct gcc ctg gtg acg gtg ccc aca gct gtc				432
Leu Ala Val Trp Ala Ala Ala Leu Val Thr 130	135	140		
ttc ggg gtg gag ggt gag gtg tgt ggt gtg cgc ctt tgc ctg ctg cgt				480
Phe Gly Val Glu Gly Glu Val Cys Gly Val Arg Leu Cys Leu Leu Arg	145	150	155	160
ttc ccc agc agg tac tgg ctg ggg gcc tac cag ctg cag agg gtg gtg				528
Phe Pro Ser Arg Tyr Trp Leu Gly Ala Tyr Gln Leu Gln Arg Val Val	165	170	175	
ctg gct ttc atg gtg ccc ttg ggc gtc atc acc acc agc tac ctg ctg				576
Leu Ala Phe Met Val Pro Leu Gly Val Ile Thr Thr Ser Tyr Leu Leu	180	185	190	
ctg ctg gcc ttc ctg cag cgg cgg caa cgg cgg cgg cag gac agc agg				624
Leu Leu Ala Phe Leu Gln Arg Arg Gln Arg Arg Arg Gln Asp Ser Arg	195	200	205	
gtc gtg gcc cgc tct gtc cgc atc ctg gtg gct tcc ttc ttc ctc tgc				672
Val Val Ala Arg Ser Val Arg Ile Leu Val Ala Ser Phe Phe Leu Cys	210	215	220	
tgg ttt ccc aac cat gtg gtc act ctc tgg ggt gtc ctg gtg aag ttt				720
Trp Phe Pro Asn His Val Val Thr Leu Trp Gly Val Leu Val Lys Phe	225	230	235	240
gac ctg gtg ccc tgg aac agt act ttc tat act atc cag acg tat gtc				768
Asp Leu Val Pro Trp Asn Ser Thr Phe Tyr Thr Ile Gln Thr Tyr Val	245	250	255	
ttc cct gtc act act tgc ttg gca cac agc aat agc tgc ctc aac cct				816
Phe Pro Val Thr Thr Cys Leu Ala His Ser Asn Ser Cys Leu Asn Pro	260	265	270	
gtg ctg tac tgt ctc ctg agg cgg gag ccc cgg cag gct ctg gca ggc				864
Val Leu Tyr Cys Leu Leu Arg Arg Glu Pro Arg Gln Ala Leu Ala Gly	275	280	285	
acc ttc agg gat ctg cgg gcg gcc agc tgc ctt cga gcc tct tcg gcc				912
Thr Phe Arg Asp Leu Arg Ala Ala Ser Cys Leu Arg Ala Ser Ser Ala	290	295	300	
tca cgc tcc agc agt gcc cgg gcc tgc tca ctc tcc cgg agc cgg gcc				960
Ser Arg Ser Ser Ser Ala Arg Ala Cys Ser Leu Ser Arg Ser Arg Ala	305	310	315	320

10/160

tcc agg ctg cca gct tcg gtt gcc cgt tct
 Ser Arg Leu Pro Ala Ser Val Ala Arg Ser
 325 330

990

<210> 8
 <211> 330
 <212> PRT
 <213> Homo sapiens

<400> 8
 Phe Leu Ala Leu Arg Leu Met Val Ala Leu Ala Tyr Gly Leu Val Gly
 1 5 10 15
 Ala Ile Gly Leu Gly Asn Leu Ala Val Leu Trp Val Leu Ser Asn
 20 25 30
 Cys Ala Arg Arg Ala Pro Gly Pro Pro Ser Asp Thr Phe Val Phe Asn
 35 40 45
 Leu Ala Leu Ala Asp Leu Gly Leu Ala Leu Thr Leu Pro Phe Trp Ala
 50 55 60
 Ala Glu Ser Ala Leu Asp Phe His Trp Pro Phe Gly Gly Ala Leu Cys
 65 70 75 80
 Lys Met Val Leu Thr Ala Thr Val Leu Asn Val Tyr Ala Ser Ile Phe
 85 90 95
 Leu Ile Thr Ala Leu Ser Val Ala Arg Tyr Trp Val Val Ala Met Ala
 100 105 110
 Ala Gly Pro Gly Thr His Leu Ser Leu Phe Trp Ala Arg Ile Ala Thr
 115 120 125
 Leu Ala Val Trp Ala Ala Ala Ala Leu Val Thr Val Pro Thr Ala Val
 130 135 140
 Phe Gly Val Glu Gly Glu Val Cys Gly Val Arg Leu Cys Leu Leu Arg
 145 150 155 160
 Phe Pro Ser Arg Tyr Trp Leu Gly Ala Tyr Gln Leu Gln Arg Val Val
 165 170 175
 Leu Ala Phe Met Val Pro Leu Gly Val Ile Thr Thr Ser Tyr Leu Leu
 180 185 190
 Leu Leu Ala Phe Leu Gln Arg Arg Gln Arg Arg Arg Gln Asp Ser Arg
 195 200 205
 Val Val Ala Arg Ser Val Arg Ile Leu Val Ala Ser Phe Phe Leu Cys
 210 215 220
 Trp Phe Pro Asn His Val Val Thr Leu Trp Gly Val Leu Val Lys Phe
 225 230 235 240
 Asp Leu Val Pro Trp Asn Ser Thr Phe Tyr Thr Ile Gln Thr Tyr Val
 245 250 255
 Phe Pro Val Thr Thr Cys Leu Ala His Ser Asn Ser Cys Leu Asn Pro
 260 265 270
 Val Leu Tyr Cys Leu Leu Arg Arg Glu Pro Arg Gln Ala Leu Ala Gly
 275 280 285
 Thr Phe Arg Asp Leu Arg Ala Ala Ser Cys Leu Arg Ala Ser Ser Ala
 290 295 300
 Ser Arg Ser Ser Ser Ala Arg Ala Cys Ser Leu Ser Arg Ser Arg Ala
 305 310 315 320
 Ser Arg Leu Pro Ala Ser Val Ala Arg Ser
 325 330

<210> 9
 <211> 969
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

11/160

<222> (1)...(969)

<400> 9

cgg gcc gtg gac gcc tgg ctc gtg ccg ctc ttc ttc gcg gcg ctg atg	48
Arg Ala Val Asp Ala Trp Leu Val Pro Leu Phe Phe Ala Ala Leu Met	
1 5 10 15	
ctg ctg ggc ctg gtg ggg aac tcg ctg gtc atc tac gtc atc tgc cgc	96
Leu Leu Gly Leu Val Gly Asn Ser Leu Val Ile Tyr Val Ile Cys Arg	
20 25 30	
cac aag ccg atg cgg acc gtg acc aac ttc tac atc gcc aac ctg gcg	144
His Lys Pro Met Arg Thr Val Thr Asn Phe Tyr Ile Ala Asn Leu Ala	
35 40 45	
gcc acg gac gtg acc ttc ctc ctg tgc tgc gtc ccc ttc acg gcc ctg	192
Ala Thr Asp Val Thr Phe Leu Leu Cys Cys Val Pro Phe Thr Ala Leu	
50 55 60	
ctg tac ccg ctg ccc ggc tgg gtg ctg ggc gac ttc atg tgc aag ttc	240
Leu Tyr Pro Leu Pro Gly Trp Val Leu Gly Asp Phe Met Cys Lys Phe	
65 70 75 80	
gtc aac tac atc cag cag gtc tcg gtg cag gcc acg tgt gcc act ctg	288
Val Asn Tyr Ile Gln Gln Val Ser Val Gln Ala Thr Cys Ala Thr Leu	
85 90 95	
acc gcc atg agt gtg gac cgc tgg tac gtg acg gtg ttc ccg ttg cgc	336
Thr Ala Met Ser Val Asp Arg Trp Tyr Val Thr Val Phe Pro Leu Arg	
100 105 110	
gcc ctg cac cgc cgc acg ccc cgc ctg gcg ctg gct gtc agc ctc agc	384
Ala Leu His Arg Arg Thr Pro Arg Leu Ala Leu Ala Val Ser Leu Ser	
115 120 125	
atc tgg gta ggc tct gcg gcg gtg tct gcg ccg gtg ctc gcc ctg cac	432
Ile Trp Val Gly Ser Ala Ala Val Ser Ala Pro Val Leu Ala Leu His	
130 135 140	
cgc ctg tca ccc ggg ccg cgc gcc tac tgc agt gag gcc ttc ccc agc	480
Arg Leu Ser Pro Gly Pro Arg Ala Tyr Cys Ser Glu Ala Phe Pro Ser	
145 150 155 160	
cgc gcc ctg gag cgc gcc ttc gca ctg tac aac ctg ctg gcg ctg tac	528
Arg Ala Leu Glu Arg Ala Phe Ala Leu Tyr Asn Leu Leu Ala Leu Tyr	
165 170 175	
ctg ctg ccg ctg ctc gcc acc tgc gcc tgc tat gcg gcc atg ctg cgc	576
Leu Leu Pro Leu Leu Ala Thr Cys Ala Cys Tyr Ala Ala Met Leu Arg	
180 185 190	
cac ctg ggc cgg gtc gcc cgc gca ggc gcc gtg ccg gcc aag gtc tgc	624
His Leu Gly Arg Val Ala Arg Ala Gly Ala Val Arg Ala Lys Val Ser	
195 200 205	
cgg ctg gtg gcg gcc gtg gtc ctg ctc ttc gcc gcc tgc tgg ggc ccc	672
Arg Leu Val Ala Ala Val Val Leu Leu Phe Ala Ala Cys Trp Gly Pro	
210 215 220	
atc cag ctg ttc ctg gtg ctg cag gcg ctg ggc ccc gcg ggc tcc tgg	720
Ile Gln Leu Phe Leu Val Leu Gln Ala Leu Gly Pro Ala Gly Ser Trp	
225 230 235 240	

12/160

cac cca cgc agc tac gcc gcc tac gcg ctt aag acc tgg gct cac tgc 768
 His Pro Arg Ser Tyr Ala Ala Tyr Ala Leu Lys Thr Trp Ala His Cys
 245 250 255
 atg tcc tac agc aac tcc gcg ctg aac ccg ctg ctc tac gcc ttc ctg 816
 Met Ser Tyr Ser Asn Ser Ala Leu Asn Pro Leu Leu Tyr Ala Phe Leu
 260 265 270
 ggc tgc cac ttc cga cag gcc ttc cgc cgc gtc tgc ccc tgc gcg ccg 864
 Gly Ser His Phe Arg Gln Ala Phe Arg Arg Val Cys Pro Cys Ala Pro
 275 280 285
 cgc cgc ccc cgc cgc ccc cgc cgg ccc gga ccc tcg gac ccc gca gcc 912
 Arg Arg Pro Arg Arg Pro Arg Arg Pro Gly Pro Ser Asp Pro Ala Ala
 290 295 300
 cca cac gcg gag ctg ctc cgc ctg ggg tcc cac ccg gcc ccc gcc agg 960
 Pro His Ala Glu Leu Leu Arg Leu Gly Ser His Pro Ala Pro Ala Arg
 305 310 315 320
 gcg cag aag 969
 Ala Gln Lys

<210> 10
 <211> 323
 <212> PRT
 <213> Homo sapiens

<400> 10
 Arg Ala Val Asp Ala Trp Leu Val Pro Leu Phe Phe Ala Ala Leu Met
 1 5 10 15
 Leu Leu Gly Leu Val Gly Asn Ser Leu Val Ile Tyr Val Ile Cys Arg
 20 25 30
 His Lys Pro Met Arg Thr Val Thr Asn Phe Tyr Ile Ala Asn Leu Ala
 35 40 45
 Ala Thr Asp Val Thr Phe Leu Leu Cys Cys Val Pro Phe Thr Ala Leu
 50 55 60
 Leu Tyr Pro Leu Pro Gly Trp Val Leu Gly Asp Phe Met Cys Lys Phe
 65 70 75 80
 Val Asn Tyr Ile Gln Gln Val Ser Val Gln Ala Thr Cys Ala Thr Leu
 85 90 95
 Thr Ala Met Ser Val Asp Arg Trp Tyr Val Thr Val Phe Pro Leu Arg
 100 105 110
 Ala Leu His Arg Arg Thr Pro Arg Leu Ala Leu Ala Val Ser Leu Ser
 115 120 125
 Ile Trp Val Gly Ser Ala Ala Val Ser Ala Pro Val Leu Ala Leu His
 130 135 140
 Arg Leu Ser Pro Gly Pro Arg Ala Tyr Cys Ser Glu Ala Phe Pro Ser
 145 150 155 160
 Arg Ala Leu Glu Arg Ala Phe Ala Leu Tyr Asn Leu Leu Ala Leu Tyr
 165 170 175
 Leu Leu Pro Leu Leu Ala Thr Cys Ala Cys Tyr Ala Ala Met Leu Arg
 180 185 190
 His Leu Gly Arg Val Ala Arg Ala Gly Ala Val Arg Ala Lys Val Ser
 195 200 205
 Arg Leu Val Ala Ala Val Val Leu Leu Phe Ala Ala Cys Trp Gly Pro
 210 215 220
 Ile Gln Leu Phe Leu Val Leu Gln Ala Leu Gly Pro Ala Gly Ser Trp
 225 230 235 240
 His Pro Arg Ser Tyr Ala Ala Tyr Ala Leu Lys Thr Trp Ala His Cys

13/160

[illegible]

```
<210> 11
<211> 1005
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> CDS
<222> (1) ... (1005)
```

<400> 11																	
gct	gcc	ctg	gaa	aag	tac	tac	ctt	tcc	att	ttt	tat	ggg	att	gag	ttc	48	
Ala	Ala	Leu	Glu	Lys	Tyr	Tyr	Leu	Ser	Ile	Phe	Tyr	Gly	Ile	Glu	Phe		
1		5			10					15							
gtt	gtg	gga	gtc	ctt	gga	aat	acc	att	gtt	gtt	tac	ggc	tac	atc	ttc	96	
Val	Val	Gly	Val	Leu	Gly	Asn	Thr	Ile	Val	Val	Tyr	Gly	Tyr	Ile	Phe		
20			25					30									
tct	ctg	aag	aac	tgg	aac	agc	agt	aat	att	tat	ctc	ttt	aac	ctc	tct	144	
Ser	Leu	Lys	Asn	Trp	Asn	Ser	Ser	Asn	Ile	Tyr	Leu	Phe	Asn	Leu	Ser		
35		40					45										
gtc	tct	gac	tta	gct	ttt	ctg	tgc	acc	ctc	ccc	atg	ctg	ata	agg	agt	192	
Val	Ser	Asp	Leu	Ala	Phe	Leu	Cys	Thr	Leu	Pro	Met	Leu	Ile	Arg	Ser		
50		55					60										
tat	gcc	aat	gga	aac	tgg	ata	tat	gga	gac	gtg	ctc	tgc	ata	agc	aac	240	
Tyr	Ala	Asn	Gly	Asn	Trp	Ile	Tyr	Gly	Asp	Val	Leu	Cys	Ile	Ser	Asn		
65		70					75					80					
cga	tat	gtg	ctt	cat	gcc	aac	ctc	tat	acc	agc	att	ctc	ttt	ctc	act	288	
Arg	Tyr	Val	Leu	His	Ala	Asn	Leu	Tyr	Thr	Ser	Ile	Leu	Phe	Leu	Thr		
85				90					95								
ttt	atc	agc	ata	gat	cga	tac	ttg	ata	att	aag	tat	cct	ttc	cga	gaa	336	
Phe	Ile	Ser	Ile	Asp	Arg	Tyr	Leu	Ile	Ile	Lys	Tyr	Pro	Phe	Arg	Glu		
100			105					110									
cac	ctt	ctg	caa	aag	aaa	gag	ttt	gct	att	tta	atc	tcc	ttg	gcc	att	384	
His	Leu	Leu	Gln	Lys	Lys	Glu	Phe	Ala	Ile	Leu	Ile	Ser	Leu	Ala	Ile		
115			120					125									
tgg	gtt	tta	gta	acc	tta	gag	tta	cta	ccc	ata	ctt	ccc	ctt	ata	aat	432	
Trp	Val	Leu	Val	Thr	Leu	Glu	Leu	Leu	Pro	Ile	Leu	Pro	Leu	Ile	Asn		
130		135					140										
cct	gtt	ata	act	gac	aat	ggc	acc	acc	tgt	aat	gat	ttt	gca	agt	tct	480	
Pro	Val	Ile	Thr	Asp	Asn	Gly	Thr	Thr	Cys	Asn	Asp	Phe	Ala	Ser	Ser		

14/160

145	150	155	160	
gga gac ccc aac tac aac ctc att tac agc atg tgt cta aca ctg ttg				528
Gly Asp Pro Asn Tyr Asn Leu Ile Tyr Ser Met Cys Leu Thr Leu Leu	165	170	175	
ggg ttc ctt att cct ctt ttt gtg atg tgt ttc ttt tat tac aag att				576
Gly Phe Leu Ile Pro Leu Phe Val Met Cys Phe Phe Tyr Tyr Lys Ile	180	185	190	
gct ctc ttc cta aag cag agg aat agg cag gtt gct act gct ctg ccc				624
Ala Leu Phe Leu Lys Gln Arg Asn Arg Gln Val Ala Thr Ala Leu Pro	195	200	205	
ctt gaa aag cct ctc aac ttg gtc atc atg gca gtg gta atc ttc tct				672
Leu Glu Lys Pro Leu Asn Leu Val Ile Met Ala Val Val Ile Phe Ser	210	215	220	
gtg ctt ttt aca ccc tat cac gtc atg cgg aat gtg agg atc gct tca				720
Val Leu Phe Thr Pro Tyr His Val Met Arg Asn Val Arg Ile Ala Ser	225	230	235	240
cgc ctg ggg agt tgg aag cag tat cag tgc act cag gtc gtc atc aac				768
Arg Leu Gly Ser Trp Lys Gln Tyr Gln Cys Thr Gln Val Val Ile Asn	245	250	255	
tcc ttt tac att gtg aca cgg cct ttg gcc ttt ctg aac agt gtc atc				816
Ser Phe Tyr Ile Val Thr Arg Pro Leu Ala Phe Leu Asn Ser Val Ile	260	265	270	
aac cct gtc ttc tat ttt ctt ttg gga gat cac ttc agg gac atg ctg				864
Asn Pro Val Phe Tyr Phe Leu Leu Gly Asp His Phe Arg Asp Met Leu	275	280	285	
atg aat caa ctg aga cac aac ttc aaa tcc ctt aca tcc ttt agc aga				912
Met Asn Gln Leu Arg His Asn Phe Lys Ser Leu Thr Ser Phe Ser Arg	290	295	300	
tgg gct cat gaa ctc cta ctt tca ttc aga gaa aat gat tct cct tcc				960
Trp Ala His Glu Leu Leu Leu Ser Phe Arg Glu Asn Asp Ser Pro Ser	305	310	315	320
tca ccc tcc tca aat ggt gcg att aca gaa gtg agc cac cgc acg				1005
Ser Pro Ser Ser Asn Gly Ala Ile Thr Glu Val Ser His Arg Thr	325	330	335	

<210> 12

<211> 335

<212> PRT

<213> Homo sapiens

<400> 12

Ala Ala Leu Glu Lys Tyr Tyr Leu Ser Ile Phe Tyr Gly Ile Glu Phe	1	5	10	15
Val Val Gly Val Leu Gly Asn Thr Ile Val Val Tyr Gly Tyr Ile Phe	20	25	30	
Ser Leu Lys Asn Trp Asn Ser Ser Asn Ile Tyr Leu Phe Asn Leu Ser	35	40	45	
Val Ser Asp Leu Ala Phe Leu Cys Thr Leu Pro Met Leu Ile Arg Ser	50	55	60	
Tyr Ala Asn Gly Asn Trp Ile Tyr Gly Asp Val Leu Cys Ile Ser Asn				

15/160

65					70					75				80
Arg	Tyr	Val	Leu	His	Ala	Asn	Leu	Tyr	Thr	Ser	Ile	Leu	Phe	Leu
				85					90					95
Phe	Ile	Ser	Ile	Asp	Arg	Tyr	Leu	Ile	Ile	Lys	Tyr	Pro	Phe	Arg
			100					105					110	
His	Leu	Leu	Gln	Lys	Lys	Glu	Phe	Ala	Ile	Leu	Ile	Ser	Leu	Ala
			115				120					125		
Trp	Val	Leu	Val	Thr	Leu	Glu	Leu	Leu	Pro	Ile	Leu	Pro	Leu	Ile
	130					135					140			
Pro	Val	Ile	Thr	Asp	Asn	Gly	Thr	Thr	Cys	Asn	Asp	Phe	Ala	Ser
145					150				155					160
Gly	Asp	Pro	Asn	Tyr	Asn	Leu	Ile	Tyr	Ser	Met	Cys	Leu	Thr	Leu
			165					170					175	
Gly	Phe	Leu	Ile	Pro	Leu	Phe	Val	Met	Cys	Phe	Phe	Tyr	Tyr	Lys
			180					185				190		
Ala	Leu	Phe	Leu	Lys	Gln	Arg	Asn	Arg	Gln	Val	Ala	Thr	Ala	Leu
	195						200				205			
Leu	Glu	Lys	Pro	Leu	Asn	Leu	Val	Ile	Met	Ala	Val	Val	Ile	Phe
	210					215				220				
Val	Leu	Phe	Thr	Pro	Tyr	His	Val	Met	Arg	Asn	Val	Arg	Ile	Ala
225					230				235					240
Arg	Leu	Gly	Ser	Trp	Lys	Gln	Tyr	Gln	Cys	Thr	Gln	Val	Val	Ile
			245					250					255	
Ser	Phe	Tyr	Ile	Val	Thr	Arg	Pro	Leu	Ala	Phe	Leu	Asn	Ser	Val
		260					265					270		
Asn	Pro	Val	Phe	Tyr	Phe	Leu	Leu	Gly	Asp	His	Phe	Arg	Asp	Met
	275					280				285				Leu
Met	Asn	Gln	Leu	Arg	His	Asn	Phe	Lys	Ser	Leu	Thr	Ser	Phe	Ser
	290					295				300				Arg
Trp	Ala	His	Glu	Leu	Leu	Leu	Ser	Phe	Arg	Glu	Asn	Asp	Ser	Pro
305					310				315					320
Ser	Pro	Ser	Ser	Asn	Gly	Ala	Ile	Thr	Glu	Val	Ser	His	Arg	Thr
			325					330					335	

<210> 13
 <211> 930
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(930)

<400> 13	
aac ttg cct ctt cag atc acc ctt tct gct ata atg ata ttc att ctg	48
Asn Leu Pro Leu Gln Ile Thr Leu Ser Ala Ile Met Ile Phe Ile Leu	
1 5 10 15	
ttt gtg tct ttt ctt ggg aac ttg gtt gtt tgc ctc atg gtt tac caa	96
Phe Val Ser Phe Leu Gly Asn Leu Val Val Cys Leu Met Val Tyr Gln	
20 25 30	
aaa gct gcc atg agg tct gca att aac atc ctc ctt gcc agc cta gct	144
Lys Ala Ala Met Arg Ser Ala Ile Asn Ile Leu Leu Ala Ser Leu Ala	
35 40 45	
ttt gca gac atg ttg ctt gca gtg ctg aac atg ccc ttt gcc ctg gta	192
Phe Ala Asp Met Leu Leu Ala Val Leu Asn Met Pro Phe Ala Leu Val	
50 55 60	
act att ctt act acc cga tgg att ttt ggg aaa ttc ttc tgt agg gta	240
Thr Ile Leu Thr Thr Arg Trp Ile Phe Gly Lys Phe Phe Cys Arg Val	

16/160

65	70	75	80	
tct gct atg ttt ttc tgg tta ttt gtg ata gaa gga gta gcc atc ctg				288
Ser Ala Met Phe Phe Trp Leu Phe Val Ile Glu Gly Val Ala Ile Leu	85	90	95	
ctc atc att agc ata gat agg ttc ctt att ata gtc cag agg cag gat				336
Leu Ile Ile Ser Ile Asp Arg Phe Leu Ile Ile Val Gln Arg Gln Asp	100	105	110	
aag cta aac cca tat aga gct aag gtt ctg att gca gtt tct tgg gca				384
Lys Leu Asn Pro Tyr Arg Ala Lys Val Leu Ile Ala Val Ser Trp Ala	115	120	125	
act tcc ttt tgt gta gct ttt cct tta gcc gta gga aac ccc gac ctg				432
Thr Ser Phe Cys Val Ala Phe Pro Leu Ala Val Gly Asn Pro Asp Leu	130	135	140	
cag ata cct tcc cga gct ccc cag tgt gtg ttt ggg tac aca acc aat				480
Gln Ile Pro Ser Arg Ala Pro Gln Cys Val Phe Gly Tyr Thr Thr Asn	145	150	155	160
cca ggc tac cag gct tat gtg att ttg att tct ctc att tct ttc ttc				528
Pro Gly Tyr Gln Ala Tyr Val Ile Leu Ile Ser Leu Ile Ser Phe Phe	165	170	175	
ata ccc ttc ctg gta ata cta cct ttc cag atg agc att gac atg ggc				576
Ile Pro Phe Leu Val Ile Leu Pro Phe Gln Met Ser Ile Asp Met Gly	180	185	190	
ttt aaa aca cgt gcc ttc acc act att ttg att ctc ttt gct gtc ttc				624
Phe Lys Thr Arg Ala Phe Thr Thr Ile Leu Ile Leu Phe Ala Val Phe	195	200	205	
att gtc tgc tgg gcc cca ttc acc act tac agc ctt gtg gca aca ttc				672
Ile Val Cys Trp Ala Pro Phe Thr Thr Tyr Ser Leu Val Ala Thr Phe	210	215	220	
agt aag cac ttt tac tat cag cac aac ttt ttt gag att agc acc tgg				720
Ser Lys His Phe Tyr Tyr Gln His Asn Phe Phe Glu Ile Ser Thr Trp	225	230	235	240
cta ctg tgg ctc tgc tac ctc aag tct gca ttg aat ccg ctg atc tac				768
Leu Leu Trp Leu Cys Tyr Leu Lys Ser Ala Leu Asn Pro Leu Ile Tyr	245	250	255	
tac tgg agg att aag aaa ttc cat gat gct tgc ctg gac atg atg cct				816
Tyr Trp Arg Ile Lys Lys Phe His Asp Ala Cys Leu Asp Met Met Pro	260	265	270	
aag tcc ttc aag ttt ttg ccg cag ctc cct ggt cac aca aag cga cgg				864
Lys Ser Phe Lys Phe Leu Pro Gln Leu Pro Gly His Thr Lys Arg Arg	275	280	285	
ata cat ttt aca cac aca cac aca cac aca cac aca cac aca cac acg				912
Ile His Phe Thr His Thr His Thr His Thr His Thr His Thr His Thr	290	295	300	
cac aca cag aaa cac atg				930
His Thr Gln Lys His Met	305	310		

17/160

<210> 14
 <211> 310
 <212> PRT
 <213> Homo sapiens

<400> 14
 Asn Leu Pro Leu Gln Ile Thr Leu Ser Ala Ile Met Ile Phe Ile Leu
 1 5 10 15
 Phe Val Ser Phe Leu Gly Asn Leu Val Cys Leu Met Val Tyr Gln
 20 25 30
 Lys Ala Ala Met Arg Ser Ala Ile Asn Ile Leu Leu Ala Ser Leu Ala
 35 40 45
 Phe Ala Asp Met Leu Leu Ala Val Leu Asn Met Pro Phe Ala Leu Val
 50 55 60
 Thr Ile Leu Thr Thr Arg Trp Ile Phe Gly Lys Phe Phe Cys Arg Val
 65 70 75 80
 Ser Ala Met Phe Phe Trp Leu Phe Val Ile Glu Gly Val Ala Ile Leu
 85 90 95
 Leu Ile Ile Ser Ile Asp Arg Phe Leu Ile Ile Val Gln Arg Gln Asp
 100 105 110
 Lys Leu Asn Pro Tyr Arg Ala Lys Val Leu Ile Ala Val Ser Trp Ala
 115 120 125
 Thr Ser Phe Cys Val Ala Phe Pro Leu Ala Val Gly Asn Pro Asp Leu
 130 135 140
 Gln Ile Pro Ser Arg Ala Pro Gln Cys Val Phe Gly Tyr Thr Thr Asn
 145 150 155 160
 Pro Gly Tyr Gln Ala Tyr Val Ile Leu Ile Ser Leu Ile Ser Phe Phe
 165 170 175
 Ile Pro Phe Leu Val Ile Leu Pro Phe Gln Met Ser Ile Asp Met Gly
 180 185 190
 Phe Lys Thr Arg Ala Phe Thr Thr Ile Leu Ile Leu Phe Ala Val Phe
 195 200 205
 Ile Val Cys Trp Ala Pro Phe Thr Thr Tyr Ser Leu Val Ala Thr Phe
 210 215 220
 Ser Lys His Phe Tyr Tyr Gln His Asn Phe Phe Glu Ile Ser Thr Trp
 225 230 235 240
 Leu Leu Trp Leu Cys Tyr Leu Lys Ser Ala Leu Asn Pro Leu Ile Tyr
 245 250 255
 Tyr Trp Arg Ile Lys Lys Phe His Asp Ala Cys Leu Asp Met Met Pro
 260 265 270
 Lys Ser Phe Lys Phe Leu Pro Gln Leu Pro Gly His Thr Lys Arg Arg
 275 280 285
 Ile His Phe Thr His Thr His Thr His Thr His Thr His Thr
 290 295 300
 His Thr Gln Lys His Met
 305 310

<210> 15
 <211> 951
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(951)

<400> 15
 agc ctg gcc cac ggc atc atc cgc tca acc gtg ctg gtt atc ttc ctc 48
 Ser Leu Ala His Gly Ile Ile Arg Ser Thr Val Leu Val Ile Phe Leu
 1 5 10 15
 gcc gcc tct ttc gtc ggc aac ata gtg ctg gcg cta gtg ttg cag cgc 96

18/160

Ala	Ala	Ser	Phe	Val	Gly	Asn	Ile	Val	Leu	Ala	Leu	Val	Leu	Gln	Arg	
			20					25					30			
aag	ccg	cag	ctg	ctg	cag	gtg	acc	aac	cgt	ttt	atc	ttt	aac	ctc	ctc	144
Lys	Pro	Gln	Leu	Leu	Gln	Val	Thr	Asn	Arg	Phe	Ile	Phe	Asn	Leu	Leu	
		35					40					45				
gtc	acc	gac	ctg	ctg	cag	att	tcg	ctc	gtg	gcc	ccc	tgg	gtg	gtg	gcc	192
Val	Thr	Asp	Leu	Leu	Gln	Ile	Ser	Leu	Val	Ala	Pro	Trp	Val	Val	Ala	
	50					55					60					
acc	tct	gtg	cct	ctc	ttc	tgg	ccc	ctc	aac	agc	cac	ttc	tgc	acg	gcc	240
Thr	Ser	Val	Pro	Leu	Phe	Trp	Pro	Leu	Asn	Ser	His	Phe	Cys	Thr	Ala	
	65				70					75					80	
ctg	gtt	agc	ctc	acc	cac	ctg	ttc	gcc	ttc	gcc	agc	gtc	aac	acc	att	288
Leu	Val	Ser	Leu	Thr	His	Leu	Phe	Ala	Phe	Ala	Ser	Val	Asn	Thr	Ile	
				85				90						95		
gtc	gtg	gtg	tca	gtg	gat	cgc	tac	ttg	tcc	atc	atc	cac	cct	ctc	tcc	336
Val	Val	Val	Ser	Val	Asp	Arg	Tyr	Leu	Ser	Ile	Ile	His	Pro	Leu	Ser	
			100					105					110			
tac	ccg	tcc	aag	atg	acc	cag	cgc	cgc	ggc	tac	ctg	ctc	ctc	tat	ggc	384
Tyr	Pro	Ser	Lys	Met	Thr	Gln	Arg	Arg	Gly	Tyr	Leu	Leu	Leu	Tyr	Gly	
		115					120					125				
acc	tgg	att	gtg	gcc	atc	ctg	cag	agc	act	cct	cca	ctc	tac	ggc	tgg	432
Thr	Trp	Ile	Val	Ala	Ile	Leu	Gln	Ser	Thr	Pro	Pro	Leu	Tyr	Gly	Trp	
	130					135					140					
ggc	cag	gct	gcc	ttt	gat	gag	cgc	aat	gct	ctc	tgc	tcc	atg	atc	tgg	480
Gly	Gln	Ala	Ala	Phe	Asp	Glu	Arg	Asn	Ala	Leu	Cys	Ser	Met	Ile	Trp	
	145				150					155					160	
ggg	gcc	agc	ccc	agc	tac	act	att	ctc	agc	gtg	gtg	tcc	ttc	atc	gtc	528
Gly	Ala	Ser	Pro	Ser	Tyr	Thr	Ile	Leu	Ser	Val	Val	Ser	Phe	Ile	Val	
				165					170					175		
att	cca	ctg	att	gtc	atg	att	gcc	tgc	tac	tcc	gtg	gtg	ttc	tgt	gca	576
Ile	Pro	Leu	Ile	Val	Met	Ile	Ala	Cys	Tyr	Ser	Val	Val	Phe	Cys	Ala	
			180					185					190			
gcc	cgg	agg	cag	cat	gct	ctg	ctg	tgc	tac	cag	tgc	aaa	gct	gct	aaa	624
Ala	Arg	Arg	Gln	His	Ala	Leu	Leu	Cys	Tyr	Gln	Cys	Lys	Ala	Ala	Lys	
		195					200					205				
gtg	atc	ttc	atc	atc	att	ttc	tcc	tat	gtg	cta	tcc	ctg	ggg	ccc	tac	672
Val	Ile	Phe	Ile	Ile	Ile	Phe	Ser	Tyr	Val	Leu	Ser	Leu	Gly	Pro	Tyr	
	210					215					220					
tgc	ttt	tta	gca	gtc	ctg	gcc	gtg	tgg	gtg	gat	gtc	gaa	acc	cag	gta	720
Cys	Phe	Leu	Ala	Val	Leu	Ala	Val	Trp	Val	Asp	Val	Glu	Thr	Gln	Val	
	225				230				235						240	
ccc	cag	tgg	gtg	atc	acc	ata	atc	atc	tgg	ctt	ttc	ttc	ctg	cag	tgc	768
Pro	Gln	Trp	Val	Ile	Thr	Ile	Ile	Ile	Trp	Leu	Phe	Phe	Leu	Gln	Cys	
				245					250					255		
tgc	atc	cac	ccc	tat	gtc	tat	ggc	tac	atg	cac	aag	acc	att	aag	aag	816
Cys	Ile	His	Pro	Tyr	Val	Tyr	Gly	Tyr	Met	His	Lys	Thr	Ile	Lys	Lys	
			260				265						270			

19/160

gaa	atc	cag	gac	atg	ctg	aag	aaa	caa	cta	aac	cag	cag	tct	tca	tct	864
Glu	Ile	Gln	Asp	Met	Leu	Lys	Lys	Gln	Leu	Asn	Gln	Gln	Ser	Ser	Ser	
		275					280				285					
gac	tct	ggc	tcc	tcc	tcc	tct	tca	gaa	gat	gaa	cga	ccc	atg	aga	tcc	912
Asp	Ser	Gly	Ser	Ser	Ser	Ser	Ser	Glu	Asp	Glu	Arg	Pro	Met	Arg	Ser	
		290				295					300					
cat	gtg	aag	aat	ggc	gag	gtt	ggc	agg	cgg	cgg	aga	cat				951
His	Val	Lys	Asn	Gly	Glu	Val	Gly	Arg	Arg	Arg	Arg	His				
305					310					315						

```
<210> 16
<211> 317
<212> PRT
<213> Homo sapiens
```

<400> 16															
Ser 1	Leu	Ala	His	Gly 5	Ile	Ile	Arg	Ser	Thr 10	Val	Leu	Val	Ile	Phe 15	Leu
Ala	Ala	Ser	Phe 20	Val	Gly	Asn	Ile	Val 25	Leu	Ala	Leu	Val	Leu 30	Gln	Arg
Lys	Pro	Gln 35	Leu	Leu	Gln	Val	Thr 40	Asn	Arg	Phe	Ile	Phe 45	Asn	Leu	Leu
Val	Thr 50	Asp	Leu	Leu	Gln	Ile 55	Ser	Leu	Val	Ala 60	Pro	Trp	Val	Val	Ala
Thr 65	Ser	Val	Pro	Leu	Phe 70	Trp	Pro	Leu	Asn 75	Ser	His	Phe	Cys	Thr	Ala 80
Leu	Val	Ser	Leu	Thr 85	His	Leu	Phe	Ala 90	Phe 90	Ala	Ser	Val	Asn	Thr 95	Ile
Val	Val	Val	Ser	Val 100	Asp	Arg	Tyr	Leu 105	Ser	Ile	Ile	His	Pro	Leu	Ser
Tyr	Pro	Ser	Lys 115	Met	Thr	Gln	Arg	Arg 120	Gly	Tyr	Leu	Leu 125	Leu	Tyr	Gly
Thr	Trp 130	Ile	Val	Ala	Ile	Leu 135	Gln	Ser	Thr	Pro	Pro 140	Leu	Tyr	Gly	Trp
Gly 145	Gln	Ala	Ala	Phe 150	Asp	Glu	Arg	Asn	Ala 155	Leu	Cys	Ser	Met	Ile	Trp 160
Gly	Ala	Ser	Pro	Ser 165	Tyr	Thr	Ile	Leu	Ser 170	Val	Val	Ser	Phe	Ile 175	Val
Ile	Pro	Leu	Ile 180	Val	Met	Ile	Ala	Cys 185	Tyr	Ser	Val	Val	Phe 190	Cys	Ala
Ala	Arg	Arg	Gln 195	His	Ala	Leu	Leu 200	Cys	Tyr	Gln	Cys	Lys 205	Ala	Ala	Lys
Val	Ile 210	Phe	Ile	Ile	Ile	Phe 215	Ser	Tyr	Val	Leu	Ser 220	Leu	Gly	Pro	Tyr
Cys 225	Phe	Leu	Ala	Val	Leu	Ala 230	Val	Trp	Val	Asp 235	Val	Glu	Thr	Gln	Val 240
Pro	Gln	Trp	Val	Ile 245	Thr	Ile	Ile	Ile	Trp 250	Leu	Phe	Phe	Leu	Gln	Cys 255
Cys	Ile	His	Pro 260	Tyr	Val	Tyr	Gly	Tyr 265	Met	His	Lys	Thr	Ile	Lys	Lys
Glu	Ile	Gln	Asp 275	Met	Leu	Lys	Lys 280	Gln	Leu	Asn	Gln	Gln	Ser	Ser	Ser
Asp	Ser 290	Gly	Ser	Ser	Ser	Ser 295	Ser	Glu	Asp	Glu	Arg 300	Pro	Met	Arg	Ser
His 305	Val	Lys	Asn	Gly 310	Glu	Val	Gly	Arg	Arg	Arg 315	Arg	His			

20/160

<210> 17
 <211> 951
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(951)

<400> 17

ccg gga cgc gcc aag atg gcc ctc gtg ctc acc ggc gtg ctc ata ttc	48
Pro Gly Arg Ala Lys Met Ala Leu Val Leu Thr Gly Val Leu Ile Phe	
1 5 10 15	
gcc ctg gcg ctc ttt ggc aat gct ctg gtg ttt tac gtg gtg acc cgc	96
Ala Leu Ala Leu Phe Gly Asn Ala Leu Val Phe Tyr Val Val Thr Arg	
20 25 30	
agc aag acc atg cgc acc gtc acc aac atc ttt ata tgc tcc ctg gcg	144
Ser Lys Thr Met Arg Thr Val Thr Asn Ile Phe Ile Cys Ser Leu Ala	
35 40 45	
ctc agt gac atg ctc atc acc ctc ttt tgc att ccc gtc acc atg ctc	192
Leu Ser Asp Met Leu Ile Thr Leu Phe Cys Ile Pro Val Thr Met Leu	
50 55 60	
cag aac att tcc gac aac tgg ctg ggg ggt gct ttc att tgc aag atg	240
Gln Asn Ile Ser Asp Asn Trp Leu Gly Gly Ala Phe Ile Cys Lys Met	
65 70 75 80	
gtg cca ttt gtc cag tct acc gct gtt gtg aca gaa atc ctc act atg	288
Val Pro Phe Val Gln Ser Thr Ala Val Val Thr Glu Ile Leu Thr Met	
85 90 95	
acc tgc att gct gtg gaa agg cac cag gga ctt gtg cat cct ttt aaa	336
Thr Cys Ile Ala Val Glu Arg His Gln Gly Leu Val His Pro Phe Lys	
100 105 110	
atg aag tgg caa tac acc aac cga agg gct ttc aca atg cta ggt gtg	384
Met Lys Trp Gln Tyr Thr Asn Arg Arg Ala Phe Thr Met Leu Gly Val	
115 120 125	
gtc tgg ctg gtg gca gtc atc gta gga tca ccc atg tgg cac atc aaa	432
Val Trp Leu Val Ala Val Ile Val Gly Ser Pro Met Trp His Ile Lys	
130 135 140	
tat gac ttc cta tat gaa aag gaa cac atc tgc tgc tta gaa gag tgg	480
Tyr Asp Phe Leu Tyr Glu Lys Glu His Ile Cys Cys Leu Glu Glu Trp	
145 150 155 160	
acc agc cct gtg cac cag aag atc tac acc acc ttc atc ctt gtc atc	528
Thr Ser Pro Val His Gln Lys Ile Tyr Thr Thr Phe Ile Leu Val Ile	
165 170 175	
ctc ttc ctc ctg cct ctt atg gtg atg ctt att ctg tac agt aaa att	576
Leu Phe Leu Leu Pro Leu Met Val Met Leu Ile Leu Tyr Ser Lys Ile	
180 185 190	
ggc tat gaa ctt tgg ata aag aaa aga aag aaa cga gct gtc att atg	624
Gly Tyr Glu Leu Trp Ile Lys Lys Arg Lys Lys Arg Ala Val Ile Met	
195 200 205	
atg gtg aca gtg gtg gct ctc ttt gct gtg tgc tgg gca cca ttc cat	672

21/160

Met	Val	Thr	Val	Val	Ala	Leu	Phe	Ala	Val	Cys	Trp	Ala	Pro	Phe	His	
210						215				220						
gtt	gtc	cat	atg	atg	att	gaa	tac	agt	gaa	ttc	ctc	tcc	cat	gtt	act	720
Val	Val	His	Met	Met	Ile	Glu	Tyr	Ser	Glu	Phe	Leu	Ser	His	Val	Thr	
225					230				235						240	
cct	tct	atg	att	ttt	gct	atc	gtg	caa	att	att	gga	ttt	tcc	aac	tcc	768
Pro	Ser	Met	Ile	Phe	Ala	Ile	Val	Gln	Ile	Ile	Gly	Phe	Ser	Asn	Ser	
				245				250						255		
atc	tgt	aat	ccc	att	gtc	tat	gca	ttt	atg	aat	gaa	aac	ttc	aaa	aaa	816
Ile	Cys	Asn	Pro	Ile	Val	Tyr	Ala	Phe	Met	Asn	Glu	Asn	Phe	Lys	Lys	
			260					265					270			
aat	gtt	ttg	tct	gca	gtt	tgt	tat	tgc	ata	gta	aat	aaa	acc	ttc	tct	864
Asn	Val	Leu	Ser	Ala	Val	Cys	Tyr	Cys	Ile	Val	Asn	Lys	Thr	Phe	Ser	
		275					280					285				
cca	gca	caa	agg	cat	gga	aat	tca	gga	att	aca	atg	atg	cgg	aag	aaa	912
Pro	Ala	Gln	Arg	His	Gly	Asn	Ser	Gly	Ile	Thr	Met	Met	Arg	Lys	Lys	
	290					295					300					
gca	aag	ttt	tcc	ctc	aga	gag	aat	cca	gtg	gag	gaa	acc				951
Ala	Lys	Phe	Ser	Leu	Arg	Glu	Asn	Pro	Val	Glu	Glu	Thr				
305					310				315							

<210> 18

<211> 317

<212> PRT

<213> Homo sapiens

<400> 18

Pro	Gly	Arg	Ala	Lys	Met	Ala	Leu	Val	Leu	Thr	Gly	Val	Leu	Ile	Phe	
1				5				10						15		
Ala	Leu	Ala	Leu	Phe	Gly	Asn	Ala	Leu	Val	Phe	Tyr	Val	Val	Thr	Arg	
		20						25					30			
Ser	Lys	Thr	Met	Arg	Thr	Val	Thr	Asn	Ile	Phe	Ile	Cys	Ser	Leu	Ala	
		35					40					45				
Leu	Ser	Asp	Met	Leu	Ile	Thr	Leu	Phe	Cys	Ile	Pro	Val	Thr	Met	Leu	
	50					55					60					
Gln	Asn	Ile	Ser	Asp	Asn	Trp	Leu	Gly	Gly	Ala	Phe	Ile	Cys	Lys	Met	
65					70					75					80	
Val	Pro	Phe	Val	Gln	Ser	Thr	Ala	Val	Val	Thr	Glu	Ile	Leu	Thr	Met	
				85					90					95		
Thr	Cys	Ile	Ala	Val	Glu	Arg	His	Gln	Gly	Leu	Val	His	Pro	Phe	Lys	
			100					105					110			
Met	Lys	Trp	Gln	Tyr	Thr	Asn	Arg	Arg	Ala	Phe	Thr	Met	Leu	Gly	Val	
		115					120					125				
Val	Trp	Leu	Val	Ala	Val	Ile	Val	Gly	Ser	Pro	Met	Trp	His	Ile	Lys	
	130						135				140					
Tyr	Asp	Phe	Leu	Tyr	Glu	Lys	Glu	His	Ile	Cys	Cys	Leu	Glu	Glu	Trp	
	145					150				155					160	
Thr	Ser	Pro	Val	His	Gln	Lys	Ile	Tyr	Thr	Thr	Phe	Ile	Leu	Val	Ile	
				165					170					175		
Leu	Phe	Leu	Leu	Pro	Leu	Met	Val	Met	Leu	Ile	Leu	Tyr	Ser	Lys	Ile	
		180						185					190			
Gly	Tyr	Glu	Leu	Trp	Ile	Lys	Lys	Arg	Lys	Lys	Arg	Ala	Val	Ile	Met	
		195					200					205				
Met	Val	Thr	Val	Val	Ala	Leu	Phe	Ala	Val	Cys	Trp	Ala	Pro	Phe	His	
	210					215					220					

22/160

Val Val His Met Met Ile Glu Tyr Ser Glu Phe Leu Ser His Val Thr
 225 230 235 240
 Pro Ser Met Ile Phe Ala Ile Val Gln Ile Ile Gly Phe Ser Asn Ser
 245 250 255
 Ile Cys Asn Pro Ile Val Tyr Ala Phe Met Asn Glu Asn Phe Lys Lys
 260 265 270
 Asn Val Leu Ser Ala Val Cys Tyr Cys Ile Val Asn Lys Thr Phe Ser
 275 280 285
 Pro Ala Gln Arg His Gly Asn Ser Gly Ile Thr Met Met Arg Lys Lys
 290 295 300
 Ala Lys Phe Ser Leu Arg Glu Asn Pro Val Glu Glu Thr
 305 310 315

<210> 19
 <211> 999
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(999)

<400> 19
 ttc ttc gca gcc aag atc gtc att ggc att gca ctg gca ggc atc atg 48
 Phe Phe Ala Ala Lys Ile Val Ile Gly Ile Ala Leu Ala Gly Ile Met
 1 5 10 15
 ctg gtc tgc ggc atc ggt aac ttt gtc ttt atc gct gcc ctc acc cgc 96
 Leu Val Cys Gly Ile Gly Asn Phe Val Phe Ile Ala Ala Leu Thr Arg
 20 25 30
 tat aag aag ttg cgc aac ctc acc aat ctg ctc att gcc aac ctg gcc 144
 Tyr Lys Lys Leu Arg Asn Leu Thr Asn Leu Leu Ile Ala Asn Leu Ala
 35 40 45
 atc tcc gac ttc ctg gtg gcc atc atc tgc tgc ccc ttc gag atg gac 192
 Ile Ser Asp Phe Leu Val Ala Ile Ile Cys Cys Pro Phe Glu Met Asp
 50 55 60
 tac tac gtg gta cgg cag ctc tcc tgg gag cat ggc cac gtg ctc tgt 240
 Tyr Tyr Val Val Arg Gln Leu Ser Trp Glu His Gly His Val Leu Cys
 65 70 75 80
 gcc tcc gtc aac tac ctg cgc acc gtc tcc ctc tac gtc tcc acc aat 288
 Ala Ser Val Asn Tyr Leu Arg Thr Val Ser Leu Tyr Val Ser Thr Asn
 85 90 95
 gcc ttg ctg gcc att gcc att gac aga tat ctc gcc atc gtt cac ccc 336
 Ala Leu Leu Ala Ile Ala Ile Asp Arg Tyr Leu Ala Ile Val His Pro
 100 105 110
 ttg aaa cca cgg atg aat tat caa acg gcc tcc ttc ctg atc gcc ttg 384
 Leu Lys Pro Arg Met Asn Tyr Gln Thr Ala Ser Phe Leu Ile Ala Leu
 115 120 125
 gtc tgg atg gtg tcc att ctc att gcc atc cca tcg gct tac ttt gca 432
 Val Trp Met Val Ser Ile Leu Ile Ala Ile Pro Ser Ala Tyr Phe Ala
 130 135 140
 aca gaa acg gtc ctc ttt att gtc aag agc cag gag aag atc ttc tgt 480
 Thr Glu Thr Val Leu Phe Ile Val Lys Ser Gln Glu Lys Ile Phe Cys
 145 150 155 160

23/160

ggc cag atc tgg cct gtg gat cag cag ctc tac tac aag tcc tac ttc 528
 Gly Gln Ile Trp Pro Val Asp Gln Gln Leu Tyr Tyr Lys Ser Tyr Phe
 165 170 175

ctc ttc atc ttt ggt gtc gag ttc gtg ggc cct gtg gtc acc atg acc 576
 Leu Phe Ile Phe Gly Val Glu Phe Val Gly Pro Val Val Thr Met Thr
 180 185 190

ctg tgc tat gcc agg atc tcc cgg gag ctc tgg ttc aag gca att cgc 624
 Leu Cys Tyr Ala Arg Ile Ser Arg Glu Leu Trp Phe Lys Ala Ile Arg
 195 200 205

aag cgg ctg cgc tgc cgc agg aag acg gtc ctg gtg ctc atg tgc att 672
 Lys Arg Leu Arg Cys Arg Lys Thr Val Leu Val Leu Met Cys Ile
 210 215 220

ctc acg gcc tat gtg ctg tgc tgg gca ccc ttc tac ggt ttc acc atc 720
 Leu Thr Ala Tyr Val Leu Cys Trp Ala Pro Phe Tyr Gly Phe Thr Ile
 225 230 235 240

gtt cgt gac ttc ttc ccc act gtg ttc gtg aag gaa aag cac tac ctc 768
 Val Arg Asp Phe Phe Pro Thr Val Phe Val Lys Glu Lys His Tyr Leu
 245 250 255

act gcc ttc tac gtg gtc gag tgc atc gcc atg agc aac agc atg atc 816
 Thr Ala Phe Tyr Val Val Glu Cys Ile Ala Met Ser Asn Ser Met Ile
 260 265 270

aac acc gtc cca ttt ttg tat ttt tgg ttg aga tgg ggc ttc act ata 864
 Asn Thr Val Pro Phe Leu Tyr Phe Trp Leu Arg Trp Gly Phe Thr Ile
 275 280 285

ttt ctc agg ctg act ctg tct caa aaa aaa aaa aaa aga aga aga aga 912
 Phe Leu Arg Leu Thr Leu Ser Gln Lys Lys Lys Lys Arg Arg Arg Arg
 290 295 300

aaa aga aaa aga act gaa agc aga gac tca aac aga tat ttg tac act 960
 Lys Arg Lys Arg Thr Glu Ser Arg Asp Ser Asn Arg Tyr Leu Tyr Thr
 305 310 315 320

cat gtt cct agc agc att att cac agc act cca gcc tgg 999
 His Val Pro Ser Ser Ile Ile His Ser Thr Pro Ala Trp
 325 330

<210> 20

<211> 333

<212> PRT

<213> Homo sapiens

<400> 20

Phe Phe Ala Ala Lys Ile Val Ile Gly Ile Ala Leu Ala Gly Ile Met
 1 5 10 15
 Leu Val Cys Gly Ile Gly Asn Phe Val Phe Ile Ala Ala Leu Thr Arg
 20 25 30
 Tyr Lys Lys Leu Arg Asn Leu Thr Asn Leu Leu Ile Ala Asn Leu Ala
 35 40 45
 Ile Ser Asp Phe Leu Val Ala Ile Ile Cys Cys Pro Phe Glu Met Asp
 50 55 60
 Tyr Tyr Val Val Arg Gln Leu Ser Trp Glu His Gly His Val Leu Cys

24/160

65					70					75				80	
Ala	Ser	Val	Asn	Tyr	Leu	Arg	Thr	Val	Ser	Leu	Tyr	Val	Ser	Thr	Asn
				85					90					95	
Ala	Leu	Leu	Ala	Ile	Ala	Ile	Asp	Arg	Tyr	Leu	Ala	Ile	Val	His	Pro
			100					105					110		
Leu	Lys	Pro	Arg	Met	Asn	Tyr	Gln	Thr	Ala	Ser	Phe	Leu	Ile	Ala	Leu
		115					120					125			
Val	Trp	Met	Val	Ser	Ile	Leu	Ile	Ala	Ile	Pro	Ser	Ala	Tyr	Phe	Ala
	130					135				140					
Thr	Glu	Thr	Val	Leu	Phe	Ile	Val	Lys	Ser	Gln	Glu	Lys	Ile	Phe	Cys
145					150				155						160
Gly	Gln	Ile	Trp	Pro	Val	Asp	Gln	Gln	Leu	Tyr	Tyr	Lys	Ser	Tyr	Phe
			165					170						175	
Leu	Phe	Ile	Phe	Gly	Val	Glu	Phe	Val	Gly	Pro	Val	Val	Thr	Met	Thr
			180				185						190		
Leu	Cys	Tyr	Ala	Arg	Ile	Ser	Arg	Glu	Leu	Trp	Phe	Lys	Ala	Ile	Arg
	195					200						205			
Lys	Arg	Leu	Arg	Cys	Arg	Arg	Lys	Thr	Val	Leu	Val	Leu	Met	Cys	Ile
	210				215				220						
Leu	Thr	Ala	Tyr	Val	Leu	Cys	Trp	Ala	Pro	Phe	Tyr	Gly	Phe	Thr	Ile
225					230				235						240
Val	Arg	Asp	Phe	Phe	Pro	Thr	Val	Phe	Val	Lys	Glu	Lys	His	Tyr	Leu
			245					250						255	
Thr	Ala	Phe	Tyr	Val	Val	Glu	Cys	Ile	Ala	Met	Ser	Asn	Ser	Met	Ile
			260				265						270		
Asn	Thr	Val	Pro	Phe	Leu	Tyr	Phe	Trp	Leu	Arg	Trp	Gly	Phe	Thr	Ile
	275					280						285			
Phe	Leu	Arg	Leu	Thr	Leu	Ser	Gln	Lys	Lys	Lys	Lys	Arg	Arg	Arg	Arg
	290				295				300						
Lys	Arg	Lys	Arg	Thr	Glu	Ser	Arg	Asp	Ser	Asn	Arg	Tyr	Leu	Tyr	Thr
305					310				315						320
His	Val	Pro	Ser	Ser	Ile	Ile	His	Ser	Thr	Pro	Ala	Trp			
			325						330						

<210> 21
 <211> 948
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(948)

<400> 21	
tcc tgg gaa cta cag atg ttt ttc ttt atg gtg ttt tca ttg ctt tat	48
Ser Trp Glu Leu Gln Met Phe Phe Phe Met Val Phe Ser Leu Leu Tyr	
1 5 10 15	
gtg gca aca atg gtg ggt aac agc ctc ata gtc atc aca gtt ata gtg	96
Val Ala Thr Met Val Gly Asn Ser Leu Ile Val Ile Thr Val Ile Val	
20 25 30	
gac cct cac cta cac tct cct atg tat ttc ctg ctt acc aat ctt tca	144
Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Thr Asn Leu Ser	
35 40 45	
atc att gat atg tct ctt gct tct ttc gcc acc cca aag atg att aca	192
Ile Ile Asp Met Ser Leu Ala Ser Phe Ala Thr Pro Lys Met Ile Thr	
50 55 60	
gat tac cta aca ggt cac aaa acc atc tct ttt gat ggc tgc ctt acc	240
Asp Tyr Leu Thr Gly His Lys Thr Ile Ser Phe Asp Gly Cys Leu Thr	

25/160

65	70	75	80	
cag ata ttc ttt ctc cac ctt ttc act gga act gag atc atc tta ctc				288
Gln Ile Phe Phe Leu His Leu Phe Thr Gly Thr Glu Ile Ile Leu Leu				
	85	90	95	
atg gcc atg tcc ttt gat agg tat att gca ata tgc aag ccc ctg cac				336
Met Ala Met Ser Phe Asp Arg Tyr Ile Ala Ile Cys Lys Pro Leu His				
	100	105	110	
tat gct tct gtc att agt ccc cag gtg tgt gtt gct ctc gtg gtg gct				384
Tyr Ala Ser Val Ile Ser Pro Gln Val Cys Val Ala Leu Val Val Ala				
	115	120	125	
tcc tgg att atg gga gtt atg cat tca atg aca cca ttt att gaa tat				432
Ser Trp Ile Met Gly Val Met His Ser Met Thr Pro Phe Ile Glu Tyr				
	130	135	140	
tta ttg att aga gtg tcc ttt ctc cat tgc ttg tct ttg ttg act tta				480
Leu Leu Ile Arg Val Ser Phe Leu His Cys Leu Ser Leu Leu Thr Leu				
	145	150	155	160
cta aag aac agc tgg tta cag gta cgt ggc ttt gtt ttt ggg ttc tgt				528
Leu Lys Asn Ser Trp Leu Gln Val Arg Gly Phe Val Phe Gly Phe Cys				
	165	170	175	
att ctg ttc tat tgt cta tct ttc act ttc tct ctc ttg gtc agc tcc				576
Ile Leu Phe Tyr Cys Leu Ser Phe Thr Phe Ser Leu Leu Val Ser Ser				
	180	185	190	
tac atc att att ctt gtt aca gtt tgg ctc aag tct tca gct gca atg				624
Tyr Ile Ile Ile Leu Val Thr Val Trp Leu Lys Ser Ser Ala Ala Met				
	195	200	205	
gca aag gca ttt tct acg ctg gct tcc cat att gca gta gta ata tta				672
Ala Lys Ala Phe Ser Thr Leu Ala Ser His Ile Ala Val Val Ile Leu				
	210	215	220	
ttc ttt gga cct tgc atc ttc atc tat gtg tgg ccc ttt acc atc tct				720
Phe Phe Gly Pro Cys Ile Phe Ile Tyr Val Trp Pro Phe Thr Ile Ser				
	225	230	235	240
cct ttg gat aaa ttt ctt gcc ata ttt tac act gtt ttc acc ccc gtc				768
Pro Leu Asp Lys Phe Leu Ala Ile Phe Tyr Thr Val Phe Thr Pro Val				
	245	250	255	
cta aac ccc att att tat aca cta agg aat agg gat atg aag gct gcc				816
Leu Asn Pro Ile Ile Tyr Thr Leu Arg Asn Arg Asp Met Lys Ala Ala				
	260	265	270	
gta agg aaa att agg act tca ata tct cac ttt cgg caa agg aca gat				864
Val Arg Lys Ile Arg Thr Ser Ile Ser His Phe Arg Gln Arg Thr Asp				
	275	280	285	
cat cta gac aaa aat tca gcc aaa aaa aca aca aat aca aag cgc act				912
His Leu Asp Lys Asn Ser Ala Lys Lys Thr Thr Asn Thr Lys Arg Thr				
	290	295	300	
cta gat cat gtg gac cta cca gat agt cac aga aca				948
Leu Asp His Val Asp Leu Pro Asp Ser His Arg Thr				
	305	310	315	

26/160

<210> 22
 <211> 316
 <212> PRT
 <213> Homo sapiens

<400> 22
 Ser Trp Glu Leu Gln Met Phe Phe Phe Met Val Phe Ser Leu Leu Tyr
 1 5 10 15
 Val Ala Thr Met Val Gly Asn Ser Leu Ile Val Ile Thr Val Ile Val
 20 25 30
 Asp Pro His Leu His Ser Pro Met Tyr Phe Leu Leu Thr Asn Leu Ser
 35 40 45
 Ile Ile Asp Met Ser Leu Ala Ser Phe Ala Thr Pro Lys Met Ile Thr
 50 55 60
 Asp Tyr Leu Thr Gly His Lys Thr Ile Ser Phe Asp Gly Cys Leu Thr
 65 70 75 80
 Gln Ile Phe Phe Leu His Leu Phe Thr Gly Thr Glu Ile Ile Leu Leu
 85 90 95
 Met Ala Met Ser Phe Asp Arg Tyr Ile Ala Ile Cys Lys Pro Leu His
 100 105 110
 Tyr Ala Ser Val Ile Ser Pro Gln Val Cys Val Ala Leu Val Val Ala
 115 120 125
 Ser Trp Ile Met Gly Val Met His Ser Met Thr Pro Phe Ile Glu Tyr
 130 135 140
 Leu Leu Ile Arg Val Ser Phe Leu His Cys Leu Ser Leu Leu Thr Leu
 145 150 155 160
 Leu Lys Asn Ser Trp Leu Gln Val Arg Gly Phe Val Phe Gly Phe Cys
 165 170 175
 Ile Leu Phe Tyr Cys Leu Ser Phe Thr Phe Ser Leu Leu Val Ser Ser
 180 185 190
 Tyr Ile Ile Ile Leu Val Thr Val Trp Leu Lys Ser Ser Ala Ala Met
 195 200 205
 Ala Lys Ala Phe Ser Thr Leu Ala Ser His Ile Ala Val Val Ile Leu
 210 215 220
 Phe Phe Gly Pro Cys Ile Phe Ile Tyr Val Trp Pro Phe Thr Ile Ser
 225 230 235 240
 Pro Leu Asp Lys Phe Leu Ala Ile Phe Tyr Thr Val Phe Thr Pro Val
 245 250 255
 Leu Asn Pro Ile Ile Tyr Thr Leu Arg Asn Arg Asp Met Lys Ala Ala
 260 265 270
 Val Arg Lys Ile Arg Thr Ser Ile Ser His Phe Arg Gln Arg Thr Asp
 275 280 285
 His Leu Asp Lys Asn Ser Ala Lys Lys Thr Thr Asn Thr Lys Arg Thr
 290 295 300
 Leu Asp His Val Asp Leu Pro Asp Ser His Arg Thr
 305 310 315

<210> 23
 <211> 954
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(954)

<400> 23
 agt gtg gta gat aca gtc atc ctc cct tcc atg att ggg att atc tgt 48
 Ser Val Val Asp Thr Val Ile Leu Pro Ser Met Ile Gly Ile Ile Cys
 1 5 10 15
 tca aca ggg ctg gtt ggc aac atc ctc att gta ttc act ata ata aga 96

27/160

Ser	Thr	Gly	Leu	Val	Gly	Asn	Ile	Leu	Ile	Val	Phe	Thr	Ile	Ile	Arg	
			20					25					30			
tcc	agg	aaa	aaa	aca	gtc	cct	gac	atc	tat	atc	tgc	aac	ctg	gct	gtg	144
Ser	Arg	Lys	Lys	Thr	Val	Pro	Asp	Ile	Tyr	Ile	Cys	Asn	Leu	Ala	Val	
		35					40					45				
gct	gat	ttg	gtc	cac	ata	gtt	gga	atg	cct	ttt	ctt	att	cac	caa	tgg	192
Ala	Asp	Leu	Val	His	Ile	Val	Gly	Met	Pro	Phe	Leu	Ile	His	Gln	Trp	
	50					55					60					
gcc	cga	ggg	gga	gag	tgg	gtg	ttt	ggg	ggg	cct	ctc	tgc	acc	atc	atc	240
Ala	Arg	Gly	Gly	Glu	Trp	Val	Phe	Gly	Gly	Pro	Leu	Cys	Thr	Ile	Ile	
	65				70					75					80	
aca	tcc	ctg	gat	act	tgt	aac	caa	ttt	gcc	tgt	agt	gcc	atc	atg	act	288
Thr	Ser	Leu	Asp	Thr	Cys	Asn	Gln	Phe	Ala	Cys	Ser	Ala	Ile	Met	Thr	
				85					90					95		
gta	atg	agt	gtg	gac	agg	tac	ttt	gcc	ctc	gtc	caa	cca	ttt	cga	ctg	336
Val	Met	Ser	Val	Asp	Arg	Tyr	Phe	Ala	Leu	Val	Gln	Pro	Phe	Arg	Leu	
			100					105					110			
aca	cgt	tgg	aga	aca	agg	tac	aag	acc	atc	cgg	atc	aat	ttg	ggc	ctt	384
Thr	Arg	Trp	Arg	Thr	Arg	Tyr	Lys	Thr	Ile	Arg	Ile	Asn	Leu	Gly	Leu	
		115					120					125				
tgg	gca	gct	tcc	ttt	atc	ctg	gca	ttg	cct	gtc	tgg	gtc	tac	tcg	aag	432
Trp	Ala	Ala	Ser	Phe	Ile	Leu	Ala	Leu	Pro	Val	Trp	Val	Tyr	Ser	Lys	
	130					135					140					
gtc	atc	aaa	ttt	aaa	gac	ggg	gtt	gag	agt	tgt	ttg	tca	aat	ttg	ctt	480
Val	Ile	Lys	Phe	Lys	Asp	Gly	Val	Glu	Ser	Cys	Leu	Ser	Asn	Leu	Leu	
	145				150					155					160	
atc	ttt	tca	aag	aaa	tat	ttt	att	tct	ttg	atc	ttt	tgt	att	att	ttc	528
Ile	Phe	Ser	Lys	Lys	Tyr	Phe	Ile	Ser	Leu	Ile	Phe	Cys	Ile	Ile	Phe	
				165					170					175		
ttt	att	tca	att	tca	ttt	att	tct	gct	ctg	atc	ttt	att	aca	ttt	ctt	576
Phe	Ile	Ser	Ile	Ser	Phe	Ile	Ser	Ala	Leu	Ile	Phe	Ile	Thr	Phe	Leu	
			180					185					190			
cta	cta	ttc	tta	gaa	aaa	caa	caa	caa	caa	aaa	aaa	aaa	cac	acg	tca	624
Leu	Leu	Phe	Leu	Glu	Lys	Gln	Gln	Gln	Gln	Lys	Lys	Lys	His	Thr	Ser	
			195				200					205				
cag	gtc	atg	cat	ctc	cta	ctc	ttg	tct	tcc	aca	ttc	ctt	gta	agt	tgg	672
Gln	Val	Met	His	Leu	Leu	Leu	Leu	Ser	Ser	Thr	Phe	Leu	Val	Ser	Trp	
	210					215					220					
att	cct	agg	tat	ttt	att	ctc	ttt	gaa	gca	att	gtg	aat	ggg	agt	tca	720
Ile	Pro	Arg	Tyr	Phe	Ile	Leu	Phe	Glu	Ala	Ile	Val	Asn	Gly	Ser	Ser	
	225				230					235					240	
ctc	atg	att	tgg	ctc	tct	gtt	tgt	ctg	tta	ttg	gtg	tat	aag	aat	gct	768
Leu	Met	Ile	Trp	Leu	Ser	Val	Cys	Leu	Leu	Leu	Val	Tyr	Lys	Asn	Ala	
				245					250					255		
tgt	gat	ttt	tgc	acc	att	cat	tat	ttt	gat	gtt	aaa	tgt	gtc	ttt	agg	816
Cys	Asp	Phe	Cys	Thr	Ile	His	Tyr	Phe	Asp	Val	Lys	Cys	Val	Phe	Arg	
			260					265					270			

28/160

aga aat tac aga caa ttg tca aag aaa aaa agc cat gga agc ttt gtg 864
 Arg Asn Tyr Arg Gln Leu Ser Lys Lys Lys Ser His Gly Ser Phe Val
 275 280 285

ccc aca acc caa aca gaa agt tta tcc tcc acc cca acc caa cac agg 912
 Pro Thr Thr Gln Thr Glu Ser Leu Ser Ser Thr Pro Thr Gln His Arg
 290 295 300

aaa gtg gtt gtt ttt ggt ttg gcc aga cca cta tgg gct act 954
 Lys Val Val Val Phe Gly Leu Ala Arg Pro Leu Trp Ala Thr
 310 315

<210> 24
 <211> 318
 <212> PRT
 <213> Homo sapiens

<400> 24
 Ser Val Val Asp Thr Val Ile Leu Pro Ser Met Ile Gly Ile Ile Cys
 1 5 10 15
 Ser Thr Gly Leu Val Gly Asn Ile Leu Ile Val Phe Thr Ile Ile Arg
 20 25 30
 Ser Arg Lys Lys Thr Val Pro Asp Ile Tyr Ile Cys Asn Leu Ala Val
 35 40 45
 Ala Asp Leu Val His Ile Val Gly Met Pro Phe Leu Ile His Gln Trp
 50 55 60
 Ala Arg Gly Gly Glu Trp Val Phe Gly Gly Pro Leu Cys Thr Ile Ile
 65 70 75 80
 Thr Ser Leu Asp Thr Cys Asn Gln Phe Ala Cys Ser Ala Ile Met Thr
 85 90 95
 Val Met Ser Val Asp Arg Tyr Phe Ala Leu Val Gln Pro Phe Arg Leu
 100 105 110
 Thr Arg Trp Arg Thr Arg Tyr Lys Thr Ile Arg Ile Asn Leu Gly Leu
 115 120 125
 Trp Ala Ala Ser Phe Ile Leu Ala Leu Pro Val Trp Val Tyr Ser Lys
 130 135 140
 Val Ile Lys Phe Lys Asp Gly Val Glu Ser Cys Leu Ser Asn Leu Leu
 145 150 155 160
 Ile Phe Ser Lys Lys Tyr Phe Ile Ser Leu Ile Phe Cys Ile Ile Phe
 165 170 175
 Phe Ile Ser Ile Ser Phe Ile Ser Ala Leu Ile Phe Ile Thr Phe Leu
 180 185 190
 Leu Leu Phe Leu Glu Lys Gln Gln Gln Gln Lys Lys Lys His Thr Ser
 195 200 205
 Gln Val Met His Leu Leu Leu Leu Ser Ser Thr Phe Leu Val Ser Trp
 210 215 220
 Ile Pro Arg Tyr Phe Ile Leu Phe Glu Ala Ile Val Asn Gly Ser Ser
 225 230 235 240
 Leu Met Ile Trp Leu Ser Val Cys Leu Leu Leu Val Tyr Lys Asn Ala
 245 250 255
 Cys Asp Phe Cys Thr Ile His Tyr Phe Asp Val Lys Cys Val Phe Arg
 260 265 270
 Arg Asn Tyr Arg Gln Leu Ser Lys Lys Lys Ser His Gly Ser Phe Val
 275 280 285
 Pro Thr Thr Gln Thr Glu Ser Leu Ser Ser Thr Pro Thr Gln His Arg
 290 295 300
 Lys Val Val Val Phe Gly Leu Ala Arg Pro Leu Trp Ala Thr
 305 310 315

<210> 25

29/160

<211> 957
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(957)

<400> 25

tgg cct cat ctg gaa gta gtt ctc ttt gtg gtt atc ttg atc ttc tac	48
Trp Pro His Leu Glu Val Val Leu Phe Val Val Ile Leu Ile Phe Tyr	
1 5 10 15	
ttg ata aca ctg ata gga aac ctg ttc atc atc atc ctg tca tac ctg	96
Leu Ile Thr Leu Ile Gly Asn Leu Phe Ile Ile Ile Leu Ser Tyr Leu	
20 25 30	
gac tcc cat ctc cac act ccc atg tac ttc ttc ctt tca aat ctc tca	144
Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu Ser	
35 40 45	
ttt ctg gat ctc tgc tac acc acc agc tct atc cct cag ttg ctg gtg	192
Phe Leu Asp Leu Cys Tyr Thr Thr Ser Ser Ile Pro Gln Leu Leu Val	
50 55 60	
aat ctc tgg ggc ccg gaa aag acc atc tct tat gct ggt tgt aca gtt	240
Asn Leu Trp Gly Pro Glu Lys Thr Ile Ser Tyr Ala Gly Cys Thr Val	
65 70 75 80	
caa ctt tac ttt gtt ctc gca ctg gga acc gca gag tgt gtc cta ctg	288
Gln Leu Tyr Phe Val Leu Ala Leu Gly Thr Ala Glu Cys Val Leu Leu	
85 90 95	
gtg gtg atg tcc tat gat cgt tat gca gct gtg tgt aga cct ttg cat	336
Val Val Met Ser Tyr Asp Arg Tyr Ala Ala Val Cys Arg Pro Leu His	
100 105 110	
tac act gtc ctc atg cac cct cgt ttc tgc cgc ttg ttg gct gcg gct	384
Tyr Thr Val Leu Met His Pro Arg Phe Cys Arg Leu Leu Ala Ala Ala	
115 120 125	
tct tgg gta aca ctt cat tcc tcc ttt act ttc tgg gta ccc ctt tgt	432
Ser Trp Val Thr Leu His Ser Ser Phe Thr Phe Trp Val Pro Leu Cys	
130 135 140	
gga cat cgc cta gtg gat cac ttc ttc tgt gaa gtt cca gca ctt ctg	480
Gly His Arg Leu Val Asp His Phe Phe Cys Glu Val Pro Ala Leu Leu	
145 150 155 160	
cgt tta tca tgt gtt gac acc cat gca aat gag ctg acc ctc atg gtc	528
Arg Leu Ser Cys Val Asp Thr His Ala Asn Glu Leu Thr Leu Met Val	
165 170 175	
atg agc tcc att ttt gtt ctc ata cct ctc att ctg att ctc act gcc	576
Met Ser Ser Ile Phe Val Leu Ile Pro Leu Ile Leu Ile Leu Thr Ala	
180 185 190	
tat ggt gcc att gcc cgg gct gta ctg agc atg caa tca acc act ggg	624
Tyr Gly Ala Ile Ala Arg Ala Val Leu Ser Met Gln Ser Thr Thr Gly	
195 200 205	
ctt cag aaa gtg ttt agg aca tgt gga gcc cat ctt atg gtt gta tct	672
Leu Gln Lys Val Phe Arg Thr Cys Gly Ala His Leu Met Val Val Ser	

30/160

210	215	220	
ctc ttt ttc att cca gtc atg tgc atg tat ctc cag cca cca tca gaa			720
Leu Phe Phe Ile Pro Val Met Cys Met Tyr Leu Gln Pro Pro Ser Glu			
225	230	235	240
aat tct cct gat cag ggc aag ttc att gcc ctc ttt tat act gtt gtc			768
Asn Ser Pro Asp Gln Gly Lys Phe Ile Ala Leu Phe Tyr Thr Val Val			
	245	250	255
aca ccg agt ctt aat cct cta atc tac act ctc aga aac aag cat gta			816
Thr Pro Ser Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys His Val			
	260	265	270
aaa ggg gca gcg aag aga cta ttg ggt gcc tgc cgc ccc atg cag agc			864
Lys Gly Ala Ala Lys Arg Leu Leu Gly Ala Cys Arg Pro Met Gln Ser			
	275	280	285
cag ccc aga act gtg agg tca agt ttc ttt gat aga aag gca aca ggt			912
Gln Pro Arg Thr Val Arg Ser Ser Phe Phe Asp Arg Lys Ala Thr Gly			
	290	295	300
tgt gag cct ggc tcc tgt gtg agg act ccg gca gca cag act tgt			957
Cys Glu Pro Gly Ser Cys Val Arg Thr Pro Ala Ala Gln Thr Cys			
305	310	315	

<210> 26

<211> 319

<212> PRT

<213> Homo sapiens

<400> 26

Trp Pro His Leu Glu Val Val Leu Phe Val Val Ile Leu Ile Phe Tyr	
1 5 10 15	
Leu Ile Thr Leu Ile Gly Asn Leu Phe Ile Ile Ile Leu Ser Tyr Leu	
20 25 30	
Asp Ser His Leu His Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu Ser	
35 40 45	
Phe Leu Asp Leu Cys Tyr Thr Thr Ser Ser Ile Pro Gln Leu Leu Val	
50 55 60	
Asn Leu Trp Gly Pro Glu Lys Thr Ile Ser Tyr Ala Gly Cys Thr Val	
65 70 75 80	
Gln Leu Tyr Phe Val Leu Ala Leu Gly Thr Ala Glu Cys Val Leu Leu	
85 90 95	
Val Val Met Ser Tyr Asp Arg Tyr Ala Ala Val Cys Arg Pro Leu His	
100 105 110	
Tyr Thr Val Leu Met His Pro Arg Phe Cys Arg Leu Leu Ala Ala Ala	
115 120 125	
Ser Trp Val Thr Leu His Ser Ser Phe Thr Phe Trp Val Pro Leu Cys	
130 135 140	
Gly His Arg Leu Val Asp His Phe Phe Cys Glu Val Pro Ala Leu Leu	
145 150 155 160	
Arg Leu Ser Cys Val Asp Thr His Ala Asn Glu Leu Thr Leu Met Val	
165 170 175	
Met Ser Ser Ile Phe Val Leu Ile Pro Leu Ile Leu Ile Leu Thr Ala	
180 185 190	
Tyr Gly Ala Ile Ala Arg Ala Val Leu Ser Met Gln Ser Thr Thr Gly	
195 200 205	
Leu Gln Lys Val Phe Arg Thr Cys Gly Ala His Leu Met Val Val Ser	
210 215 220	
Leu Phe Phe Ile Pro Val Met Cys Met Tyr Leu Gln Pro Pro Ser Glu	

31/160

225		230		235		240
Asn Ser Pro Asp Gln Gly Lys Phe Ile Ala Leu Phe Tyr Thr Val Val						
	245			250		255
Thr Pro Ser Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn Lys His Val						
	260		265		270	
Lys Gly Ala Ala Lys Arg Leu Leu Gly Ala Cys Arg Pro Met Gln Ser						
	275		280		285	
Gln Pro Arg Thr Val Arg Ser Ser Phe Phe Asp Arg Lys Ala Thr Gly						
	290		295		300	
Cys Glu Pro Gly Ser Cys Val Arg Thr Pro Ala Ala Gln Thr Cys						
305	310		315			

<210> 27
 <211> 963
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(963)

<400> 27
 gtt cgt gtc gtg ccc cgc acc gtg ttt ttt ttg ttt ttt ttt ttg ttt 48
 Val Arg Val Val Pro Arg Thr Val Phe Phe Leu Phe Phe Phe Leu Phe
 1 5 10 15

att ttg gtt ctt gtt tca aat atc ttg aca gtg atc atc ctc tcc cag 96
 Ile Leu Val Leu Val Ser Asn Ile Leu Thr Val Ile Ile Leu Ser Gln
 20 25 30

ctg gtg gca aga aga cag aag tcc tcc tac aac tat ctc ttg gca ctc 144
 Leu Val Ala Arg Arg Gln Lys Ser Ser Tyr Asn Tyr Leu Leu Ala Leu
 35 40 45

gct gct gcc gac atc ttg gtc ctc ttt ttc ata gtg ttt gtg gac ttc 192
 Ala Ala Ala Asp Ile Leu Val Leu Phe Phe Ile Val Phe Val Asp Phe
 50 55 60

ctg ttg gaa gat ttc atc ttg aac atg cag atg cct cag gtc ccc gac 240
 Leu Leu Glu Asp Phe Ile Leu Asn Met Gln Met Pro Gln Val Pro Asp
 65 70 75 80

aag atc ata gaa gtg ctg gaa ttc tca tcc atc cac acc tcc ata tgg 288
 Lys Ile Ile Glu Val Leu Glu Phe Ser Ser Ile His Thr Ser Ile Trp
 85 90 95

att act gta ccg tta acc att gac agg tat atc gct gtc tgc cac ccg 336
 Ile Thr Val Pro Leu Thr Ile Asp Arg Tyr Ile Ala Val Cys His Pro
 100 105 110

ctc aag tac cac acg gtc tca tac cca gcc cgc acc cgg aaa gtc att 384
 Leu Lys Tyr His Thr Val Ser Tyr Pro Ala Arg Thr Arg Lys Val Ile
 115 120 125

gta agt gtt tac atc acc tgc ttc ctg acc agc atc ccc tat tac tgg 432
 Val Ser Val Tyr Ile Thr Cys Phe Leu Thr Ser Ile Pro Tyr Tyr Trp
 130 135 140

tgg ccc aac atc tgg act gaa gac tac atc agc acc tct gtg cat cac 480
 Trp Pro Asn Ile Trp Thr Glu Asp Tyr Ile Ser Thr Ser Val His His
 145 150 155 160

32/160

gtc ctc atc tgg atc cac tgc ttc acc gtc tac ctg gtg ccc tgc tcc 528
 Val Leu Ile Trp Ile His Cys Phe Thr Val Tyr Leu Val Pro Cys Ser
 165 170 175

atc ttc ttc atc ttg aac tca atc att gtg tac aag ctc agg agg aag 576
 Ile Phe Phe Ile Leu Asn Ser Ile Ile Val Tyr Lys Leu Arg Arg Lys
 180 185 190

agc aat ttt cgt ctc cgt ggc tac tcc acg ggg aag acc acc gcc atc 624
 Ser Asn Phe Arg Leu Arg Gly Tyr Ser Thr Gly Lys Thr Thr Ala Ile
 195 200 205

ttg ttc acc att acc tcc atc ttt gcc aca ctt tgg gcc ccc cgc atc 672
 Leu Phe Thr Ile Thr Ser Ile Phe Ala Thr Leu Trp Ala Pro Arg Ile
 210 215 220

atc atg att ctt tac cac ctc tat ggg gcg ccc atc cag aac cgc tgg 720
 Ile Met Ile Leu Tyr His Leu Tyr Gly Ala Pro Ile Gln Asn Arg Trp
 225 230 235 240

ctg gta cac atc atg tcc gac att gcc aac atg cta gcc ctt ctg aac 768
 Leu Val His Ile Met Ser Asp Ile Ala Asn Met Leu Ala Leu Leu Asn
 245 250 255

aca gcc atc aac ttc ttc ctc tac tgc ttc atc agc aag cgg ttc cgc 816
 Thr Ala Ile Asn Phe Phe Leu Tyr Cys Phe Ile Ser Lys Arg Phe Arg
 260 265 270

acc atg gca gcc gcc acg ctc aag gct ttc ttc aag tgc cag aag caa 864
 Thr Met Ala Ala Ala Thr Leu Lys Ala Phe Phe Lys Cys Gln Lys Gln
 275 280 285

cct gta caa att caa cct ttc aag cag ata tct tta agt cca aca cac 912
 Pro Val Gln Ile Gln Pro Phe Lys Gln Ile Ser Leu Ser Pro Thr His
 290 295 300

aca cac aca cac aca cac aca cac aca cac aca cac act tct aaa gac 960
 Thr His Thr His Thr His Thr His Thr His Thr His Thr Ser Lys Asp
 305 310 315 320

act 963
 Thr

<210> 28

<211> 321

<212> PRT

<213> Homo sapiens

<400> 28

Val Arg Val Val Pro Arg Thr Val Phe Phe Leu Phe Phe Phe Leu Phe
 1 5 10 15
 Ile Leu Val Leu Val Ser Asn Ile Leu Thr Val Ile Ile Leu Ser Gln
 20 25 30
 Leu Val Ala Arg Arg Gln Lys Ser Ser Tyr Asn Tyr Leu Leu Ala Leu
 35 40 45
 Ala Ala Ala Asp Ile Leu Val Leu Phe Phe Ile Val Phe Val Asp Phe
 50 55 60
 Leu Leu Glu Asp Phe Ile Leu Asn Met Gln Met Pro Gln Val Pro Asp
 65 70 75 80

33/160

Lys Ile Ile Glu Val Leu Glu Phe Ser Ser Ile His Thr Ser Ile Trp
 85 90 95
 Ile Thr Val Pro Leu Thr Ile Asp Arg Tyr Ile Ala Val Cys His Pro
 100 105 110
 Leu Lys Tyr His Thr Val Ser Tyr Pro Ala Arg Thr Arg Lys Val Ile
 115 120 125
 Val Ser Val Tyr Ile Thr Cys Phe Leu Thr Ser Ile Pro Tyr Tyr Trp
 130 135 140
 Trp Pro Asn Ile Trp Thr Glu Asp Tyr Ile Ser Thr Ser Val His His
 145 150 155 160
 Val Leu Ile Trp Ile His Cys Phe Thr Val Tyr Leu Val Pro Cys Ser
 165 170 175
 Ile Phe Phe Ile Leu Asn Ser Ile Ile Val Tyr Lys Leu Arg Arg Lys
 180 185 190
 Ser Asn Phe Arg Leu Arg Gly Tyr Ser Thr Gly Lys Thr Thr Ala Ile
 195 200 205
 Leu Phe Thr Ile Thr Ser Ile Phe Ala Thr Leu Trp Ala Pro Arg Ile
 210 215 220
 Ile Met Ile Leu Tyr His Leu Tyr Gly Ala Pro Ile Gln Asn Arg Trp
 225 230 235 240
 Leu Val His Ile Met Ser Asp Ile Ala Asn Met Leu Ala Leu Leu Asn
 245 250 255
 Thr Ala Ile Asn Phe Phe Leu Tyr Cys Phe Ile Ser Lys Arg Phe Arg
 260 265 270
 Thr Met Ala Ala Ala Thr Leu Lys Ala Phe Phe Lys Cys Gln Lys Gln
 275 280 285
 Pro Val Gln Ile Gln Pro Phe Lys Gln Ile Ser Leu Ser Pro Thr His
 290 295 300
 Thr His Thr His Thr His Thr His Thr His Thr His Thr Ser Lys Asp
 305 310 315 320
 Thr

<210> 29
 <211> 969
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) ... (969)

<400> 29
 atg ggc ccc ggc gag gcg ctg ctg gcg ggt ctc ctg gtg atg gta ctg 48
 Met Gly Pro Gly Glu Ala Leu Leu Ala Gly Leu Leu Val Met Val Leu
 1 5 10 15

 gcc gtg gcg ctg cta tcc aac gca ctg gtg ctg ctt tgt tgc gcc tac 96
 Ala Val Ala Leu Leu Ser Asn Ala Leu Val Leu Leu Cys Cys Ala Tyr
 20 25 30

 agc gct gag ctc cgc act cga gcc tca ggc gtc ctc ctg gtg aat ctg 144
 Ser Ala Glu Leu Arg Thr Arg Ala Ser Gly Val Leu Leu Val Asn Leu
 35 40 45

 tct ctg ggc cac ctg ctg ctg gcg gcg ctg gac atg ccc ttc acg ctg 192
 Ser Leu Gly His Leu Leu Leu Ala Ala Leu Asp Met Pro Phe Thr Leu
 50 55 60

 ctc ggt gtg atg cgc ggg cgg aca ccg tcg gcg ccc ggc gca tgc caa 240
 Leu Gly Val Met Arg Gly Arg Thr Pro Ser Ala Pro Gly Ala Cys Gln
 65 70 75 80

34/160

gtc att ggc ttc ctg gac acc ttc ctg gcg tcc aac gcg gcg ctg agc	288
Val Ile Gly Phe Leu Asp Thr Phe Leu Ala Ser Asn Ala Ala Leu Ser	
85 90 95	
gtg gcg gcg ctg agc gca gac cag tgg ctg gca gtg ggc ttc cca ctg	336
Val Ala Ala Leu Ser Ala Asp Gln Trp Leu Ala Val Gly Phe Pro Leu	
100 105 110	
cgc tac gcc gga cgc ctg cga ccg cgc tat gcc ggc ctg ctg ctg ggc	384
Arg Tyr Ala Gly Arg Leu Arg Pro Arg Tyr Ala Gly Leu Leu Leu Gly	
115 120 125	
tgt gcc tgg gga cag tgc ctg gcc ttc tca ggc gct gca ctt ggc tgc	432
Cys Ala Trp Gly Gln Ser Leu Ala Phe Ser Gly Ala Ala Leu Gly Cys	
130 135 140	
tgc tgg ctt ggc tac agc agc gcc ttc gcg tcc tgt tgc ctg cgc ctg	480
Ser Trp Leu Gly Tyr Ser Ser Ala Phe Ala Ser Cys Ser Leu Arg Leu	
145 150 155 160	
ccg ccc gag cct gag cgt ccg cgc ttc gca gcc ttc acc gcc acg ctc	528
Pro Pro Glu Pro Glu Arg Pro Arg Phe Ala Ala Phe Thr Ala Thr Leu	
165 170 175	
cat gcc gtg ggc ttc gtg ctg ccg ctg gcg gtg ctc tgc ctc acc tgc	576
His Ala Val Gly Phe Val Leu Pro Leu Ala Val Leu Cys Leu Thr Ser	
180 185 190	
ctc cag gtg cac cgg gtg gca cgc aga cac tgc cag cgc atg gac acc	624
Leu Gln Val His Arg Val Ala Arg Arg His Cys Gln Arg Met Asp Thr	
195 200 205	
cgg cgc cgc cac cgc gcc acc agg aag att ggc att gct att gcg acc	672
Arg Arg Arg His Arg Ala Thr Arg Lys Ile Gly Ile Ala Ile Ala Thr	
210 215 220	
ttc ctc atc tgc ttt gcc ccg tat gtc atg acc agg ctg gcg gag ctc	720
Phe Leu Ile Cys Phe Ala Pro Tyr Val Met Thr Arg Leu Ala Glu Leu	
225 230 235 240	
gtg ccc ttc gtc acc gtg aac gcc cag tgg ggc atc ctc agc aag tgc	768
Val Pro Phe Val Thr Val Asn Ala Gln Trp Gly Ile Leu Ser Lys Cys	
245 250 255	
ctg acc tac agc aag gcg gtg gcc gac ccg ttc acg tac tct ctg ctc	816
Leu Thr Tyr Ser Lys Ala Val Ala Asp Pro Phe Thr Tyr Ser Leu Leu	
260 265 270	
cgc cgg ccg ttc cgc caa gtc ctg gcc ggc atg gtg cac cgg ctg ctg	864
Arg Arg Pro Phe Arg Gln Val Leu Ala Gly Met Val His Arg Leu Leu	
275 280 285	
aag aga acc ccg cgc cca gca tcc acc cat gac agc tct ctg gat gtg	912
Lys Arg Thr Pro Arg Pro Ala Ser Thr His Asp Ser Ser Leu Asp Val	
290 295 300	
gcc ggc atg gtg cac cag ctg ctg aag aga acc ccg cgc cca gcg tcc	960
Ala Gly Met Val His Gln Leu Leu Lys Arg Thr Pro Arg Pro Ala Ser	
305 310 315 320	
acc cac aac	969
Thr His Asn	

35/160

<210> 30
 <211> 323
 <212> PRT
 <213> Homo sapiens

<400> 30
 Met Gly Pro Gly Glu Ala Leu Leu Ala Gly Leu Leu Val Met Val Leu
 1 5 10 15
 Ala Val Ala Leu Leu Ser Asn Ala Leu Val Leu Leu Cys Cys Ala Tyr
 20 25 30
 Ser Ala Glu Leu Arg Thr Arg Ala Ser Gly Val Leu Leu Val Asn Leu
 35 40 45
 Ser Leu Gly His Leu Leu Leu Ala Ala Leu Asp Met Pro Phe Thr Leu
 50 55 60
 Leu Gly Val Met Arg Gly Arg Thr Pro Ser Ala Pro Gly Ala Cys Gln
 65 70 75 80
 Val Ile Gly Phe Leu Asp Thr Phe Leu Ala Ser Asn Ala Ala Leu Ser
 85 90 95
 Val Ala Ala Leu Ser Ala Asp Gln Trp Leu Ala Val Gly Phe Pro Leu
 100 105 110
 Arg Tyr Ala Gly Arg Leu Arg Pro Arg Tyr Ala Gly Leu Leu Leu Gly
 115 120 125
 Cys Ala Trp Gly Gln Ser Leu Ala Phe Ser Gly Ala Ala Leu Gly Cys
 130 135 140
 Ser Trp Leu Gly Tyr Ser Ser Ala Phe Ala Ser Cys Ser Leu Arg Leu
 145 150 155 160
 Pro Pro Glu Pro Glu Arg Pro Arg Phe Ala Ala Phe Thr Ala Thr Leu
 165 170 175
 His Ala Val Gly Phe Val Leu Pro Leu Ala Val Leu Cys Leu Thr Ser
 180 185 190
 Leu Gln Val His Arg Val Ala Arg Arg His Cys Gln Arg Met Asp Thr
 195 200 205
 Arg Arg Arg His Arg Ala Thr Arg Lys Ile Gly Ile Ala Ile Ala Thr
 210 215 220
 Phe Leu Ile Cys Phe Ala Pro Tyr Val Met Thr Arg Leu Ala Glu Leu
 225 230 235 240
 Val Pro Phe Val Thr Val Asn Ala Gln Trp Gly Ile Leu Ser Lys Cys
 245 250 255
 Leu Thr Tyr Ser Lys Ala Val Ala Asp Pro Phe Thr Tyr Ser Leu Leu
 260 265 270
 Arg Arg Pro Phe Arg Gln Val Leu Ala Gly Met Val His Arg Leu Leu
 275 280 285
 Lys Arg Thr Pro Arg Pro Ala Ser Thr His Asp Ser Ser Leu Asp Val
 290 295 300
 Ala Gly Met Val His Gln Leu Leu Lys Arg Thr Pro Arg Pro Ala Ser
 305 310 315 320
 Thr His Asn

<210> 31
 <211> 981
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(981)

<400> 31

36/160

ttg gaa ggc atc aaa cac tgg att ttc atc ccc ttt ttc ttt atg tac	48
Leu Glu Gly Ile Lys His Trp Ile Phe Ile Pro Phe Phe Phe Met Tyr	
1 5 10 15	
atg gtt gcc atc tca ggc aat tgt ttc att ctg atc att att aag acc	96
Met Val Ala Ile Ser Gly Asn Cys Phe Ile Leu Ile Ile Ile Lys Thr	
20 25 30	
aac cct cgt ctg cac aca ccc atg tac tat cta cta tcc ttg ctg gcc	144
Asn Pro Arg Leu His Thr Pro Met Tyr Tyr Leu Leu Ser Leu Leu Ala	
35 40 45	
ctc act gac ctg ggg ctg tgt gtg tcc acg ttg ccc acc act atg ggg	192
Leu Thr Asp Leu Gly Leu Cys Val Ser Thr Leu Pro Thr Thr Met Gly	
50 55 60	
atc ttc tgg ttt aac tcc cag agt atc tac ttt gga gcg tgt caa atc	240
Ile Phe Trp Phe Asn Ser Gln Ser Ile Tyr Phe Gly Ala Cys Gln Ile	
65 70 75 80	
cag atg ttc tgc atc cac tct ttt tcc ttc atg gag tcc tca gtg ctc	288
Gln Met Phe Cys Ile His Ser Phe Ser Phe Met Glu Ser Ser Val Leu	
85 90 95	
ctc atg atg tcc ttt gac cgc ttt gtg gcc atc tgc cac cct ctg agg	336
Leu Met Met Ser Phe Asp Arg Phe Val Ala Ile Cys His Pro Leu Arg	
100 105 110	
tat tcg gtc att atc act ggc cag caa gtg gtc aga gca ggc cta att	384
Tyr Ser Val Ile Ile Thr Gly Gln Gln Val Val Arg Ala Gly Leu Ile	
115 120 125	
gtc atc ttc cgg gga cct gtg gcc act atc cct att gtc ctc ctc ctg	432
Val Ile Phe Arg Gly Pro Val Ala Thr Ile Pro Ile Val Leu Leu Leu	
130 135 140	
aag gct ttt ccc tac tgt gga tct gtg gtc ctc tcc cac tca ttt tgc	480
Lys Ala Phe Pro Tyr Cys Gly Ser Val Val Leu Ser His Ser Phe Cys	
145 150 155 160	
ctg cac cag gaa gtg ata cag ctg gcc tgc aca gat acc acc ttc aat	528
Leu His Gln Glu Val Ile Gln Leu Ala Cys Thr Asp Thr Thr Phe Asn	
165 170 175	
aat ctg tat gga ctg atg gtg gta gtt ttc act gtg atg ctg gac ctg	576
Asn Leu Tyr Gly Leu Met Val Val Val Phe Thr Val Met Leu Asp Leu	
180 185 190	
gtg ctc atc gca ctg tcc tat gga ctc atc ctg cac aca gta gca ggc	624
Val Leu Ile Ala Leu Ser Tyr Gly Leu Ile Leu His Thr Val Ala Gly	
195 200 205	
ctg gcc tcc caa gag gag cag cgc cgt gcc ttt cag aca tgc acc gct	672
Leu Ala Ser Gln Glu Glu Gln Arg Arg Ala Phe Gln Thr Cys Thr Ala	
210 215 220	
cat ctc tgt gct gtg cta gta ttc ttt gtg ccc atg atg ggg ctg tcc	720
His Leu Cys Ala Val Leu Val Phe Phe Val Pro Met Met Gly Leu Ser	
225 230 235 240	
ctg gtg cac cgt ttt ggg aag cat gcc cca cct gct att cat ctt ctt	768

37/160

Leu	Val	His	Arg	Phe	Gly	Lys	His	Ala	Pro	Pro	Ala	Ile	His	Leu	Leu		
				245					250					255			
atg	gcc	aat	gtc	tac	ctt	ttt	gtg	cct	ccc	atg	ctt	aac	cca	atc	ata	816	
Met	Ala	Asn	Val	Tyr	Leu	Phe	Val	Pro	Pro	Met	Leu	Asn	Pro	Ile	Ile		
			260					265				270					
tac	agc	att	aag	acc	aag	gag	atc	cac	cgt	gcc	att	atc	aaa	ctc	cta	864	
Tyr	Ser	Ile	Lys	Thr	Lys	Glu	Ile	His	Arg	Ala	Ile	Ile	Lys	Leu	Leu		
			275				280					285					
gaa	tgc	aga	agt	ctc	agg	agc	caa	tgc	aat	caa	ctg	gaa	gaa	agg	gta	912	
Glu	Cys	Arg	Ser	Leu	Arg	Ser	Gln	Cys	Asn	Gln	Leu	Glu	Glu	Arg	Val		
	290					295				300							
tca	gtg	atg	gaa	gat	gaa	atg	aat	gaa	atg	aag	caa	gaa	gag	aag	ttt	960	
Ser	Val	Met	Glu	Asp	Glu	Met	Asn	Glu	Met	Lys	Gln	Glu	Glu	Lys	Phe		
305					310					315					320		
aga	gaa	aaa	aga	ata	aaa	aga										981	
Arg	Glu	Lys	Arg	Ile	Lys	Arg											
				325													

<210> 32

<211> 327

<212> PRT

<213> Homo sapiens

<400> 32

Leu	Glu	Gly	Ile	Lys	His	Trp	Ile	Phe	Ile	Pro	Phe	Phe	Phe	Met	Tyr		
1				5					10					15			
Met	Val	Ala	Ile	Ser	Gly	Asn	Cys	Phe	Ile	Leu	Ile	Ile	Ile	Lys	Thr		
			20					25					30				
Asn	Pro	Arg	Leu	His	Thr	Pro	Met	Tyr	Tyr	Leu	Leu	Ser	Leu	Leu	Ala		
		35				40						45					
Leu	Thr	Asp	Leu	Gly	Leu	Cys	Val	Ser	Thr	Leu	Pro	Thr	Thr	Met	Gly		
50					55					60							
Ile	Phe	Trp	Phe	Asn	Ser	Gln	Ser	Ile	Tyr	Phe	Gly	Ala	Cys	Gln	Ile		
65				70					75					80			
Gln	Met	Phe	Cys	Ile	His	Ser	Phe	Ser	Phe	Met	Glu	Ser	Ser	Val	Leu		
			85					90					95				
Leu	Met	Met	Ser	Phe	Asp	Arg	Phe	Val	Ala	Ile	Cys	His	Pro	Leu	Arg		
		100					105						110				
Tyr	Ser	Val	Ile	Ile	Thr	Gly	Gln	Gln	Val	Val	Arg	Ala	Gly	Leu	Ile		
		115				120						125					
Val	Ile	Phe	Arg	Gly	Pro	Val	Ala	Thr	Ile	Pro	Ile	Val	Leu	Leu	Leu		
130					135						140						
Lys	Ala	Phe	Pro	Tyr	Cys	Gly	Ser	Val	Val	Leu	Ser	His	Ser	Phe	Cys		
145				150					155					160			
Leu	His	Gln	Glu	Val	Ile	Gln	Leu	Ala	Cys	Thr	Asp	Thr	Thr	Phe	Asn		
			165					170					175				
Asn	Leu	Tyr	Gly	Leu	Met	Val	Val	Val	Phe	Thr	Val	Met	Leu	Asp	Leu		
		180				185						190					
Val	Leu	Ile	Ala	Leu	Ser	Tyr	Gly	Leu	Ile	Leu	His	Thr	Val	Ala	Gly		
		195				200						205					
Leu	Ala	Ser	Gln	Glu	Glu	Gln	Arg	Arg	Ala	Phe	Gln	Thr	Cys	Thr	Ala		
210						215					220						
His	Leu	Cys	Ala	Val	Leu	Val	Phe	Phe	Val	Pro	Met	Met	Gly	Leu	Ser		
225				230					235					240			
Leu	Val	His	Arg	Phe	Gly	Lys	His	Ala	Pro	Pro	Ala	Ile	His	Leu	Leu		
			245					250					255				
Met	Ala	Asn	Val	Tyr	Leu	Phe	Val	Pro	Pro	Met	Leu	Asn	Pro	Ile	Ile		

260							265					270				
Tyr	Ser	Ile	Lys	Thr	Lys	Glu	Ile	His	Arg	Ala	Ile	Ile	Lys	Leu	Leu	
275							280					285				
Glu	Cys	Arg	Ser	Leu	Arg	Ser	Gln	Cys	Asn	Gln	Leu	Glu	Glu	Arg	Val	
290							295					300				
Ser	Val	Met	Glu	Asp	Glu	Met	Asn	Glu	Met	Lys	Gln	Glu	Glu	Lys	Phe	
305							310					315				
Arg	Glu	Lys	Arg	Ile	Lys	Arg										
325																

```
<220>
<221> CDS
<222> (1) ... (972)
```

<400> 33																	
cac	agt	act	gct	gac	ctt	gtc	ctc	ttc	tcc	gtg	gtt	atg	gcg	gtc	ttc		
His	Ser	Thr	Ala	Asp	Leu	Val	Leu	Phe	Ser	Val	Val	Met	Ala	Val	Phe	48	
				5						10		15					
aca	gtg	gcc	ctc	tgt	ggg	aat	gtc	ctc	ctc	atc	ttc	ctc	atc	tac	atg		
Thr	Val	Ala	Leu	Cys	Gly	Asn	Val	Leu	Leu	Ile	Phe	Leu	Ile	Tyr	Met	96	
				20						25		30					
gac	cct	cac	ctt	cac	acc	ccc	atg	tac	ttc	ttc	ctc	agc	cag	ctc	tcc		
Asp	Pro	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ser	Gln	Leu	Ser	144	
				35						40		45					
ctc	atg	gac	ctc	atg	ttg	gtc	tgt	acc	aat	gtg	cca	aag	atg	gca	gcc		
Leu	Met	Asp	Leu	Met	Leu	Val	Cys	Thr	Asn	Val	Pro	Lys	Met	Ala	Ala	192	
				50						55		60					
aac	ttc	ctg	tct	ggc	agg	aag	tcc	atc	tcc	ttt	gtg	ggc	tgt	ggc	ata		
Asn	Phe	Leu	Ser	Gly	Arg	Lys	Ser	Ile	Ser	Phe	Val	Gly	Cys	Gly	Ile	240	
				65						70		75				80	
caa	att	ggc	ctc	ttt	gtc	tgt	ctt	gtg	gga	tct	gag	ggg	ctc	ttg	ctg		
Gln	Ile	Gly	Leu	Phe	Val	Cys	Leu	Val	Gly	Ser	Glu	Gly	Leu	Leu	Leu	288	
				85						90		95					
gga	ctc	atg	gct	tat	gac	cgc	tat	gtg	gcc	att	agc	cac	cca	ctt	cac		
Gly	Leu	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Ser	His	Pro	Leu	His	336	
				100						105		110					
tat	ccc	atc	ctc	atg	aat	cag	agg	gtc	tgt	ctc	cag	att	act	ggg	agc		
Tyr	Pro	Ile	Leu	Met	Asn	Gln	Arg	Val	Cys	Leu	Gln	Ile	Thr	Gly	Ser	384	
				115						120		125					
tcc	tgg	gcc	ttt	ggg	ata	atc	gat	ggc	ttg	atc	cag	atg	gtg	gta	gta		
Ser	Trp	Ala	Phe	Gly	Ile	Ile	Asp	Gly	Leu	Ile	Gln	Met	Val	Val	Val	432	
				130						135		140					
atg	aat	ttc	ccc	tac	tgt	ggc	ttg	agg	aag	gtg	aac	cat	ttc	ttc	tgt		
Met	Asn	Phe	Pro	Tyr	Cys	Gly	Leu	Arg	Lys	Val	Asn	His	Phe	Phe	Cys	480	
				145						150		155				160	
gag	atg	cta	tcc	ttg	ttg	aag	ctg	gcc	tgt	gtg	ata	ttt	gct	tgc	tgt		
Glu	Met	Leu	Ser	Leu	Leu	Lys	Leu	Ala	Cys	Val	Ile	Phe	Ala	Cys	Cys	528	

39/160

165										170					175					
gtc	ttc	atg	ctt	ctc	ttc	cca	ttc	tcc	atc	atc	gtg	gcc	tcc	tat	gct	576				
Val	Phe	Met	Leu	Leu	Phe	Pro	Phe	Ser	Ile	Ile	Val	Ala	Ser	Tyr	Ala					
			180					185					190							
cac	att	cta	ggg	act	gtg	ctg	caa	atg	cac	tct	gct	cag	gcc	tgg	aaa	624				
His	Ile	Leu	Gly	Thr	Val	Leu	Gln	Met	His	Ser	Ala	Gln	Ala	Trp	Lys					
		195					200					205								
aag	gcc	ctg	gcc	acc	tgc	tcc	tcc	cac	ctg	aca	gct	ttt	ttt	ttt	tgc	672				
Lys	Ala	Leu	Ala	Thr	Cys	Ser	Ser	His	Leu	Thr	Ala	Phe	Phe	Phe	Cys					
	210					215					220									
caa	cta	cct	tac	caa	atc	ctt	tcc	cat	caa	gtt	gtc	tgt	tca	ttt	tat	720				
Gln	Leu	Pro	Tyr	Gln	Ile	Leu	Ser	His	Gln	Val	Val	Cys	Ser	Phe	Tyr					
225					230					235					240					
tgg	gtg	att	ttg	ggg	cat	aga	tgt	gac	aaa	tct	tca	ttg	caa	tca	agt	768				
Trp	Val	Ile	Leu	Gly	His	Arg	Cys	Asp	Lys	Ser	Ser	Leu	Gln	Ser	Ser					
				245				250						255						
aca	gtg	tca	ctt	tca	ttt	gcg	ggt	ctt	aat	cca	att	cta	tat	ggc	agc	816				
Thr	Val	Ser	Leu	Ser	Phe	Ala	Val	Leu	Asn	Pro	Ile	Leu	Tyr	Gly	Ser					
			260					265					270							
gtc	gcc	cgc	tcc	ttt	cgg	cgc	agg	gcg	gga	gcc	ctt	ctt	gtg	tgc	aga	864				
Val	Ala	Arg	Ser	Phe	Arg	Arg	Arg	Ala	Gly	Ala	Leu	Leu	Val	Cys	Arg					
		275					280					285								
aaa	aaa	cca	cag	aat	agc	tca	gaa	aat	ttc	act	ttt	acc	ccc	act	tct	912				
Lys	Lys	Pro	Gln	Asn	Ser	Ser	Glu	Asn	Phe	Thr	Phe	Thr	Pro	Thr	Ser					
	290					295					300									
ttc	ctc	ctt	tct	cct	tac	atc	acg	cac	aca	cac	aca	cac	aca	cat	gca	960				
Phe	Leu	Leu	Ser	Pro	Tyr	Ile	Thr	His	Thr	His	Thr	His	Thr	His	Ala					
305					310					315					320					
cac	aca	cac	gtc													972				
His	Thr	His	Val																	

<210> 34

<211> 324

<212> PRT

<213> Homo sapiens

<400> 34

His	Ser	Thr	Ala	Asp	Leu	Val	Leu	Phe	Ser	Val	Val	Met	Ala	Val	Phe
1				5					10					15	
Thr	Val	Ala	Leu	Cys	Gly	Asn	Val	Leu	Ile	Phe	Leu	Ile	Tyr	Met	
		20						25				30			
Asp	Pro	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ser	Gln	Leu	Ser
	35						40					45			
Leu	Met	Asp	Leu	Met	Leu	Val	Cys	Thr	Asn	Val	Pro	Lys	Met	Ala	Ala
	50					55					60				
Asn	Phe	Leu	Ser	Gly	Arg	Lys	Ser	Ile	Ser	Phe	Val	Gly	Cys	Gly	Ile
65					70					75					80
Gln	Ile	Gly	Leu	Phe	Val	Cys	Leu	Val	Gly	Ser	Glu	Gly	Leu	Leu	Leu
				85					90				95		
Gly	Leu	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Ser	His	Pro	Leu	His

40/160

[illegible]

```
<210> 35
<211> 975
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> CDS
<222> (1) ... (975)
```

<400> 35																	
ctc	tgt	ttc	ttg	cag	act	gag	caa	ttg	ata	act	ctg	tgg	gtc	ctc	ttt	48	
Leu	Cys	Phe	Leu	Gln	Thr	Glu	Gln	Leu	Ile	Thr	Leu	Trp	Val	Leu	Phe		
1				5					10					15			
gtt	ttt	acc	att	gtt	gga	aac	tcc	gtt	gtg	ctt	ttt	tcc	aca	tgg	agg	96	
Val	Phe	Thr	Ile	Val	Gly	Asn	Ser	Val	Val	Leu	Phe	Ser	Thr	Trp	Arg		
			20					25					30				
aga	aag	aag	aag	tca	aga	atg	acc	ttc	ttt	gtg	act	cag	ctg	gcc	atc	144	
Arg	Lys	Lys	Lys	Ser	Arg	Met	Thr	Phe	Phe	Val	Thr	Gln	Leu	Ala	Ile		
		35					40					45					
aca	gtg	gga	ttt	ttg	ttg	gac	ttt	ctc	atc	cta	ttc	att	atg	cct	ctt	192	
Thr	Val	Gly	Phe	Leu	Leu	Asp	Phe	Leu	Ile	Leu	Phe	Ile	Met	Pro	Leu		
	50					55					60						
cac	ttc	tct	ttg	gtc	tat	ctc	ttt	cac	tat	gag	agc	tca	cct	gat	ttt	240	
His	Phe	Ser	Leu	Val	Tyr	Leu	Phe	His	Tyr	Glu	Ser	Ser	Pro	Asp	Phe		
65					70					75				80			
tgg	tgc	tta	caa	agc	tac	ttt	ttt	tgt	gtt	gtg	ctg	ctc	tac	gcc	tct	288	

41/160

[illegible]

42/160

325

<210> 36
 <211> 325
 <212> PRT
 <213> Homo sapiens

<400> 36
 Leu Cys Phe Leu Gln Thr Glu Gln Leu Ile Thr Leu Trp Val Leu Phe
 1 5 10 15
 Val Phe Thr Ile Val Gly Asn Ser Val Val Leu Phe Ser Thr Trp Arg
 20 25 30
 Arg Lys Lys Lys Ser Arg Met Thr Phe Phe Val Thr Gln Leu Ala Ile
 35 40 45
 Thr Val Gly Phe Leu Leu Asp Phe Leu Ile Leu Phe Ile Met Pro Leu
 50 55 60
 His Phe Ser Leu Val Tyr Leu Phe His Tyr Glu Ser Ser Pro Asp Phe
 65 70 75 80
 Trp Cys Leu Gln Ser Tyr Phe Phe Cys Val Val Leu Leu Tyr Ala Ser
 85 90 95
 Thr Tyr Val Leu Val Ser Leu Ser Ile Asp Arg Tyr His Ala Ile Val
 100 105 110
 Tyr Pro Met Lys Phe Leu Gln Gly Glu Lys Gln Ala Arg Val Leu Ile
 115 120 125
 Val Ile Ala Trp Ser Leu Ser Phe Leu Phe Ser Ile Pro Thr Leu Ile
 130 135 140
 Ile Phe Gly Lys Arg Thr Leu Ser Asn Gly Glu Val Gln Cys Trp Ala
 145 150 155 160
 Leu Trp Pro Asp Asp Ser Tyr Trp Thr Pro Tyr Met Thr Ile Val Ala
 165 170 175
 Phe Leu Val Tyr Phe Ile Pro Leu Thr Ile Ile Ser Ile Met Tyr Gly
 180 185 190
 Ile Val Ile Arg Thr Ile Trp Ile Lys Ser Lys Thr Tyr Glu Thr Ala
 195 200 205
 Lys Ile Lys Ala Ile Lys Tyr Ser Ile Ile Ile Ile Leu Ala Phe Ile
 210 215 220
 Cys Cys Trp Ser Pro Tyr Phe Leu Phe Asp Ile Leu Asp Asn Phe Asn
 225 230 235 240
 Leu Leu Pro Asp Thr Gln Glu Arg Phe Tyr Ala Ser Val Ile Ile Gln
 245 250 255
 Asn Leu Pro Ala Leu Asn Ser Ala Ile Asn Pro Leu Ile Tyr Tyr Ser
 260 265 270
 Val Ser Gln Lys Asn Lys Arg Lys Arg Lys Arg Arg Ser Arg Arg Lys
 275 280 285
 Lys Lys Glu Lys Glu Arg Arg Arg Arg Lys Lys Arg Arg Arg Lys
 290 295 300
 Lys Lys Glu Gly Arg Arg Gly Gly Glu Gly Arg Gly Lys Lys Glu Glu
 305 310 315 320
 Glu Arg Arg Lys Glu
 325

<210> 37
 <211> 969
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(969)

43/160

<400> 37

aac	ctg	gag	ctg	tgg	aaa	ata	ttt	tct	gct	gtg	ttt	ctt	gtc	atg	tat	48
Asn	Leu	Glu	Leu	Trp	Lys	Ile	Phe	Ser	Ala	Val	Phe	Leu	Val	Met	Tyr	
1				5					10					15		
gta	gcc	aca	gtg	ctg	gaa	aat	cta	ctt	att	gtg	gta	act	att	atc	aca	96
Val	Ala	Thr	Val	Leu	Glu	Asn	Leu	Leu	Ile	Val	Val	Thr	Ile	Ile	Thr	
			20					25					30			
agt	cag	agt	ctg	agg	tca	cct	atg	tat	ttt	ttt	ctt	acc	ttc	ttg	tcc	144
Ser	Gln	Ser	Leu	Arg	Ser	Pro	Met	Tyr	Phe	Phe	Leu	Thr	Phe	Leu	Ser	
		35					40					45				
ctt	ttg	gat	gtc	atg	ttc	tca	tct	gtc	gtt	gcc	ccc	aag	gtg	att	gta	192
Leu	Leu	Asp	Val	Met	Phe	Ser	Ser	Val	Val	Ala	Pro	Lys	Val	Ile	Val	
	50					55					60					
gac	acc	ctc	tcc	aag	agc	act	acc	atc	tct	ctc	aaa	ggc	tgc	ctc	acc	240
Asp	Thr	Leu	Ser	Lys	Ser	Thr	Thr	Ile	Ser	Leu	Lys	Gly	Cys	Leu	Thr	
65					70					75					80	
cag	ctg	ttt	gtg	gag	cat	ttc	ttt	ggc	ggc	gtg	ggg	atc	atc	ctc	ctc	288
Gln	Leu	Phe	Val	Glu	His	Phe	Phe	Gly	Gly	Val	Gly	Ile	Ile	Leu	Leu	
				85				90						95		
act	gtg	atg	gcc	tat	gac	cgc	tac	gtg	gcc	atc	tgt	aag	ccc	ctg	cac	336
Thr	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Lys	Pro	Leu	His	
			100					105					110			
tac	acg	atc	atc	atg	agt	cca	cgg	gtg	tgc	tgc	cta	atg	gta	gga	ggg	384
Tyr	Thr	Ile	Ile	Met	Ser	Pro	Arg	Val	Cys	Cys	Leu	Met	Val	Gly	Gly	
		115					120					125				
gct	tgg	gtg	ggg	gga	ttt	atg	cac	gca	atg	ata	caa	ctt	ctc	ttc	atg	432
Ala	Trp	Val	Gly	Gly	Phe	Met	His	Ala	Met	Ile	Gln	Leu	Leu	Phe	Met	
	130					135					140					
tat	caa	ata	ccc	ttc	tgt	ggc	cct	aat	atc	ata	gat	cac	ttt	ata	tgt	480
Tyr	Gln	Ile	Pro	Phe	Cys	Gly	Pro	Asn	Ile	Ile	Asp	His	Phe	Ile	Cys	
145					150				155						160	
gat	ttg	ttt	cag	ttg	ttg	aca	ctt	gcc	tgc	acg	gac	acc	cac	atc	ctg	528
Asp	Leu	Phe	Gln	Leu	Leu	Thr	Leu	Ala	Cys	Thr	Asp	Thr	His	Ile	Leu	
			165					170						175		
ggc	ctc	tta	gtt	acc	ctc	aac	agt	ggg	atg	atg	tgt	gtg	gcc	atc	ttt	576
Gly	Leu	Leu	Val	Thr	Leu	Asn	Ser	Gly	Met	Met	Cys	Val	Ala	Ile	Phe	
			180					185					190			
ctt	atc	tta	att	gcg	tcc	tac	acg	gtc	atc	cta	tgc	tcc	ctg	aag	tct	624
Leu	Ile	Leu	Ile	Ala	Ser	Tyr	Thr	Val	Ile	Leu	Cys	Ser	Leu	Lys	Ser	
		195					200					205				
tac	agc	tct	aaa	ggg	cgg	cac	aaa	gcc	ctc	tct	acc	tgc	agc	tcc	cac	672
Tyr	Ser	Ser	Lys	Gly	Arg	His	Lys	Ala	Leu	Ser	Thr	Cys	Ser	Ser	His	
	210					215					220					
ctc	acg	gtg	gtt	gta	ttg	ttc	ttt	gtc	ccc	tgt	att	ttc	ttg	tac	atg	720
Leu	Thr	Val	Val	Val	Leu	Phe	Phe	Val	Pro	Cys	Ile	Phe	Leu	Tyr	Met	
225					230					235					240	

44/160

```

agg cct gtg gtc act cac ccc ata gac aag gca atg gct gtg tca gac 768
Arg Pro Val Val Thr His Pro Ile Asp Lys Ala Met Ala Val Ser Asp
                245                250                255

tca atc atc aca ccc atg tta aat ccc ttg atc tat aca ctg agg aat 816
Ser Ile Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn
                260                265                270

gca gag gac ata aga gag ata ctg agg ctg atg ttt cgt gcc ccc ttt 864
Ala Glu Asp Ile Arg Glu Ile Leu Arg Leu Met Phe Arg Ala Pro Phe
                275                280                285

tgt cct tta ttt tat ttt att ttt cca ggc tgg tct caa aat cct gag 912
Cys Pro Leu Phe Tyr Phe Ile Phe Pro Gly Trp Ser Gln Asn Pro Glu
                290                295                300

ctc agg tcg ccc tcc tcg gcc tcc caa agt tct gga gtt aca ggt gtg 960
Leu Arg Ser Pro Ser Ser Ala Ser Gln Ser Ser Gly Val Thr Gly Val
305                310                315                320

agc cac tgc 969
Ser His Cys

```

<210> 38
 <211> 323
 <212> PRT
 <213> Homo sapiens

```

<400> 38
Asn Leu Glu Leu Trp Lys Ile Phe Ser Ala Val Phe Leu Val Met Tyr
1      5      10      15
Val Ala Thr Val Leu Glu Asn Leu Leu Ile Val Val Thr Ile Ile Thr
20      25      30
Ser Gln Ser Leu Arg Ser Pro Met Tyr Phe Phe Leu Thr Phe Leu Ser
35      40      45
Leu Leu Asp Val Met Phe Ser Ser Val Val Ala Pro Lys Val Ile Val
50      55      60
Asp Thr Leu Ser Lys Ser Thr Thr Ile Ser Leu Lys Gly Cys Leu Thr
65      70      75      80
Gln Leu Phe Val Glu His Phe Phe Gly Gly Val Gly Ile Ile Leu Leu
85      90      95
Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu His
100     105     110
Tyr Thr Ile Ile Met Ser Pro Arg Val Cys Cys Leu Met Val Gly Gly
115     120     125
Ala Trp Val Gly Gly Phe Met His Ala Met Ile Gln Leu Leu Phe Met
130     135     140
Tyr Gln Ile Pro Phe Cys Gly Pro Asn Ile Ile Asp His Phe Ile Cys
145     150     155     160
Asp Leu Phe Gln Leu Thr Leu Ala Cys Thr Asp Thr His Ile Leu
165     170     175
Gly Leu Leu Val Thr Leu Asn Ser Gly Met Met Cys Val Ala Ile Phe
180     185     190
Leu Ile Leu Ile Ala Ser Tyr Thr Val Ile Leu Cys Ser Leu Lys Ser
195     200     205
Tyr Ser Ser Lys Gly Arg His Lys Ala Leu Ser Thr Cys Ser Ser His
210     215     220
Leu Thr Val Val Val Leu Phe Phe Val Pro Cys Ile Phe Leu Tyr Met
225     230     235     240
Arg Pro Val Val Thr His Pro Ile Asp Lys Ala Met Ala Val Ser Asp
245     250     255

```

45/160

Ser Ile Ile Thr Pro Met Leu Asn Pro Leu Ile Tyr Thr Leu Arg Asn
 260 265 270
 Ala Glu Asp Ile Arg Glu Ile Leu Arg Leu Met Phe Arg Ala Pro Phe
 275 280 285
 Cys Pro Leu Phe Tyr Phe Ile Phe Pro Gly Trp Ser Gln Asn Pro Glu
 290 295 300
 Leu Arg Ser Pro Ser Ser Ala Ser Gln Ser Ser Gly Val Thr Gly Val
 305 310 315 320
 Ser His Cys

<210> 39
 <211> 924
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(924)

<400> 39
 gtg cac acg gcc tac ctg gtg ctg agc tcc ctg gcc atg ttc acc tgc 48
 Val His Thr Ala Tyr Leu Val Leu Ser Ser Leu Ala Met Phe Thr Cys
 1 5 10 15
 ctg tgc ggg atg gca ggc aac agc atg gtg atc tgg ctg ctg ggc ttt 96
 Leu Cys Gly Met Ala Gly Asn Ser Met Val Ile Trp Leu Leu Gly Phe
 20 25 30
 cga atg cac agg aac ccc ttc tgc atc tat atc ctc aac ctg gcg gca 144
 Arg Met His Arg Asn Pro Phe Cys Ile Tyr Ile Leu Asn Leu Ala Ala
 35 40 45
 gcc gac ctc ctc ttc ctc ttc agc atg gct tcc acg ctc agc ctg gaa 192
 Ala Asp Leu Leu Phe Leu Phe Ser Met Ala Ser Thr Leu Ser Leu Glu
 50 55 60
 acc cag ccc ctg gtc aat acc act gac aag gtc cac gag ctg atg aag 240
 Thr Gln Pro Leu Val Asn Thr Thr Asp Lys Val His Glu Leu Met Lys
 65 70 75 80
 aga ctg atg tac ttt gcc tac aca gtg ggc ctg agc ctg ctg acg gcc 288
 Arg Leu Met Tyr Phe Ala Tyr Thr Val Gly Leu Ser Leu Leu Thr Ala
 85 90 95
 atc agc acc cag cgc tgt ctc tct gtc ctc ttc cct atc tgg ttc aag 336
 Ile Ser Thr Gln Arg Cys Leu Ser Val Leu Phe Pro Ile Trp Phe Lys
 100 105 110
 tgt cac cgg ccc agg cac ctg tca gcc tgg gtg tgt ggc ctg ctg tgg 384
 Cys His Arg Pro Arg His Leu Ser Ala Trp Val Cys Gly Leu Leu Trp
 115 120 125
 aca ctc tgt ctc ctg atg aac ggg ttg acc tct tcc ttc tgc agc aag 432
 Thr Leu Cys Leu Leu Met Asn Gly Leu Thr Ser Ser Phe Cys Ser Lys
 130 135 140
 ttc ttg aaa ttc aat gaa gat cgg tgc ttc agg gtg gac atg gtc cag 480
 Phe Leu Lys Phe Asn Glu Asp Arg Cys Phe Arg Val Asp Met Val Gln
 145 150 155 160
 gcc gcc ctc atc atg ggg gtc tta acc cca gtg atg act ctg tcc agc 528

46/160

Ala	Ala	Leu	Ile	Met	Gly	Val	Leu	Thr	Pro	Val	Met	Thr	Leu	Ser	Ser		
				165					170					175			
ctg	acc	ctc	ttt	gtc	tgg	gtg	cgg	agg	agc	tcc	cag	cag	tgg	cgg	cgg	576	
Leu	Thr	Leu	Phe	Val	Trp	Val	Arg	Arg	Ser	Ser	Gln	Gln	Trp	Arg	Arg		
			180					185					190				
cag	ccc	aca	cgg	ctg	ttc	gtg	gtg	gtc	ctg	gcc	tct	gtc	ctg	gtg	ttc	624	
Gln	Pro	Thr	Arg	Leu	Phe	Val	Val	Val	Leu	Ala	Ser	Val	Leu	Val	Phe		
			195					200				205					
ctc	atc	tgt	tcc	ctg	cct	ctg	agc	atc	tac	tgg	ttt	gtg	ctc	tac	tgg	672	
Leu	Ile	Cys	Ser	Leu	Pro	Leu	Ser	Ile	Tyr	Trp	Phe	Val	Leu	Tyr	Trp		
	210					215					220						
ttg	agc	ctg	ccg	ccc	gag	atg	cag	gtc	ctg	tgc	ttc	agc	ttg	tca	cgc	720	
Leu	Ser	Leu	Pro	Pro	Glu	Met	Gln	Val	Leu	Cys	Phe	Ser	Leu	Ser	Arg		
225					230					235					240		
ctc	tcc	tcg	tcc	gta	agc	agc	agc	gcc	aac	ccc	gtc	atc	tac	ttc	ctg	768	
Leu	Ser	Ser	Ser	Val	Ser	Ser	Ser	Ala	Asn	Pro	Val	Ile	Tyr	Phe	Leu		
				245					250					255			
gtg	ggc	agc	cgg	agg	agc	cac	agg	ctg	ccc	acc	aga	cag	ggg	cgg	tgc	816	
Val	Gly	Ser	Arg	Arg	Ser	His	Arg	Leu	Pro	Thr	Arg	Gln	Gly	Arg	Cys		
			260					265					270				
ctc	aca	ctg	tca	acc	cga	ttc	cgt	gag	aac	tct	atc	acg	aga	aca	gca	864	
Leu	Thr	Leu	Ser	Thr	Arg	Phe	Arg	Glu	Asn	Ser	Ile	Thr	Arg	Thr	Ala		
		275					280					285					
cca	cgg	ggg	aaa	tcc	acc	ccc	agg	atc	caa	tca	cct	tcc	acc	agg	cca	912	
Pro	Arg	Gly	Lys	Ser	Thr	Pro	Arg	Ile	Gln	Ser	Pro	Ser	Thr	Arg	Pro		
	290					295					300						
cac	atc	cta	caa													924	
His	Ile	Leu	Gln														
305																	

<210> 40

<211> 308

<212> PRT

<213> Homo sapiens

<400> 40

Val	His	Thr	Ala	Tyr	Leu	Val	Leu	Ser	Ser	Leu	Ala	Met	Phe	Thr	Cys		
1				5					10					15			
Leu	Cys	Gly	Met	Ala	Gly	Asn	Ser	Met	Val	Ile	Trp	Leu	Leu	Gly	Phe		
			20					25					30				
Arg	Met	His	Arg	Asn	Pro	Phe	Cys	Ile	Tyr	Ile	Leu	Asn	Leu	Ala	Ala		
		35					40					45					
Ala	Asp	Leu	Leu	Phe	Leu	Phe	Ser	Met	Ala	Ser	Thr	Leu	Ser	Leu	Glu		
	50					55					60						
Thr	Gln	Pro	Leu	Val	Asn	Thr	Thr	Asp	Lys	Val	His	Glu	Leu	Met	Lys		
	65				70				75					80			
Arg	Leu	Met	Tyr	Phe	Ala	Tyr	Thr	Val	Gly	Leu	Ser	Leu	Leu	Thr	Ala		
			85					90						95			
Ile	Ser	Thr	Gln	Arg	Cys	Leu	Ser	Val	Leu	Phe	Pro	Ile	Trp	Phe	Lys		
			100					105					110				
Cys	His	Arg	Pro	Arg	His	Leu	Ser	Ala	Trp	Val	Cys	Gly	Leu	Leu	Trp		

47/160

Thr	Leu	115	Cys	Leu	Leu	Met	Asn	120	Gly	Leu	Thr	Ser	Ser	125	Phe	Cys	Ser	Lys
	130						135						140					
Phe	Leu	Lys	Phe	Asn	Glu	Asp	Arg	Cys	Phe	Arg	Val	Asp	Met	Val	Gln			
145				150					155						160			
Ala	Ala	Leu	Ile	Met	Gly	Val	Leu	Thr	Pro	Val	Met	Thr	Leu	Ser	Ser			
				165					170						175			
Leu	Thr	Leu	Phe	Val	Trp	Val	Arg	Arg	Ser	Ser	Gln	Gln	Trp	Arg	Arg			
				180					185						190			
Gln	Pro	Thr	Arg	Leu	Phe	Val	Val	Val	Leu	Ala	Ser	Val	Leu	Val	Phe			
		195							200						205			
Leu	Ile	Cys	Ser	Leu	Pro	Leu	Ser	Ile	Tyr	Trp	Phe	Val	Leu	Tyr	Trp			
	210						215					220						
Leu	Ser	Leu	Pro	Pro	Glu	Met	Gln	Val	Leu	Cys	Phe	Ser	Leu	Ser	Arg			
225					230						235				240			
Leu	Ser	Ser	Ser	Val	Ser	Ser	Ser	Ala	Asn	Pro	Val	Ile	Tyr	Phe	Leu			
				245					250						255			
Val	Gly	Ser	Arg	Arg	Ser	His	Arg	Leu	Pro	Thr	Arg	Gln	Gly	Arg	Cys			
				260					265						270			
Leu	Thr	Leu	Ser	Thr	Arg	Phe	Arg	Glu	Asn	Ser	Ile	Thr	Arg	Thr	Ala			
		275							280						285			
Pro	Arg	Gly	Lys	Ser	Thr	Pro	Arg	Ile	Gln	Ser	Pro	Ser	Thr	Arg	Pro			
	290						295					300						
His	Ile	Leu	Gln															
305																		

<210> 41
 <211> 951
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(951)

<400> 41
 ccg tgt gtg gct ggc gtc atc cct gtc atc tac tac agt gtc ctg ctg 48
 Pro Cys Val Ala Gly Val Ile Pro Val Ile Tyr Tyr Ser Val Leu Leu
 1 5 10 15

ggc ttg ggg ctg cct ggt gac ctc ctg acc gca gtg gcc ctg gcg cgc 96
 Gly Leu Gly Leu Pro Gly Asp Leu Leu Thr Ala Val Ala Leu Ala Arg
 20 25 30

ctt gcc acc agg acc agg agg ccc tcc tac tac tac ctt ctg gcg ctc 144
 Leu Ala Thr Arg Thr Arg Arg Pro Ser Tyr Tyr Tyr Leu Leu Ala Leu
 35 40 45

aca gcc tcg gat atc atc atc cag gtg gtc atc gtg ttc gcg ggc ttc 192
 Thr Ala Ser Asp Ile Ile Ile Gln Val Val Ile Val Phe Ala Gly Phe
 50 55 60

ctc ctg cag gga gca gtg ctg gcc cgc cag gtg ccc cag gct gtg gtg 240
 Leu Leu Gln Gly Ala Val Leu Ala Arg Gln Val Pro Gln Ala Val Val
 65 70 75 80

cgc acg gcc aac atc ctg gag ttt gct gcc aac cac gcc tca gtc tgg 288
 Arg Thr Ala Asn Ile Leu Glu Phe Ala Ala Asn His Ala Ser Val Trp
 85 90 95

atc gcc atc ctg ctc acg gtt gac cgc tac act gcc ctg tgc cac ccc 336

48/160

Ile	Ala	Ile	Leu	Leu	Thr	Val	Asp	Arg	Tyr	Thr	Ala	Leu	Cys	His	Pro		
			100					105					110				
ctg	cac	cat	cgg	gcc	gcc	tcg	tcc	cca	ggc	cgg	acc	cgc	cgg	gcc	att	384	
Leu	His	His	Arg	Ala	Ala	Ser	Ser	Pro	Gly	Arg	Thr	Arg	Arg	Ala	Ile		
			115				120					125					
gct	gct	gtc	ctg	agt	gct	gcc	ctg	ttg	acc	ggc	atc	ccc	ttc	tac	tgg	432	
Ala	Ala	Val	Leu	Ser	Ala	Ala	Leu	Leu	Thr	Gly	Ile	Pro	Phe	Tyr	Trp		
			130				135				140						
tgg	ctg	gac	atg	tgg	aga	gac	acc	gac	tca	ccc	aga	aca	ctg	gac	gag	480	
Trp	Leu	Asp	Met	Trp	Arg	Asp	Thr	Asp	Ser	Pro	Arg	Thr	Leu	Asp	Glu		
					150					155					160		
gtc	ctc	aag	tgg	gct	cac	tgt	ctc	act	gtc	tat	ttc	atc	cct	tgt	ggc	528	
Val	Leu	Lys	Trp	Ala	His	Cys	Leu	Thr	Val	Tyr	Phe	Ile	Pro	Cys	Gly		
				165					170					175			
gtg	ttc	ctg	gtc	acc	aac	tcg	gcc	atc	atc	cac	cgg	cta	cgg	agg	agg	576	
Val	Phe	Leu	Val	Thr	Asn	Ser	Ala	Ile	Ile	His	Arg	Leu	Arg	Arg	Arg		
			180					185					190				
ggc	cgg	agt	ggg	ctg	cag	ccc	cgg	gtg	ggc	aag	agc	aca	gcc	atc	ctc	624	
Gly	Arg	Ser	Gly	Leu	Gln	Pro	Arg	Val	Gly	Lys	Ser	Thr	Ala	Ile	Leu		
		195					200					205					
ctg	ggc	atc	acc	aca	ctg	ttc	acc	ctc	ctg	tgg	gcg	ccc	cgg	gtc	ttc	672	
Leu	Gly	Ile	Thr	Thr	Leu	Phe	Thr	Leu	Leu	Trp	Ala	Pro	Arg	Val	Phe		
	210					215					220						
gtc	atg	ctc	tac	cac	atg	tac	gtg	gcc	cct	gtc	cac	cgg	gac	tgg	agg	720	
Val	Met	Leu	Tyr	His	Met	Tyr	Val	Ala	Pro	Val	His	Arg	Asp	Trp	Arg		
	225				230				235					240			
gtc	cac	ctg	gcc	ttg	gat	gtg	gcc	aat	atg	gtg	gcc	atg	ctc	cac	acg	768	
Val	His	Leu	Ala	Leu	Asp	Val	Ala	Asn	Met	Val	Ala	Met	Leu	His	Thr		
			245					250					255				
gca	gcc	aac	ttc	ggc	ctc	tac	tgc	ttt	gtc	agc	aag	act	ttc	cgg	gcc	816	
Ala	Ala	Asn	Phe	Gly	Leu	Tyr	Cys	Phe	Val	Ser	Lys	Thr	Phe	Arg	Ala		
			260					265					270				
act	ttt	tgc	tct	tgt	tgc	cca	agc	tgt	agt	gca	atg	ggg	cga	tct	cag	864	
Thr	Phe	Cys	Ser	Cys	Cys	Pro	Ser	Cys	Ser	Ala	Met	Gly	Arg	Ser	Gln		
		275				280					285						
ctc	act	gca	acc	tcc	tcc	tcc	cgg	gtt	caa	gca	gtt	ctc	ctg	cct	cag	912	
Leu	Thr	Ala	Thr	Ser	Ser	Ser	Arg	Val	Gln	Ala	Val	Leu	Leu	Pro	Gln		
		290				295					300						
cct	ccc	gag	gag	ctg	gga	cta	cag	gcg	cgt	gcc	acc	aca				951	
Pro	Pro	Glu	Glu	Leu	Gly	Leu	Gln	Ala	Arg	Ala	Thr	Thr					
				305		310				315							

<210> 42

<211> 317

<212> PRT

<213> Homo sapiens

<400> 42

Pro Cys Val Ala Gly Val Ile Pro Val Ile Tyr Tyr Ser Val Leu Leu

49/160

```

1           5           10           15
Gly Leu Gly Leu Pro Gly Asp Leu Leu Thr Ala Val Ala Leu Ala Arg
20
Leu Ala Thr Arg Thr Arg Arg Pro Ser Tyr Tyr Tyr Leu Leu Ala Leu
35
Thr Ala Ser Asp Ile Ile Ile Gln Val Val Ile Val Phe Ala Gly Phe
50
Leu Leu Gln Gly Ala Val Leu Ala Arg Gln Val Pro Gln Ala Val Val
65
Arg Thr Ala Asn Ile Leu Glu Phe Ala Ala Asn His Ala Ser Val Trp
85
Ile Ala Ile Leu Leu Thr Val Asp Arg Tyr Thr Ala Leu Cys His Pro
100
Leu His His Arg Ala Ala Ser Ser Pro Gly Arg Thr Arg Arg Ala Ile
115
Ala Ala Val Leu Ser Ala Ala Leu Leu Thr Gly Ile Pro Phe Tyr Trp
130
135
140

Trp Leu Asp Met Trp Arg Asp Thr Asp Ser Pro Arg Thr Leu Asp Glu
145
Val Leu Lys Trp Ala His Cys Leu Thr Val Tyr Phe Ile Pro Cys Gly
165
Val Phe Leu Val Thr Asn Ser Ala Ile Ile His Arg Leu Arg Arg Arg
180
Gly Arg Ser Gly Leu Gln Pro Arg Val Gly Lys Ser Thr Ala Ile Leu
195
Leu Gly Ile Thr Thr Leu Phe Thr Leu Leu Trp Ala Pro Arg Val Phe
210
Val Met Leu Tyr His Met Tyr Val Ala Pro Val His Arg Asp Trp Arg
225
Val His Leu Ala Leu Asp Val Ala Asn Met Val Ala Met Leu His Thr
245
Ala Ala Asn Phe Gly Leu Tyr Cys Phe Val Ser Lys Thr Phe Arg Ala
260
Thr Phe Cys Ser Cys Cys Pro Ser Cys Ser Ala Met Gly Arg Ser Gln
275
Leu Thr Ala Thr Ser Ser Ser Arg Val Gln Ala Val Leu Leu Pro Gln
290
Pro Pro Glu Glu Leu Gly Leu Gln Ala Arg Ala Thr Thr
305
310
315

```

<210> 43
 <211> 957
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(957)

```

<400> 43
gac cca gaa ctg aag tta atc cct ttc agc ctg ttc ctg tcc atg tac   48
Asp Pro Glu Leu Lys Leu Ile Pro Phe Ser Leu Phe Leu Ser Met Tyr
1           5           10           15

ctg gtc acc atc ctg ggg aac ctg ctc att ctc ctg gct gtc atc tct   96
Leu Val Thr Ile Leu Gly Asn Leu Leu Ile Leu Leu Ala Val Ile Ser
20           25           30

gac tcc cac ctc cac acc ccc atg tac ttc ctt ctc ttt aat ctc tcc   144
Asp Ser His Leu His Thr Pro Met Tyr Phe Leu Leu Phe Asn Leu Ser
35           40           45

```

50/160

ttt	act	gac	atc	tgt	tta	acc	aca	acc	aca	gtc	cca	aag	atc	cta	gtg	192
Phe	Thr	Asp	Ile	Cys	Leu	Thr	Thr	Thr	Thr	Val	Pro	Lys	Ile	Leu	Val	
50						55					60					
aac	atc	caa	gct	cag	aat	cag	agt	atc	act	tac	aca	ggc	tgc	ctc	acc	240
Asn	Ile	Gln	Ala	Gln	Asn	Gln	Ser	Ile	Thr	Tyr	Thr	Gly	Cys	Leu	Thr	
65					70				75						80	
cag	atc	tgt	ctt	gtc	ttg	gtt	ttt	gct	ggc	ttg	gaa	agt	tgc	ttt	ctt	288
Gln	Ile	Cys	Leu	Val	Leu	Val	Phe	Ala	Gly	Leu	Glu	Ser	Cys	Phe	Leu	
				85					90					95		
gca	gtc	atg	gcc	tac	gac	cgc	tat	gtg	gcc	att	tgc	cac	cca	ctg	agg	336
Ala	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	His	Pro	Leu	Arg	
			100					105					110			
tac	aca	gtc	ctc	atg	aat	gtc	cat	ttc	tgg	ggc	ttg	ctg	att	ctt	ctc	384
Tyr	Thr	Val	Leu	Met	Asn	Val	His	Phe	Trp	Gly	Leu	Leu	Ile	Leu	Leu	
		115				120						125				
tcc	atg	ttc	atg	agc	act	atg	gat	gcc	ctg	gtt	cag	agt	ctg	atg	gta	432
Ser	Met	Phe	Met	Ser	Thr	Met	Asp	Ala	Leu	Val	Gln	Ser	Leu	Met	Val	
	130					135					140					
ttg	cag	ctg	tcc	ttc	tgc	aaa	aac	gtt	gaa	atc	cct	ttg	ttc	ttc	tgt	480
Leu	Gln	Leu	Ser	Phe	Cys	Lys	Asn	Val	Glu	Ile	Pro	Leu	Phe	Phe	Cys	
145					150				155						160	
gaa	ctc	gcc	tgt	tct	gac	acc	ctc	atc	aac	aac	atc	ctc	ata	tat	ttt	528
Glu	Leu	Ala	Cys	Ser	Asp	Thr	Leu	Ile	Asn	Asn	Ile	Leu	Ile	Tyr	Phe	
				165					170					175		
gca	agt	agt	gta	ttt	ggc	gca	att	cct	ctc	tct	gga	ata	att	ttc	tct	576
Ala	Ser	Ser	Val	Phe	Gly	Ala	Ile	Pro	Leu	Ser	Gly	Ile	Ile	Phe	Ser	
			180					185					190			
tat	tct	caa	ata	gtc	acc	tct	gtt	ctg	aga	atg	cca	tca	gca	aga	gga	624
Tyr	Ser	Gln	Ile	Val	Thr	Ser	Val	Leu	Arg	Met	Pro	Ser	Ala	Arg	Gly	
		195					200					205				
aag	tat	aaa	gcg	ttt	tcc	acc	tgt	ggc	tgt	cac	ctc	tct	gtt	ttt	tcc	672
Lys	Tyr	Lys	Ala	Phe	Ser	Thr	Cys	Gly	Cys	His	Leu	Ser	Val	Phe	Ser	
	210					215					220					
ttg	ttc	tat	ggg	aca	gct	ttt	ggg	gtg	tac	att	agt	tct	gct	gtt	gct	720
Leu	Phe	Tyr	Gly	Thr	Ala	Phe	Gly	Val	Tyr	Ile	Ser	Ser	Ala	Val	Ala	
225					230				235						240	
gag	tct	tcc	cga	att	act	gct	gtg	gct	tca	gtg	atg	tac	act	gtg	gtc	768
Glu	Ser	Ser	Arg	Ile	Thr	Ala	Val	Ala	Ser	Val	Met	Tyr	Thr	Val	Val	
				245					250					255		
cct	caa	atg	atg	aac	ccc	ttc	atc	tac	agc	ctg	aga	aat	aag	gag	atg	816
Pro	Gln	Met	Met	Asn	Pro	Phe	Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Glu	Met	
				260				265					270			
aag	aaa	gct	ttg	agg	aaa	ctt	att	gaa	tgc	ctg	act	ctt	tgt	ttt	gtt	864
Lys	Lys	Ala	Leu	Arg	Lys	Leu	Ile	Glu	Cys	Leu	Thr	Leu	Cys	Phe	Val	
		275				280						285				
ttg	ttt	ttt	tct	ctg	aga	tgg	agt	ctt	tct	ctg	tct	ccc	agg	ctg	gag	912
Leu	Phe	Phe	Ser	Leu	Arg	Trp	Ser	Leu	Ser	Leu	Ser	Pro	Arg	Leu	Glu	

51/160

290	295	300	
tgc aat ggc acg acc tcg gct cac tgc aac ttc cgc ctc cgg gtt			957
Cys Asn Gly Thr Thr Ser Ala His Cys Asn Phe Arg Leu Arg Val			
305	310	315	

<210> 44
 <211> 319
 <212> PRT
 <213> Homo sapiens

<400> 44

Asp	Pro	Glu	Leu	Lys	Leu	Ile	Pro	Phe	Ser	Leu	Phe	Leu	Ser	Met	Tyr
1				5					10					15	
Leu	Val	Thr	Ile	Leu	Gly	Asn	Leu	Leu	Ile	Leu	Leu	Ala	Val	Ile	Ser
			20					25					30		
Asp	Ser	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Leu	Leu	Phe	Asn	Leu	Ser
		35					40					45			
Phe	Thr	Asp	Ile	Cys	Leu	Thr	Thr	Thr	Val	Pro	Lys	Ile	Leu	Val	
	50					55				60					
Asn	Ile	Gln	Ala	Gln	Asn	Gln	Ser	Ile	Thr	Tyr	Thr	Gly	Cys	Leu	Thr
65					70					75					80
Gln	Ile	Cys	Leu	Val	Leu	Val	Phe	Ala	Gly	Leu	Glu	Ser	Cys	Phe	Leu
				85					90					95	
Ala	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	His	Pro	Leu	Arg
			100					105					110		
Tyr	Thr	Val	Leu	Met	Asn	Val	His	Phe	Trp	Gly	Leu	Leu	Ile	Leu	Leu
		115					120					125			
Ser	Met	Phe	Met	Ser	Thr	Met	Asp	Ala	Leu	Val	Gln	Ser	Leu	Met	Val
	130					135					140				
Leu	Gln	Leu	Ser	Phe	Cys	Lys	Asn	Val	Glu	Ile	Pro	Leu	Phe	Phe	Cys
145					150					155					160
Glu	Leu	Ala	Cys	Ser	Asp	Thr	Leu	Ile	Asn	Asn	Ile	Leu	Ile	Tyr	Phe
				165					170					175	
Ala	Ser	Ser	Val	Phe	Gly	Ala	Ile	Pro	Leu	Ser	Gly	Ile	Ile	Phe	Ser
			180					185					190		
Tyr	Ser	Gln	Ile	Val	Thr	Ser	Val	Leu	Arg	Met	Pro	Ser	Ala	Arg	Gly
		195					200					205			
Lys	Tyr	Lys	Ala	Phe	Ser	Thr	Cys	Gly	Cys	His	Leu	Ser	Val	Phe	Ser
	210					215					220				
Leu	Phe	Tyr	Gly	Thr	Ala	Phe	Gly	Val	Tyr	Ile	Ser	Ser	Ala	Val	Ala
225					230					235					240
Glu	Ser	Ser	Arg	Ile	Thr	Ala	Val	Ala	Ser	Val	Met	Tyr	Thr	Val	Val
				245					250					255	
Pro	Gln	Met	Met	Asn	Pro	Phe	Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Glu	Met
			260					265					270		
Lys	Lys	Ala	Leu	Arg	Lys	Leu	Ile	Glu	Cys	Leu	Thr	Leu	Cys	Phe	Val
		275					280					285			
Leu	Phe	Phe	Ser	Leu	Arg	Trp	Ser	Leu	Ser	Leu	Ser	Pro	Arg	Leu	Glu
	290					295					300				
Cys	Asn	Gly	Thr	Thr	Ser	Ala	His	Cys	Asn	Phe	Arg	Leu	Arg	Val	
305					310					315					

<210> 45
 <211> 984
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS

52/160

<222> (1)...(984)

<400> 45

gcc act gaa ttc cag gtt ctt ctc ttc ctt ctc ttc ctc ctc ctc tac	48
Ala Thr Glu Phe Gln Val Leu Leu Phe Leu Leu Phe Leu Leu Leu Tyr	
1 5 10 15	
ttg atg atc ctc tgt ggc aac aca gcc atc atc tgg gtg gtg tgc aca	96
Leu Met Ile Leu Cys Gly Asn Thr Ala Ile Ile Trp Val Val Cys Thr	
20 25 30	
cac agc acc ctc cgc acc ccg atg tat ttc ttc ctg tcc aac ctg tct	144
His Ser Thr Leu Arg Thr Pro Met Tyr Phe Phe Leu Ser Asn Leu Ser	
35 40 45	
ttc ctg gaa ctc tgc tac acc acc gtg gta gta ccc ttg atg ctt tcc	192
Phe Leu Glu Leu Cys Tyr Thr Thr Val Val Val Pro Leu Met Leu Ser	
50 55 60	
aac att ttg ggg gcc cag aag ccc att tcg ttg gct gga tgt ggg gcc	240
Asn Ile Leu Gly Ala Gln Lys Pro Ile Ser Leu Ala Gly Cys Gly Ala	
65 70 75 80	
caa atg ttc ttc ttt gtc acc ctc ggc agc acg gac tgt ttc ctc ttg	288
Gln Met Phe Phe Phe Val Thr Leu Gly Ser Thr Asp Cys Phe Leu Leu	
85 90 95	
gcg atc atg gcc tat gac cgc tat gtg gct atc tgc cac ccg ctg cac	336
Ala Ile Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His	
100 105 110	
tac acc ctc atc atg acc cgc gag ctg tgc acg cag atg ctg ggt ggg	384
Tyr Thr Leu Ile Met Thr Arg Glu Leu Cys Thr Gln Met Leu Gly Gly	
115 120 125	
gcc ctg ggc ctg gcc ctc ttc ccc tcc ctg cag ctc acc gcc tta atc	432
Ala Leu Gly Leu Ala Leu Phe Pro Ser Leu Gln Leu Thr Ala Leu Ile	
130 135 140	
ttc acc ctg ccc ttt tgc ggc cac cac cag gaa atc aac cac ttc ctc	480
Phe Thr Leu Pro Phe Cys Gly His His Gln Glu Ile Asn His Phe Leu	
145 150 155 160	
tgc gat gtg cct ccc gtc ctg cgc ctg gcc tgc gct gac atc cgc gtg	528
Cys Asp Val Pro Pro Val Leu Arg Leu Ala Cys Ala Asp Ile Arg Val	
165 170 175	
cac cag gct gtc ctc tat gtc gtg agc atc ctc gtg ctg acc atc ccc	576
His Gln Ala Val Leu Tyr Val Val Ser Ile Leu Val Leu Thr Ile Pro	
180 185 190	
ttc ctg ctc atc tgc gtc tcc tac gtg ttc atc acc tgt gcc atc ctg	624
Phe Leu Leu Ile Cys Val Ser Tyr Val Phe Ile Thr Cys Ala Ile Leu	
195 200 205	
agc atc cgt tct gcc gag ggc cgc cgc cgg gcc ttc tcc acc tgc tcc	672
Ser Ile Arg Ser Ala Glu Gly Arg Arg Arg Ala Phe Ser Thr Cys Ser	
210 215 220	
ttc cac ctc acc gtg gtc ctg ctg cac ttt cct ccc ctg cag gtt cac	720
Phe His Leu Thr Val Val Leu Leu His Phe Pro Pro Leu Gln Val His	
225 230 235 240	

[illegible]

```
<210> 46
<211> 328
<212> PRT
<213> Homo sapiens
```

<400>	46														
Ala	Thr	Glu	Phe	Gln	Val	Leu	Leu	Phe	Leu	Leu	Phe	Leu	Leu	Leu	Tyr
1				5					10					15	
Leu	Met	Ile	Leu	Cys	Gly	Asn	Thr	Ala	Ile	Ile	Trp	Val	Val	Cys	Thr
		20						25				30			
His	Ser	Thr	Leu	Arg	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ser	Asn	Leu	Ser
		35					40					45			
Phe	Leu	Glu	Leu	Cys	Tyr	Thr	Thr	Val	Val	Val	Pro	Leu	Met	Leu	Ser
		50				55					60				
Asn	Ile	Leu	Gly	Ala	Gln	Lys	Pro	Ile	Ser	Leu	Ala	Gly	Cys	Gly	Ala
65				70						75				80	
Gln	Met	Phe	Phe	Phe	Val	Thr	Leu	Gly	Ser	Thr	Asp	Cys	Phe	Leu	Leu
				85					90					95	
Ala	Ile	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	His	Pro	Leu	His
			100					105					110		
Tyr	Thr	Leu	Ile	Met	Thr	Arg	Glu	Leu	Cys	Thr	Gln	Met	Leu	Gly	Gly
		115					120					125			
Ala	Leu	Gly	Leu	Ala	Leu	Phe	Pro	Ser	Leu	Gln	Leu	Thr	Ala	Leu	Ile
		130				135					140				
Phe	Thr	Leu	Pro	Phe	Cys	Gly	His	His	Gln	Glu	Ile	Asn	His	Phe	Leu
145				150						155					160
Cys	Asp	Val	Pro	Pro	Val	Leu	Arg	Leu	Ala	Cys	Ala	Asp	Ile	Arg	Val
				165					170					175	
His	Gln	Ala	Val	Leu	Tyr	Val	Val	Ser	Ile	Leu	Val	Leu	Thr	Ile	Pro
			180					185					190		
Phe	Leu	Leu	Ile	Cys	Val	Ser	Tyr	Val	Phe	Ile	Thr	Cys	Ala	Ile	Leu
		195					200					205			
Ser	Ile	Arg	Ser	Ala	Glu	Gly	Arg	Arg	Arg	Ala	Phe	Ser	Thr	Cys	Ser
		210				215					220				
Phe	His	Leu	Thr	Val	Val	Leu	Leu	His	Phe	Pro	Pro	Leu	Gln	Val	His
225				230						235					240

54/160

His Phe Phe Lys Asn Ser Ala Pro Phe Lys Thr Leu Leu Ile Pro Phe
 245 250 255
 Ile Gln Pro Phe Gly Tyr Val Asn Val Ile Pro Met Leu Asn Pro Leu
 260 265 270
 Ile Tyr Ser Leu Arg Asn Lys Glu Val Lys Glu Ala Leu Arg Lys Ile
 275 280 285
 Leu Asn Arg Ala Lys Thr Gln Val Thr Gln Thr His Arg Glu Thr Gly
 290 295 300
 Ser His Ile His Arg Gln Thr Asp Gly Cys Arg Pro Arg Gln Thr Gly
 305 310 315 320
 Arg Tyr Leu His Arg Gln Thr Glu
 325

<210> 47
 <211> 939
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(939)

<400> 47
 gac cct cag atg gag atc atc ttc ttc gtg gtc ttc ctc ata gtt tac 48
 Asp Pro Gln Met Glu Ile Ile Phe Phe Val Val Phe Leu Ile Val Tyr
 1 5 10 15
 ctg gtt aat gta gtg ggg aat att ggt atg att atc ctg att aca aca 96
 Leu Val Asn Val Val Gly Asn Ile Gly Met Ile Ile Leu Ile Thr Thr
 20 25 30
 gac act cag ctt cac aca ccc atg tat ttt ttc ctc tgc aac ctc tcc 144
 Asp Thr Gln Leu His Thr Pro Met Tyr Phe Phe Leu Cys Asn Leu Ser
 35 40 45
 ttt gtt gac ctg ggc tac tcc tca gcc att gcc ccc agg atg ctg gct 192
 Phe Val Asp Leu Gly Tyr Ser Ser Ala Ile Ala Pro Arg Met Leu Ala
 50 55 60
 gac ttc cta aca aat cac aaa gtt atc tcc ttc tcc agc tgt gcc acc 240
 Asp Phe Leu Thr Asn His Lys Val Ile Ser Phe Ser Ser Cys Ala Thr
 65 70 75 80
 cag ttt gct ttt ttt gta ggt ttt gtg gat gct gag tgc tat gtc ctg 288
 Gln Phe Ala Phe Phe Val Gly Phe Val Asp Ala Glu Cys Tyr Val Leu
 85 90 95
 gca gcc atg gcc tat ggt cgt ttt gtg gcc att tgt cga ccc ctc cac 336
 Ala Ala Met Ala Tyr Gly Arg Phe Val Ala Ile Cys Arg Pro Leu His
 100 105 110
 tat agc acc ttc atg tcc aag cag gtc tgc ttg gct ctc atg ctg ggc 384
 Tyr Ser Thr Phe Met Ser Lys Gln Val Cys Leu Ala Leu Met Leu Gly
 115 120 125
 tct tac ctg gct ggt cta gtg agt tta gta gcc cac act acc ctc acc 432
 Ser Tyr Leu Ala Gly Leu Val Ser Leu Val Ala His Thr Thr Leu Thr
 130 135 140
 ttc agc ctg agt tac tgt ggt tgc tgc ata tat tta aag gaa aga gca 480
 Phe Ser Leu Ser Tyr Cys Gly Cys Cys Ile Tyr Leu Lys Glu Arg Ala
 145 150 155 160

55/160

```

gga cat aga aaa tta aat tat agt atc ttt ttt atc ctt ttt tct tta 528
Gly His Arg Lys Leu Asn Tyr Ser Ile Phe Phe Ile Leu Phe Ser Leu
165 170 175

ttt ttc tcc ctc atc ata atc ctc atc tcc tac atc ttc att ctc att 576
Phe Phe Ser Leu Ile Ile Ile Leu Ile Ser Tyr Ile Phe Ile Leu Ile
180 185 190

gcc atc ctg agg atg cgt tct gct gaa agt agg cgc aaa gcg ttc tcc 624
Ala Ile Leu Arg Met Arg Ser Ala Glu Ser Arg Arg Lys Ala Phe Ser
195 200 205

acc tgc ggg tcc cac ctg gtg gca gtg act gtg ttt tat gga acc ctg 672
Thr Cys Gly Ser His Leu Val Ala Val Thr Val Phe Tyr Gly Thr Leu
210 215 220

ttc tgc atg tac gtt aga cct ccc acg gac agg tca gtg gaa cag tcc 720
Phe Cys Met Tyr Val Arg Pro Pro Thr Asp Arg Ser Val Glu Gln Ser
225 230 235 240

aaa gtc att gct gtt ttc tac act ttt gta agc cct atg ttg aac ccc 768
Lys Val Ile Ala Val Phe Tyr Thr Phe Val Ser Pro Met Leu Asn Pro
245 250 255

atc atc tat agt ttg agg aac aag gat gtg aaa caa gct ttt tgg aaa 816
Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Gln Ala Phe Trp Lys
260 265 270

ctg atc aga aga aac aaa agc atg gcc tgt ggc agg gtg gga aag aca 864
Leu Ile Arg Arg Asn Lys Ser Met Ala Cys Gly Arg Val Gly Lys Thr
275 280 285

aaa tgt tca gag agg cca gag aaa gac cca tcc att tgc agc gac agt 912
Lys Cys Ser Glu Arg Pro Glu Lys Asp Pro Ser Ile Cys Ser Asp Ser
290 295 300

gaa att gtg gct gct gtt gtg aag gaa 939
Glu Ile Val Ala Ala Val Val Lys Glu
305 310

```

<210> 48

<211> 313

<212> PRT

<213> Homo sapiens

<400> 48

```

Asp Pro Gln Met Glu Ile Ile Phe Phe Val Val Phe Leu Ile Val Tyr
1 5 10 15
Leu Val Asn Val Val Gly Asn Ile Gly Met Ile Ile Leu Ile Thr Thr
20 25 30
Asp Thr Gln Leu His Thr Pro Met Tyr Phe Phe Leu Cys Asn Leu Ser
35 40 45
Phe Val Asp Leu Gly Tyr Ser Ser Ala Ile Ala Pro Arg Met Leu Ala
50 55 60
Asp Phe Leu Thr Asn His Lys Val Ile Ser Phe Ser Ser Cys Ala Thr
65 70 75 80
Gln Phe Ala Phe Phe Val Gly Phe Val Asp Ala Glu Cys Tyr Val Leu
85 90 95
Ala Ala Met Ala Tyr Gly Arg Phe Val Ala Ile Cys Arg Pro Leu His
100 105 110
Tyr Ser Thr Phe Met Ser Lys Gln Val Cys Leu Ala Leu Met Leu Gly

```


56/160

```

      115      120      125
Ser Tyr Leu Ala Gly Leu Val Ser Leu Val Ala His Thr Thr Leu Thr
      130      135      140
Phe Ser Leu Ser Tyr Cys Gly Cys Cys Ile Tyr Leu Lys Glu Arg Ala
145      150      155      160
Gly His Arg Lys Leu Asn Tyr Ser Ile Phe Phe Ile Leu Phe Ser Leu
      165      170      175
Phe Phe Ser Leu Ile Ile Ile Leu Ile Ser Tyr Ile Phe Ile Leu Ile
      180      185      190
Ala Ile Leu Arg Met Arg Ser Ala Glu Ser Arg Arg Lys Ala Phe Ser
      195      200      205

Thr Cys Gly Ser His Leu Val Ala Val Thr Val Phe Tyr Gly Thr Leu
      210      215      220
Phe Cys Met Tyr Val Arg Pro Pro Thr Asp Arg Ser Val Glu Gln Ser
225      230      235      240
Lys Val Ile Ala Val Phe Tyr Thr Phe Val Ser Pro Met Leu Asn Pro
      245      250      255
Ile Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Gln Ala Phe Trp Lys
      260      265      270
Leu Ile Arg Arg Asn Lys Ser Met Ala Cys Gly Arg Val Gly Lys Thr
      275      280      285
Lys Cys Ser Glu Arg Pro Glu Lys Asp Pro Ser Ile Cys Ser Asp Ser
      290      295      300
Glu Ile Val Ala Ala Val Val Lys Glu
305      310

```

<210> 49
 <211> 942
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(942)

```

<400> 49
aac tca gag gta cag aga gtt ctc ttt gtg gtc ttt ttg ctg atc tat   48
Asn Ser Glu Val Gln Arg Val Leu Phe Val Val Phe Leu Leu Ile Tyr
  1              5              10              15

gtg gtc acg gtt tgt ggc aac atg ctc att gtg gtc act atc acc tcc   96
Val Val Thr Val Cys Gly Asn Met Leu Ile Val Val Thr Ile Thr Ser
      20              25              30

agc ccc acg ctg gct tcc cct gtg tat ttt ttc ctg gcc aac cta tcc   144
Ser Pro Thr Leu Ala Ser Pro Val Tyr Phe Phe Leu Ala Asn Leu Ser
      35              40              45

ttt att gac acc ttt tat tct tct tct atg gct cct aaa ctc att gct   192
Phe Ile Asp Thr Phe Tyr Ser Ser Ser Met Ala Pro Lys Leu Ile Ala
      50              55              60

gac tca ttg tat gag ggg aga acc atc tct tat gag tgc tgc atg gct   240
Asp Ser Leu Tyr Glu Gly Arg Thr Ile Ser Tyr Glu Cys Cys Met Ala
      65              70              75              80

cag ctc ttt gga gct cat ttt ttg gga ggt gtt gag atc att ctg ctc   288
Gln Leu Phe Gly Ala His Phe Leu Gly Gly Val Glu Ile Ile Leu Leu
      85              90              95

aca gtg atg gct tat gac cgc tat gtg gcc atc tgt aag ccc ctg cac   336

```

57/160

Thr	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Lys	Pro	Leu	His		
			100					105					110				
aat	act	acc	atc	atg	acc	agg	cat	ctc	tgt	gcc	atg	ctt	gta	ggg	gtg	384	
Asn	Thr	Thr	Ile	Met	Thr	Arg	His	Leu	Cys	Ala	Met	Leu	Val	Gly	Val		
		115					120					125					
gct	tgg	ctt	ggg	ggc	ttc	ctg	cat	tca	ttg	gtt	cag	ctc	ctc	ctg	gtc	432	
Ala	Trp	Leu	Gly	Gly	Phe	Leu	His	Ser	Leu	Val	Gln	Leu	Leu	Leu	Val		
	130					135					140						
ctt	tgg	ttg	ccc	ttc	tgt	ggg	ccc	aat	gtg	atc	aat	cac	ttt	gcc	ttt	480	
Leu	Trp	Leu	Pro	Phe	Cys	Gly	Pro	Asn	Val	Ile	Asn	His	Phe	Ala	Phe		
145					150					155					160		
gcc	tgc	acc	aat	acg	tat	gtc	att	ggg	ctg	ctg	gtg	gtt	gcc	aac	agt	528	
Ala	Cys	Thr	Asn	Thr	Tyr	Val	Ile	Gly	Leu	Leu	Val	Val	Ala	Asn	Ser		
				165					170					175			
ggg	tta	atc	tgc	ctg	ttg	aac	ttc	ctc	atg	ctg	gct	gcc	tcc	tac	att	576	
Gly	Leu	Ile	Cys	Leu	Leu	Asn	Phe	Leu	Met	Leu	Ala	Ala	Ser	Tyr	Ile		
			180					185					190				
gtc	atc	ctg	tac	tcc	ttg	agg	tcc	cac	agt	gca	gat	ggg	aga	tgc	aaa	624	
Val	Ile	Leu	Tyr	Ser	Leu	Arg	Ser	His	Ser	Ala	Asp	Gly	Arg	Cys	Lys		
		195					200					205					
gcc	ctc	tcc	acc	tgt	gga	gcc	cac	ttc	att	gtt	gtt	gcc	ttg	ttc	ttt	672	
Ala	Leu	Ser	Thr	Cys	Gly	Ala	His	Phe	Ile	Val	Val	Ala	Leu	Phe	Phe		
	210					215					220						
gtg	ccc	tgt	ata	ttt	act	tat	gtg	cat	cca	ttt	tct	act	tta	cct	ata	720	
Val	Pro	Cys	Ile	Phe	Thr	Tyr	Val	His	Pro	Phe	Ser	Thr	Leu	Pro	Ile		
225					230					235					240		
gac	aaa	aat	atg	gca	tta	ttt	tat	ggg	att	ctg	aca	cct	atg	ttg	aat	768	
Asp	Lys	Asn	Met	Ala	Leu	Phe	Tyr	Gly	Ile	Leu	Thr	Pro	Met	Leu	Asn		
				245				250						255			
cca	ctc	att	tat	acc	ctg	aga	aat	gaa	gag	gta	aaa	aat	gcc	atg	aga	816	
Pro	Leu	Ile	Tyr	Thr	Leu	Arg	Asn	Glu	Glu	Val	Lys	Asn	Ala	Met	Arg		
			260					265					270				
aag	ctc	ttt	aca	tgg	cag	gcc	aac	att	cag	att	cag	gaa	ata	cag	aga	864	
Lys	Leu	Phe	Thr	Trp	Gln	Ala	Asn	Ile	Gln	Ile	Gln	Glu	Ile	Gln	Arg		
		275					280					285					
atg	cca	caa	aga	tac	tcc	tca	aga	aga	gca	act	cca	aga	cac	ata	aat	912	
Met	Pro	Gln	Arg	Tyr	Ser	Ser	Arg	Arg	Ala	Thr	Pro	Arg	His	Ile	Asn		
	290					295					300						
gtc	aga	ttc	acc	aaa	gtt	gaa	atg	aag	gaa							942	
Val	Arg	Phe	Thr	Lys	Val	Glu	Met	Lys	Glu								
305					310												

<210> 50

<211> 314

<212> PRT

<213> Homo sapiens

<400> 50

Asn Ser Glu Val Gln Arg Val Leu Phe Val Val Phe Leu Leu Ile Tyr

58/160

```

      1           5           10           15
Val Val Thr Val Cys Gly Asn Met Leu Ile Val Val Thr Ile Thr Ser
      20           25           30
Ser Pro Thr Leu Ala Ser Pro Val Tyr Phe Phe Leu Ala Asn Leu Ser
      35           40           45
Phe Ile Asp Thr Phe Tyr Ser Ser Ser Met Ala Pro Lys Leu Ile Ala
      50           55           60
Asp Ser Leu Tyr Glu Gly Arg Thr Ile Ser Tyr Glu Cys Cys Met Ala
      65           70           75           80

Gln Leu Phe Gly Ala His Phe Leu Gly Gly Val Glu Ile Ile Leu Leu
      85           90           95
Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu His
      100          105          110
Asn Thr Thr Ile Met Thr Arg His Leu Cys Ala Met Leu Val Gly Val
      115          120          125
Ala Trp Leu Gly Gly Phe Leu His Ser Leu Val Gln Leu Leu Leu Val
      130          135          140
Leu Trp Leu Pro Phe Cys Gly Pro Asn Val Ile Asn His Phe Ala Phe
      145          150          155          160
Ala Cys Thr Asn Thr Tyr Val Ile Gly Leu Leu Val Val Ala Asn Ser
      165          170          175
Gly Leu Ile Cys Leu Leu Asn Phe Leu Met Leu Ala Ala Ser Tyr Ile
      180          185          190
Val Ile Leu Tyr Ser Leu Arg Ser His Ser Ala Asp Gly Arg Cys Lys
      195          200          205
Ala Leu Ser Thr Cys Gly Ala His Phe Ile Val Val Ala Leu Phe Phe
      210          215          220
Val Pro Cys Ile Phe Thr Tyr Val His Pro Phe Ser Thr Leu Pro Ile
      225          230          235          240
Asp Lys Asn Met Ala Leu Phe Tyr Gly Ile Leu Thr Pro Met Leu Asn
      245          250          255
Pro Leu Ile Tyr Thr Leu Arg Asn Glu Glu Val Lys Asn Ala Met Arg
      260          265          270
Lys Leu Phe Thr Trp Gln Ala Asn Ile Gln Ile Gln Glu Ile Gln Arg
      275          280          285
Met Pro Gln Arg Tyr Ser Ser Arg Arg Ala Thr Pro Arg His Ile Asn
      290          295          300
Val Arg Phe Thr Lys Val Glu Met Lys Glu
      305          310

```

<210> 51
 <211> 972
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(972)

```

<400> 51
gac atg gaa tca tct ttc tca ttt gga gtg atc ctt gct gtc ctg gcc 48
Asp Met Glu Ser Ser Phe Ser Phe Gly Val Ile Leu Ala Val Leu Ala
      1           5           10           15

tcc ctc atc att gct act aac aca cta gtg gct gtg gct gtg ctg ctg 96
Ser Leu Ile Ile Ala Thr Asn Thr Leu Val Ala Val Ala Val Leu Leu
      20           25           30

ttg atc cac aag aat gat ggt gtc agt ctc tgc ttc acc ttg aat ctg 144
Leu Ile His Lys Asn Asp Gly Val Ser Leu Cys Phe Thr Leu Asn Leu
      35           40           45

```

59/160

gct	gtg	gct	gac	acc	ttg	att	ggg	gtg	gcc	atc	tct	ggc	cta	ctc	aca	192
Ala	Val	Ala	Asp	Thr	Leu	Ile	Gly	Val	Ala	Ile	Ser	Gly	Leu	Leu	Thr	
	50					55					60					
gac	cag	ctc	tcc	agc	cct	tct	cgg	ccc	aca	cag	aag	acc	ctg	tgc	agc	240
Asp	Gln	Leu	Ser	Ser	Pro	Ser	Arg	Pro	Thr	Gln	Lys	Thr	Leu	Cys	Ser	
	65				70					75					80	
ctg	cgg	atg	gca	ttt	gtc	act	tcc	tcc	gca	gct	gcc	tct	gtc	ctc	acg	288
Leu	Arg	Met	Ala	Phe	Val	Thr	Ser	Ser	Ala	Ala	Ala	Ser	Val	Leu	Thr	
				85					90					95		
gtc	atg	ctg	atc	acc	ttt	gac	agg	tac	ctt	gcc	atc	aag	cag	ccc	ttc	336
Val	Met	Leu	Ile	Thr	Phe	Asp	Arg	Tyr	Leu	Ala	Ile	Lys	Gln	Pro	Phe	
			100					105					110			
cgc	tac	ttg	aag	atc	atg	agt	ggg	ttc	gtg	gcc	ggg	gcc	tgc	att	gcc	384
Arg	Tyr	Leu	Lys	Ile	Met	Ser	Gly	Phe	Val	Ala	Gly	Ala	Cys	Ile	Ala	
		115					120					125				
ggg	ctg	tgg	tta	gtg	tct	tac	ctc	att	ggc	ttc	ctc	cca	ctc	gga	atc	432
Gly	Leu	Trp	Leu	Val	Ser	Tyr	Leu	Ile	Gly	Phe	Leu	Pro	Leu	Gly	Ile	
	130					135						140				
ccc	atg	ttc	cag	cag	act	gcc	tac	aaa	ggg	cag	tgc	agc	ttc	ttt	gct	480
Pro	Met	Phe	Gln	Gln	Thr	Ala	Tyr	Lys	Gly	Gln	Cys	Ser	Phe	Phe	Ala	
	145					150				155					160	
gta	ttt	cac	cct	cac	ttc	gtg	ctg	acc	ctc	tcc	tgc	gtt	ggc	ttc	ttc	528
Val	Phe	His	Pro	His	Phe	Val	Leu	Thr	Leu	Ser	Cys	Val	Gly	Phe	Phe	
				165					170					175		
cca	gcc	atg	ctc	ctc	ttt	gtc	ttc	ttc	tac	tgc	gac	atg	ctc	aag	att	576
Pro	Ala	Met	Leu	Leu	Phe	Val	Phe	Phe	Tyr	Cys	Asp	Met	Leu	Lys	Ile	
			180					185					190			
gcc	tcc	atg	cac	agc	cag	cag	att	cga	aag	atg	gaa	cat	gca	gga	gcc	624
Ala	Ser	Met	His	Ser	Gln	Gln	Ile	Arg	Lys	Met	Glu	His	Ala	Gly	Ala	
		195					200					205				
atg	gct	gga	gct	ctc	cgt	act	gtg	tct	gtt	ctc	att	ggg	agc	ttt	gct	672
Met	Ala	Gly	Ala	Leu	Arg	Thr	Val	Ser	Val	Leu	Ile	Gly	Ser	Phe	Ala	
	210					215					220					
cta	tcc	tgg	acc	ccc	ttc	ctt	atc	act	ggc	att	gtg	cag	gtg	gcc	tgc	720
Leu	Ser	Trp	Thr	Pro	Phe	Leu	Ile	Thr	Gly	Ile	Val	Gln	Val	Ala	Cys	
	225				230					235					240	
cag	gag	tgt	cac	ctc	tac	cta	gtg	ctg	gaa	cgg	tac	ctg	tgg	ctg	ctc	768
Gln	Glu	Cys	His	Leu	Tyr	Leu	Val	Leu	Glu	Arg	Tyr	Leu	Trp	Leu	Leu	
				245					250					255		
ggc	gtg	ggc	aac	tcc	ctg	ctc	aac	cca	ctc	atc	tat	gcc	tat	tgg	cag	816
Gly	Val	Gly	Asn	Ser	Leu	Leu	Asn	Pro	Leu	Ile	Tyr	Ala	Tyr	Trp	Gln	
			260				265						270			
aag	gag	ttc	cgt	aac	att	ctg	ctc	ttc	tgc	ctc	aca	tgt	gtc	tct	att	864
Lys	Glu	Phe	Arg	Asn	Ile	Leu	Leu	Phe	Cys	Leu	Thr	Cys	Val	Ser	Ile	
		275				280						285				
acc	tct	ttg	aga	aag	aag	ctc	ttt	cgt	tgt	att	cac	cat	gtg	gct	aac	912
Thr	Ser	Leu	Arg	Lys	Lys	Leu	Phe	Arg	Cys	Ile	His	His	Val	Ala	Asn	

60/160

290	295	300	
ttt ata tgt ata cat atg cat aca cac aca cac aca cac aca cac aca	960		
Phe Ile Cys Ile His Met His Thr His Thr His Thr His Thr His Thr			
305 310 315 320			
cac aca cac aca	972		
His Thr His Thr			

<210> 52
 <211> 324
 <212> PRT
 <213> Homo sapiens

<400> 52

Asp Met Glu Ser Ser Phe Ser Phe Gly Val Ile Leu Ala Val Leu Ala	
1 5 10 15	
Ser Leu Ile Ile Ala Thr Asn Thr Leu Val Ala Val Ala Val Leu Leu	
20 25 30	
Leu Ile His Lys Asn Asp Gly Val Ser Leu Cys Phe Thr Leu Asn Leu	
35 40 45	
Ala Val Ala Asp Thr Leu Ile Gly Val Ala Ile Ser Gly Leu Leu Thr	
50 55 60	
Asp Gln Leu Ser Ser Pro Ser Arg Pro Thr Gln Lys Thr Leu Cys Ser	
65 70 75 80	
Leu Arg Met Ala Phe Val Thr Ser Ser Ala Ala Ala Ser Val Leu Thr	
85 90 95	
Val Met Leu Ile Thr Phe Asp Arg Tyr Leu Ala Ile Lys Gln Pro Phe	
100 105 110	
Arg Tyr Leu Lys Ile Met Ser Gly Phe Val Ala Gly Ala Cys Ile Ala	
115 120 125	
Gly Leu Trp Leu Val Ser Tyr Leu Ile Gly Phe Leu Pro Leu Gly Ile	
130 135 140	
Pro Met Phe Gln Gln Thr Ala Tyr Lys Gly Gln Cys Ser Phe Phe Ala	
145 150 155 160	
Val Phe His Pro His Phe Val Leu Thr Leu Ser Cys Val Gly Phe Phe	
165 170 175	
Pro Ala Met Leu Leu Phe Val Phe Phe Tyr Cys Asp Met Leu Lys Ile	
180 185 190	
Ala Ser Met His Ser Gln Gln Ile Arg Lys Met Glu His Ala Gly Ala	
195 200 205	
Met Ala Gly Ala Leu Arg Thr Val Ser Val Leu Ile Gly Ser Phe Ala	
210 215 220	
Leu Ser Trp Thr Pro Phe Leu Ile Thr Gly Ile Val Gln Val Ala Cys	
225 230 235 240	
Gln Glu Cys His Leu Tyr Leu Val Leu Glu Arg Tyr Leu Trp Leu Leu	
245 250 255	
Gly Val Gly Asn Ser Leu Leu Asn Pro Leu Ile Tyr Ala Tyr Trp Gln	
260 265 270	
Lys Glu Phe Arg Asn Ile Leu Leu Phe Cys Leu Thr Cys Val Ser Ile	
275 280 285	
Thr Ser Leu Arg Lys Lys Leu Phe Arg Cys Ile His His Val Ala Asn	
290 295 300	
Phe Ile Cys Ile His Met His Thr His Thr His Thr His Thr	
305 310 315 320	
His Thr His Thr	

<210> 53
 <211> 987

61/160

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(987)

<400> 53

tcc	cag	gac	tgg	aga	acc	atc	atc	ccg	gct	ctc	ttg	gtg	gct	gtc	tgc	48
Ser	Gln	Asp	Trp	Arg	Thr	Ile	Ile	Pro	Ala	Leu	Leu	Val	Ala	Val	Cys	
1				5					10					15		
ctg	gtg	ggc	ttc	gtg	gga	aac	ctg	tgt	gtg	att	ggc	atc	ctc	ctt	cac	96
Leu	Val	Gly	Phe	Val	Gly	Asn	Leu	Cys	Val	Ile	Gly	Ile	Leu	Leu	His	
		20					25						30			
aat	gct	tgg	aaa	gga	aag	cca	tcc	atg	atc	cac	tcc	ctg	att	ctg	aat	144
Asn	Ala	Trp	Lys	Gly	Lys	Pro	Ser	Met	Ile	His	Ser	Leu	Ile	Leu	Asn	
		35					40					45				
ctc	agc	ctg	gct	gat	ctc	tcc	ctc	ctg	ctg	ttt	tct	gca	cct	atc	cga	192
Leu	Ser	Leu	Ala	Asp	Leu	Ser	Leu	Leu	Phe	Ser	Ser	Ala	Pro	Ile	Arg	
	50					55					60					
gct	acg	gcg	tac	tcc	aaa	agt	ggt	tgg	gat	cta	ggc	tgg	ttt	gtc	tgc	240
Ala	Thr	Ala	Tyr	Ser	Lys	Ser	Val	Trp	Asp	Leu	Gly	Trp	Phe	Val	Cys	
65					70				75					80		
aag	tcc	tct	gac	tgg	ttt	atc	cac	aca	tgc	atg	gca	gcc	aag	agc	ctg	288
Lys	Ser	Ser	Asp	Trp	Phe	Ile	His	Thr	Cys	Met	Ala	Ala	Lys	Ser	Leu	
			85						90					95		
aca	atc	gtt	gtg	gtg	gcc	aaa	gta	tgc	ttc	atg	tat	gca	agt	gac	cca	336
Thr	Ile	Val	Val	Val	Ala	Lys	Val	Cys	Phe	Met	Tyr	Ala	Ser	Asp	Pro	
		100						105					110			
gcc	aag	caa	gtg	agt	atc	cac	aac	tac	acc	atc	tgg	tca	gtg	ctg	gtg	384
Ala	Lys	Gln	Val	Ser	Ile	His	Asn	Tyr	Thr	Ile	Trp	Ser	Val	Leu	Val	
		115					120					125				
gcc	atc	tgg	act	gtg	gct	agc	ctg	tta	ccc	ctg	ccg	gaa	tgg	ttc	ttt	432
Ala	Ile	Trp	Thr	Val	Ala	Ser	Leu	Leu	Pro	Leu	Pro	Glu	Trp	Phe	Phe	
	130					135					140					
agc	acc	atc	agg	cat	cat	gaa	ggt	gtg	gaa	atg	tgc	ctc	gtg	gat	gta	480
Ser	Thr	Ile	Arg	His	His	Glu	Gly	Val	Glu	Met	Cys	Leu	Val	Asp	Val	
145					150					155				160		
cca	gct	gtg	gct	gaa	gag	ttt	atg	tcg	atg	ttt	ggg	aag	ctc	tac	cca	528
Pro	Ala	Val	Ala	Glu	Glu	Phe	Met	Ser	Met	Phe	Gly	Lys	Leu	Tyr	Pro	
			165					170						175		
ctc	ctg	gca	ttt	ggc	ctt	cca	tta	ttt	ttt	gcc	agc	ttt	tat	ttc	tgg	576
Leu	Leu	Ala	Phe	Gly	Leu	Pro	Leu	Phe	Phe	Ala	Ser	Phe	Tyr	Phe	Trp	
		180					185						190			
aga	gct	tat	gac	caa	tgt	aaa	aaa	cga	gga	act	aag	act	caa	aat	ctt	624
Arg	Ala	Tyr	Asp	Gln	Cys	Lys	Lys	Arg	Gly	Thr	Lys	Thr	Gln	Asn	Leu	
		195					200					205				
aga	aac	cag	ata	cgc	tca	aag	caa	gtc	aca	gtg	atg	ctg	ctg	agc	att	672
Arg	Asn	Gln	Ile	Arg	Ser	Lys	Gln	Val	Thr	Val	Met	Leu	Leu	Ser	Ile	
	210					215					220					

62/160

gcc atc atc tct gct ctc ttg tgg ctc ccc gaa tgg gta gct tgg ctg 720
 Ala Ile Ile Ser Ala Leu Leu Trp Leu Pro Glu Trp Val Ala Trp Leu
 225 230 235 240

tgg gta tgg cat ctg aag gct gca ggc ccg gcc cca cca caa ggt ttc 768
 Trp Val Trp His Leu Lys Ala Ala Gly Pro Ala Pro Pro Gln Gly Phe
 245 250 255

ata gcc ctg tct caa gtc ttg atg ttt tcc atc tct tca gca aat cct 816
 Ile Ala Leu Ser Gln Val Leu Met Phe Ser Ile Ser Ser Ala Asn Pro
 260 265 270

ctc att ttt ctt gtg atg tcg gaa gag ttc agg gaa ggc ttg aaa gat 864
 Leu Ile Phe Leu Val Met Ser Glu Glu Phe Arg Glu Gly Leu Lys Asp
 275 280 285

tcc atc tta aga atc cac ttt gtt tgc tca tcc atg aga agc agt tac 912
 Ser Ile Leu Arg Ile His Phe Val Cys Ser Ser Met Arg Ser Ser Tyr
 290 295 300

tca tct gtt aaa gtt ttc tta tgc gat agc agc aat tca ggc aca tca 960
 Ser Ser Val Lys Val Phe Leu Cys Asp Ser Ser Asn Ser Gly Thr Ser
 305 310 315 320

tca gac tcc act tct aat gcc agg tct 987
 Ser Asp Ser Thr Ser Asn Ala Arg Ser
 325

<210> 54

<211> 329

<212> PRT

<213> Homo sapiens

<400> 54

Ser Gln Asp Trp Arg Thr Ile Ile Pro Ala Leu Leu Val Ala Val Cys
 1 5 10 15
 Leu Val Gly Phe Val Gly Asn Leu Cys Val Ile Gly Ile Leu Leu His
 20 25 30
 Asn Ala Trp Lys Gly Lys Pro Ser Met Ile His Ser Leu Ile Leu Asn
 35 40 45
 Leu Ser Leu Ala Asp Leu Ser Leu Leu Phe Ser Ala Pro Ile Arg
 50 55 60
 Ala Thr Ala Tyr Ser Lys Ser Val Trp Asp Leu Gly Trp Phe Val Cys
 65 70 75 80
 Lys Ser Ser Asp Trp Phe Ile His Thr Cys Met Ala Ala Lys Ser Leu
 85 90 95
 Thr Ile Val Val Val Ala Lys Val Cys Phe Met Tyr Ala Ser Asp Pro
 100 105 110
 Ala Lys Gln Val Ser Ile His Asn Tyr Thr Ile Trp Ser Val Leu Val
 115 120 125
 Ala Ile Trp Thr Val Ala Ser Leu Leu Pro Leu Pro Glu Trp Phe Phe
 130 135 140
 Ser Thr Ile Arg His His Glu Gly Val Glu Met Cys Leu Val Asp Val
 145 150 155 160
 Pro Ala Val Ala Glu Phe Met Ser Met Phe Gly Lys Leu Tyr Pro
 165 170 175
 Leu Leu Ala Phe Gly Leu Pro Leu Phe Phe Ala Ser Phe Tyr Phe Trp
 180 185 190
 Arg Ala Tyr Asp Gln Cys Lys Lys Arg Gly Thr Lys Thr Gln Asn Leu

63/160

[illegible]

```
<210> 55
<211> 954
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> CDS  
<222> (1) ... (954)
```

<400>	55																
tgc	tac	aag	cag	acc	ctg	agc	ttc	acg	ggg	ctg	acg	tgc	atc	gtt	tcc		48
Cys	Tyr	Lys	Gln	Thr	Leu	Ser	Phe	Thr	Gly	Leu	Thr	Cys	Ile	Val	Ser		
1				5					10					15			
ctt	gtc	gcg	ctg	aca	gga	aac	gcg	gtt	gtg	ctc	tgg	ctc	ctg	ggc	tgc		96
Leu	Val	Ala	Leu	Thr	Gly	Asn	Ala	Val	Val	Leu	Trp	Leu	Leu	Gly	Cys		
			20					25					30				
cgc	atg	cgc	agg	aac	gct	gtc	tcc	atc	tac	atc	ctc	aac	ctg	gtc	gcg		144
Arg	Met	Arg	Arg	Asn	Ala	Val	Ser	Ile	Tyr	Ile	Leu	Asn	Leu	Val	Ala		
		35					40					45					
gcc	gac	ttc	ctc	ttc	ctt	agc	ggc	cac	att	ata	tgt	tgc	ccg	tta	cgc		192
Ala	Asp	Phe	Leu	Phe	Leu	Ser	Gly	His	Ile	Ile	Cys	Ser	Pro	Leu	Arg		
	50					55					60						
ctc	atc	aat	atc	cgc	cat	ccc	atc	tcc	aaa	atc	ctc	agt	cct	gtg	atg		240
Leu	Ile	Asn	Ile	Arg	His	Pro	Ile	Ser	Lys	Ile	Leu	Ser	Pro	Val	Met		
65					70				75					80			
acc	ttt	ccc	tac	ttt	ata	ggc	cta	agc	atg	ctg	agc	gcc	atc	agc	acc		288
Thr	Phe	Pro	Tyr	Phe	Ile	Gly	Leu	Ser	Met	Leu	Ser	Ala	Ile	Ser	Thr		
				85					90					95			
gag	cgc	tgc	ctc	atc	aaa	cac	tgc	ata	tct	gcc	ctg	tgg	ccc	atc	tgg		336
Glu	Arg	Cys	Leu	Ile	Lys	His	Cys	Ile	Ser	Ala	Leu	Trp	Pro	Ile	Trp		
			100				105						110				
tac	cac	tgc	cgt	cgc	ccc	aca	cac	ctg	tca	gca	gtc	ctg	tgt	gcc	ctg		384
Tyr	His	Cys	Arg	Arg	Pro	Thr	His	Leu	Ser	Ala	Val	Leu	Cys	Ala	Leu		
		115					120					125					
ctc	tgg	gcc	ccg	tcc	ctg	ctg	ctt	gcc	ttc	ctg	gaa	ggt	tac	tac	tgt		432

64/160

Leu Trp Ala Pro Ser Leu Leu Leu Ala Phe Leu Glu Gly Tyr Tyr Cys
 130 135 140

gct ttt ctg ttt aag att ggg gac tac agt tgg ttt cag aca ttt gat 480
 Ala Phe Leu Phe Lys Ile Gly Asp Tyr Ser Trp Phe Gln Thr Phe Asp
 145 150 155 160

ttc atc aca ggc acg tgg ctg att ttt aaa ttt gtg gtt ctc ttc tat 528
 Phe Ile Thr Gly Thr Trp Leu Ile Phe Lys Phe Val Val Leu Phe Tyr
 165 170 175

gtt ccc ctg aaa atc atg ttc tgt tct gag att gga att aca agc gtg 576
 Val Pro Leu Lys Ile Met Phe Cys Ser Glu Ile Gly Ile Thr Ser Val
 180 185 190

agc cac cgc gcc cag ccg aca atc tct tta acc cat atg gtt gca tca 624
 Ser His Arg Ala Gln Pro Thr Ile Ser Leu Thr His Met Val Ala Ser
 195 200 205

tat cta gga gta atg ttg ctg ctc ttc ctt att tgc agc ctg ccc tta 672
 Tyr Leu Gly Val Met Leu Leu Leu Phe Leu Ile Cys Ser Leu Pro Leu
 210 215 220

ggc att aag tgg ttc cta tta ttc tgg atc ctc gtg gat ttt gat atc 720
 Gly Ile Lys Trp Phe Leu Leu Phe Trp Ile Leu Val Asp Phe Asp Ile
 225 230 235 240

ttc ctt tgt cat ttg caa cca gtt tca gat gtc ctg tcc tct ctt aac 768
 Phe Leu Cys His Leu Gln Pro Val Ser Asp Val Leu Ser Ser Leu Asn
 245 250 255

agc agt gcc aac ccc atc att tac ttc ttc atg ggc tcc ttt agg cag 816
 Ser Ser Ala Asn Pro Ile Ile Tyr Phe Phe Met Gly Ser Phe Arg Gln
 260 265 270

cgt gtt ttt tgt tgt tgt tgt tgt tgc tgc tgc tgc ttt aca aaa 864
 Arg Val Phe Cys Cys Cys Cys Cys Cys Cys Cys Cys Phe Thr Lys
 275 280 285

ttc ctg tta gga ata act ttt gtg tcc agg cgc ggt ggc tca cac ctg 912
 Phe Leu Leu Gly Ile Thr Phe Val Ser Arg Arg Gly Gly Ser His Leu
 290 295 300

cat tcc ggc cat tcc agg cat gtc ccc tcc cat tcc agg cat 954
 His Ser Gly His Ser Arg His Val Pro Ser His Ser Arg His
 305 310 315

<210> 56

<211> 318

<212> PRT

<213> Homo sapiens

<400> 56

Cys Tyr Lys Gln Thr Leu Ser Phe Thr Gly Leu Thr Cys Ile Val Ser
 1 5 10 15
 Leu Val Ala Leu Thr Gly Asn Ala Val Val Leu Trp Leu Leu Gly Cys
 20 25 30
 Arg Met Arg Arg Asn Ala Val Ser Ile Tyr Ile Leu Asn Leu Val Ala
 35 40 45

65/160

Ala Asp Phe Leu Phe Leu Ser Gly His Ile Ile Cys Ser Pro Leu Arg
 50 55 60
 Leu Ile Asn Ile Arg His Pro Ile Ser Lys Ile Leu Ser Pro Val Met
 65 70 75 80
 Thr Phe Pro Tyr Phe Ile Gly Leu Ser Met Leu Ser Ala Ile Ser Thr
 85 90 95
 Glu Arg Cys Leu Ile Lys His Cys Ile Ser Ala Leu Trp Pro Ile Trp
 100 105 110
 Tyr His Cys Arg Arg Pro Thr His Leu Ser Ala Val Leu Cys Ala Leu
 115 120 125
 Leu Trp Ala Pro Ser Leu Leu Leu Ala Phe Leu Glu Gly Tyr Tyr Cys
 130 135 140
 Ala Phe Leu Phe Lys Ile Gly Asp Tyr Ser Trp Phe Gln Thr Phe Asp
 145 150 155 160
 Phe Ile Thr Gly Thr Trp Leu Ile Phe Lys Phe Val Val Leu Phe Tyr
 165 170 175
 Val Pro Leu Lys Ile Met Phe Cys Ser Glu Ile Gly Ile Thr Ser Val
 180 185 190
 Ser His Arg Ala Gln Pro Thr Ile Ser Leu Thr His Met Val Ala Ser
 195 200 205
 Tyr Leu Gly Val Met Leu Leu Phe Leu Ile Cys Ser Leu Pro Leu
 210 215 220
 Gly Ile Lys Trp Phe Leu Leu Phe Trp Ile Leu Val Asp Phe Asp Ile
 225 230 235 240
 Phe Leu Cys His Leu Gln Pro Val Ser Asp Val Leu Ser Ser Leu Asn
 245 250 255
 Ser Ser Ala Asn Pro Ile Ile Tyr Phe Phe Met Gly Ser Phe Arg Gln
 260 265 270
 Arg Val Phe Cys Cys Cys Cys Cys Cys Cys Cys Cys Cys Phe Thr Lys
 275 280 285
 Phe Leu Leu Gly Ile Thr Phe Val Ser Arg Arg Gly Gly Ser His Leu
 290 295 300
 His Ser Gly His Ser Arg His Val Pro Ser His Ser Arg His
 305 310 315

<210> 57
 <211> 972
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(972)

<400> 57
 gag cga ctg ctc cga ctc atc tct gct ggg gtc tgt ggc ctc atc ctg 48
 Glu Arg Leu Leu Arg Leu Ile Ser Ala Gly Val Cys Gly Leu Ile Leu
 1 5 10 15
 ctg gtg ggg ctg tca gct aat ggg ctc atg ctg ctg gtg gtg ggc cgg 96
 Leu Val Gly Leu Ser Ala Asn Gly Leu Met Leu Leu Val Val Gly Arg
 20 25 30
 ggc ccg ggc tcc ccc cac ccg ctc cac tcc ctg acc cac agc ctc atg 144
 Gly Pro Gly Ser Pro His Pro Leu His Ser Leu Thr His Ser Leu Met
 35 40 45
 atg aac atc acg cca tct gac ctg ctc ttc ctg gcc tgc gtg gtg cct 192
 Met Asn Ile Thr Pro Ser Asp Leu Leu Phe Leu Ala Cys Val Val Pro
 50 55 60
 gtg ctg ctg ctg agc ttc ctg cag cac aac tgg tgg ctg ggc cct gcc 240

66/160

Val 65	Leu	Leu	Leu	Ser	Phe 70	Leu	Gln	His	Asn	Trp 75	Trp	Leu	Gly	Pro	Ala 80	
atc	tgc	acc	att	agc	cag	gcc	acc	aac	aca	gcc	acc	acg	ttc	tgc	atc	288
Ile	Cys	Thr	Ile	Ser 85	Gln	Ala	Thr	Asn	Thr 90	Ala	Thr	Thr	Phe	Cys 95	Ile	
ttc	tat	agc	atg	gtg	gcc	aca	gct	ctc	ctg	cgc	cat	gtg	gct	gtg	gcc	336
Phe	Tyr	Ser	Met 100	Val	Ala	Thr	Ala	Leu 105	Leu	Arg	His	Val 110	Ala	Val	Ala	
cgg	cct	gac	ctg	gcc	ttc	cca	gcc	ggc	tgg	ggc	acc	ctc	ttg	ctg	ctc	384
Arg	Pro	Asp 115	Leu	Ala	Phe	Pro	Ala 120	Gly	Trp	Gly	Thr	Leu 125	Leu	Leu	Leu	
tgt	ggg	gcc	atg	tgg	gcc	ctg	ggc	ctt	aca	gaa	tcc	ctg	ccc	aac	tgg	432
Cys	Gly 130	Ala	Met	Trp	Ala 135	Leu	Gly	Leu	Thr	Glu	Ser 140	Leu	Pro	Asn	Trp	
ctg	ttc	cag	agg	gtg	gca	gtg	gag	gag	gag	aca	gcg	ggg	gct	ccc	aag	480
Leu	Phe	Gln	Arg	Val 150	Ala	Val	Glu	Glu	Glu	Thr 155	Ala	Gly	Ala	Pro	Lys 160	
acc	cag	gcc	tgc	ctc	ttg	ctc	ctg	agc	cct	gct	ggg	acc	tcc	tgc	tac	528
Thr	Gln	Ala	Cys 165	Leu	Leu	Leu	Leu	Ser	Pro 170	Ala	Gly	Thr	Ser	Cys 175	Tyr	
atc	agc	ctg	ctg	gga	gcc	ctg	gcc	ttc	ctg	cca	tgc	acg	ctg	ggg	ctg	576
Ile	Ser	Leu	Leu 180	Gly	Ala	Leu	Ala	Phe 185	Leu	Pro	Cys	Thr	Leu 190	Gly	Leu	
ggc	tgc	tct	ttc	agc	cac	gtg	ggc	tgg	ctc	ctg	tgg	acc	cag	ccc	caa	624
Gly	Cys 195	Ser	Phe	Ser	His	Val 200	Gly	Trp	Leu	Leu	Trp	Thr 205	Gln	Pro	Gln	
gag	aac	ata	ggg	ctc	agc	ctt	gtg	gtg	ctg	gtg	gtt	ttt	gtg	ctg	atg	672
Glu	Asn 210	Ile	Gly	Leu	Ser	Leu 215	Val	Val	Leu	Val	Val 220	Phe	Val	Leu	Met	
tgg	ggg	ccc	tgc	tcc	atg	ctg	ggt	tat	gtg	gca	gcc	atg	ggc	tac	ctg	720
Trp	Gly 225	Pro	Cys	Ser	Met 230	Leu	Gly	Tyr	Val	Ala 235	Ala	Met	Gly	Tyr	Leu 240	
cct	gcc	aca	ccg	gct	gct	ttt	gtg	gcc	tcc	agc	ctc	tgc	acc	atc	ctg	768
Pro	Ala	Thr	Pro	Ala 245	Ala	Phe	Val	Ala	Ser 250	Ser	Leu	Cys	Thr	Ile 255	Leu	
gcc	tac	tcc	aat	tgc	gct	gtc	agc	cct	atc	ctc	tgc	ttc	tac	ctc	tcc	816
Ala	Tyr	Ser	Asn 260	Cys	Ala	Val	Ser	Pro 265	Ile	Leu	Cys	Phe	Tyr 270	Leu	Ser	
cgc	ccc	ttc	cag	gca	gga	ctc	agg	gac	ctc	ttc	tgc	agg	ccg	atg	atg	864
Arg	Pro	Phe 275	Gln	Ala	Gly	Leu	Arg 280	Asp	Leu	Phe	Cys	Arg 285	Pro	Met	Met	
gcc	agg	cat	ccc	aga	ggt	cct	ggg	caa	caa	gag	cga	gac	tct	gtc	tca	912
Ala	Arg 290	His	Pro	Arg	Gly	Pro 295	Gly	Gln	Gln	Glu	Arg 300	Asp	Ser	Val	Ser	
aat	aat	aaa	aca	aaa	acc	aaa	aca	cac	aca	cac	aca	cac	aca	cac	aca	960
Asn	Asn	Lys	Thr	Lys	Thr 310	Lys	Thr	His	Thr	His 315	Thr	His	Thr	His	Thr 320	

67/160

cac aca cac aca
His Thr His Thr

972

<210> 58
<211> 324
<212> PRT
<213> Homo sapiens

<400> 58
Glu Arg Leu Leu Arg Leu Ile Ser Ala Gly Val Cys Gly Leu Ile Leu
1 5 10 15
Leu Val Gly Leu Ser Ala Asn Gly Leu Met Leu Leu Val Val Gly Arg
20 25 30
Gly Pro Gly Ser Pro His Pro Leu His Ser Leu Thr His Ser Leu Met
35 40 45
Met Asn Ile Thr Pro Ser Asp Leu Leu Phe Leu Ala Cys Val Val Pro
50 55 60
Val Leu Leu Leu Ser Phe Leu Gln His Asn Trp Trp Leu Gly Pro Ala
65 70 75 80
Ile Cys Thr Ile Ser Gln Ala Thr Asn Thr Ala Thr Thr Phe Cys Ile
85 90 95
Phe Tyr Ser Met Val Ala Thr Ala Leu Leu Arg His Val Ala Val Ala
100 105 110
Arg Pro Asp Leu Ala Phe Pro Ala Gly Trp Gly Thr Leu Leu Leu Leu
115 120 125
Cys Gly Ala Met Trp Ala Leu Gly Leu Thr Glu Ser Leu Pro Asn Trp
130 135 140
Leu Phe Gln Arg Val Ala Val Glu Glu Glu Thr Ala Gly Ala Pro Lys
145 150 155 160
Thr Gln Ala Cys Leu Leu Leu Ser Pro Ala Gly Thr Ser Cys Tyr
165 170 175
Ile Ser Leu Leu Gly Ala Leu Ala Phe Leu Pro Cys Thr Leu Gly Leu
180 185 190
Gly Cys Ser Phe Ser His Val Gly Trp Leu Leu Trp Thr Gln Pro Gln
195 200 205
Glu Asn Ile Gly Leu Ser Leu Val Val Leu Val Val Phe Val Leu Met
210 215 220
Trp Gly Pro Cys Ser Met Leu Gly Tyr Val Ala Ala Met Gly Tyr Leu
225 230 235 240
Pro Ala Thr Pro Ala Ala Phe Val Ala Ser Ser Leu Cys Thr Ile Leu
245 250 255
Ala Tyr Ser Asn Cys Ala Val Ser Pro Ile Leu Cys Phe Tyr Leu Ser
260 265 270
Arg Pro Phe Gln Ala Gly Leu Arg Asp Leu Phe Cys Arg Pro Met Met
275 280 285
Ala Arg His Pro Arg Gly Pro Gly Gln Gln Glu Arg Asp Ser Val Ser
290 295 300
Asn Asn Lys Thr Lys Thr Lys Thr His Thr His Thr His Thr
305 310 315 320
His Thr His Thr

<210> 59
<211> 873
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)... (873)

68/160

<400> 59

tct tta gca ctc tac aat gtc ttt cca ttt ttt ttc tgg ctt ctt ttt	48
Ser Leu Ala Leu Tyr Asn Val Phe Pro Phe Phe Phe Trp Leu Leu Phe	
1 5 10 15	
gtg ggg gca ctg ctg ggc aac ggc gcg ctg ctg gtc gtg gtg ctg cgc	96
Val Gly Ala Leu Leu Gly Asn Gly Ala Leu Leu Val Val Val Leu Arg	
20 25 30	
acg ccg gga ctg cgc gac gcg ctc tac ctg gcg cac ctg tgc gtc gtg	144
Thr Pro Gly Leu Arg Asp Ala Leu Tyr Leu Ala His Leu Cys Val Val	
35 40 45	
gac ctg ctg gcg gcc gcc tcc atc atg ccg ctg ggc ctg ctg gcc gca	192
Asp Leu Leu Ala Ala Ala Ser Ile Met Pro Leu Gly Leu Leu Ala Ala	
50 55 60	
ccg ccg ccc ggg ctg ggc cgc gtg cgc ctg ggc ccc gcg cca tgc cgc	240
Pro Pro Pro Gly Leu Gly Arg Val Arg Leu Gly Pro Ala Pro Cys Arg	
65 70 75 80	
gcc gct cgc ttc ctc tcc gcc gct ctg ctg ccg gcc tgc acg ctc ggg	288
Ala Ala Arg Phe Leu Ser Ala Ala Leu Leu Pro Ala Cys Thr Leu Gly	
85 90 95	
gtg gcc gca ctt ggc ctg gca cgc tac cgc ctc atc gtg cac ccg ctg	336
Val Ala Ala Leu Gly Leu Ala Arg Tyr Arg Leu Ile Val His Pro Leu	
100 105 110	
cgg cca ggc tcg cgg ccg ccg cct gtg ctc gtg ctc acc gcc gtg tgg	384
Arg Pro Gly Ser Arg Pro Pro Pro Val Leu Val Leu Thr Ala Val Trp	
115 120 125	
gcc gcg gcg gga ctg ctg ggc gcg ctc tcc ctg ctc ggc ccg ccg ccc	432
Ala Ala Ala Gly Leu Leu Gly Ala Leu Ser Leu Leu Gly Pro Pro Pro	
130 135 140	
gca ccg ccc cct gct cct gct cgc tgc tcg gtc ctg gct ggg ggc ctc	480
Ala Pro Pro Pro Ala Pro Ala Arg Cys Ser Val Leu Ala Gly Gly Leu	
145 150 155 160	
ggg ccc ttc cgg ccg ctc tgg gcc ctg ctg gcc ttc gcg ctg ccc gcc	528
Gly Pro Phe Arg Pro Leu Trp Ala Leu Leu Ala Phe Ala Leu Pro Ala	
165 170 175	
ctc ctg ctg ctc ggc gcc tac ggc ggc atc ttc gtg gtg gcg ccg ctg	576
Leu Leu Leu Leu Gly Ala Tyr Gly Gly Ile Phe Val Val Ala Pro Leu	
180 185 190	
gcc gtg ggc caa ttt gca gcc tgc tgg ctg cct tat ggc tgc gcg tgc	624
Ala Val Gly Gln Phe Ala Ala Cys Trp Leu Pro Tyr Gly Cys Ala Cys	
195 200 205	
ctg gcg ccc gca gcg cgg gcc gcg gaa gcc gaa gcg gct gtc acc tgg	672
Leu Ala Pro Ala Ala Arg Ala Ala Glu Ala Glu Ala Ala Val Thr Trp	
210 215 220	
gtc gcc tac tcg gcc ttc gcg gct cac ccc ttc ctg tac ggg ctg ctg	720
Val Ala Tyr Ser Ala Phe Ala Ala His Pro Phe Leu Tyr Gly Leu Leu	
225 230 235 240	

69/160

cag cgc ccc gtg cgc ttg gca ctg ggc cgc ctc tct cgc ctg agg agc 768
Gln Arg Pro Val Arg Leu Ala Leu Gly Arg Leu Ser Arg Leu Arg Ser
245 250 255

agc tgg gcg gtg agg acc aca tct gga tca aga ctg ctc aga ggc cct 816
Ser Trp Ala Val Arg Thr Thr Ser Gly Ser Arg Leu Leu Arg Gly Pro

260 265 270

tgc agt gtg ctt gac caa acg ctg tca agt tca ggg ccc agc ctg gct 864
 Cys Ser Val Leu Asp Gln Thr Leu Ser Ser Ser Gly Pro Ser Leu Ala
 275 280 285

ggg tcc tcc 873
Gly Ser Ser
290

```
<210> 60
<211> 291
<212> PRT
<213> Homo sapiens
```

[illegible]

70/160

<210> 61
 <211> 1326
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(1326)

<400> 61
 aca cac ctt cca tca gca tgc tcc caa atc cca gct ctc gaa gag agc 48
 Thr His Leu Pro Ser Ala Ser Ser Gln Ile Pro Ala Leu Glu Glu Ser
 1 5 10 15

tgt gag gct gtg gaa gcc cga gaa atc atg tgg ttt aag act cgt caa 96
 Cys Glu Ala Val Glu Ala Arg Glu Ile Met Trp Phe Lys Thr Arg Gln
 20 25 30

gga cag ata gca aag cag cca tgc cct gca gga act ata ggt gta tca 144
 Gly Gln Ile Ala Lys Gln Pro Cys Pro Ala Gly Thr Ile Gly Val Ser
 35 40 45

act tat cta tgc ctt gct cct gat gga att tgg gat ccc caa ggt cca 192
 Thr Tyr Leu Cys Leu Ala Pro Asp Gly Ile Trp Asp Pro Gln Gly Pro
 50 55 60

gat ctc agc aac tgt tct tct cct tgg gtc aat cat ata aca cag aag 240
 Asp Leu Ser Asn Cys Ser Ser Pro Trp Val Asn His Ile Thr Gln Lys
 65 70 75 80

cgc tct tgc aga gcc tat gtc cag tca gag gaa aat ttc aac cct aac 288
 Arg Ser Cys Arg Ala Tyr Val Gln Ser Glu Glu Asn Phe Asn Pro Asn
 85 90 95

tgt tca ttt tgg agc tac tcc aag cgt aca atg aca ggt tat tgg tca 336
 Cys Ser Phe Trp Ser Tyr Ser Lys Arg Thr Met Thr Gly Tyr Trp Ser
 100 105 110

aca caa ggc tgt cgg ctc ctg aca aca aat aag aca cat act aca tgc 384
 Thr Gln Gly Cys Arg Leu Leu Thr Thr Asn Lys Thr His Thr Thr Cys
 115 120 125

tct tgt aac cac cta aca aat ttt gca gta ctg atg gca cat gtg gaa 432
 Ser Cys Asn His Leu Thr Asn Phe Ala Val Leu Met Ala His Val Glu
 130 135 140

cac agt gat gcg gtc cat gac ctc ctt ctg gat gtg atc acg tgg gtt 480
 His Ser Asp Ala Val His Asp Leu Leu Leu Asp Val Ile Thr Trp Val
 145 150 155 160

gga att ttg ctg tcc ctt gtt tgt ctc ctg att tgc atc ttc aca ttt 528
 Gly Ile Leu Leu Ser Leu Val Cys Leu Leu Ile Cys Ile Phe Thr Phe
 165 170 175

tgc ttt ttc cgg ggg ctc cag agt gac cgt aac acc atc cac aag aac 576
 Cys Phe Phe Arg Gly Leu Gln Ser Asp Arg Asn Thr Ile His Lys Asn
 180 185 190

ctc tgc atc agt ctc ttt gta gca gag ctg ctc ttc ctg att ggg atc 624
 Leu Cys Ile Ser Leu Phe Val Ala Glu Leu Leu Phe Leu Ile Gly Ile
 195 200 205

aac cga act gac caa cca att gcc tgt gct gtt ttc gct gcc ctg tta 672

71/160

Asn	Arg	Thr	Asp	Gln	Pro	Ile	Ala	Cys	Ala	Val	Phe	Ala	Ala	Leu	Leu	
210						215					220					
cat	ttc	ttc	ttc	ttg	gct	gcc	ttc	acc	tgg	atg	ttc	ctg	gag	ggg	gtg	720
His	Phe	Phe	Phe	Leu	Ala	Ala	Phe	Thr	Trp	Met	Phe	Leu	Glu	Gly	Val	
225					230				235						240	
cag	ctt	tat	atc	atg	ctg	gtg	gag	gtt	ttt	gag	agt	gaa	cat	tca	cgt	768
Gln	Leu	Tyr	Ile	Met	Leu	Val	Glu	Val	Phe	Glu	Ser	Glu	His	Ser	Arg	
				245					250					255		
agg	aaa	tac	ttt	tat	ctg	gtc	ggc	tat	ggg	atg	cct	gca	ctc	att	gtg	816
Arg	Lys	Tyr	Phe	Tyr	Leu	Val	Gly	Tyr	Gly	Met	Pro	Ala	Leu	Ile	Val	
			260					265					270			
gct	gtg	tca	gct	gca	gta	gac	tac	agg	agt	tat	gga	aca	gat	aaa	gta	864
Ala	Val	Ser	Ala	Ala	Val	Asp	Tyr	Arg	Ser	Tyr	Gly	Thr	Asp	Lys	Val	
		275					280					285				
tgt	tgg	ctc	cga	ctt	gac	acc	tac	ttc	att	tgg	agt	ttt	ata	gga	cca	912
Cys	Trp	Leu	Arg	Leu	Asp	Thr	Tyr	Phe	Ile	Trp	Ser	Phe	Ile	Gly	Pro	
	290					295					300					
gca	act	ttg	ata	att	atg	ctt	aat	gta	atc	ttc	ctt	ggg	att	gct	tta	960
Ala	Thr	Leu	Ile	Ile	Met	Leu	Asn	Val	Ile	Phe	Leu	Gly	Ile	Ala	Leu	
305					310					315					320	
tat	aaa	atg	ttt	cat	cat	act	gct	ata	ctg	aaa	cct	gaa	tca	ggc	tgt	1008
Tyr	Lys	Met	Phe	His	His	Thr	Ala	Ile	Leu	Lys	Pro	Glu	Ser	Gly	Cys	
				325					330					335		
ctt	gat	aac	atc	aag	tca	tgg	gtt	ata	ggg	gca	ata	gct	ctt	ctc	tgc	1056
Leu	Asp	Asn	Ile	Lys	Ser	Trp	Val	Ile	Gly	Ala	Ile	Ala	Leu	Leu	Cys	
			340					345					350			
cta	tta	gga	ttg	acc	tgg	gcc	ttt	gga	ctc	atg	tat	att	aat	gaa	agc	1104
Leu	Leu	Gly	Leu	Thr	Trp	Ala	Phe	Gly	Leu	Met	Tyr	Ile	Asn	Glu	Ser	
		355					360					365				
aca	gtc	atc	atg	gcc	tat	ctc	ttc	acc	att	ttc	aat	tct	cta	cag	gga	1152
Thr	Val	Ile	Met	Ala	Tyr	Leu	Phe	Thr	Ile	Phe	Asn	Ser	Leu	Gln	Gly	
		370				375					380					
atg	ttt	ata	ttt	att	ttc	cat	tgt	gtc	cta	cag	aag	aag	gta	cga	aaa	1200
Met	Phe	Ile	Phe	Ile	Phe	His	Cys	Val	Leu	Gln	Lys	Lys	Val	Arg	Lys	
385					390				395						400	
gag	tat	ggg	aaa	tgc	ctg	cga	aca	cat	tgc	tgt	agt	ggc	aaa	agt	aca	1248
Glu	Tyr	Gly	Lys	Cys	Leu	Arg	Thr	His	Cys	Cys	Ser	Gly	Lys	Ser	Thr	
				405					410					415		
gag	agt	tcc	att	ggg	tca	ggg	aaa	aca	tct	ggg	tct	cga	act	cct	gga	1296
Glu	Ser	Ser	Ile	Gly	Ser	Gly	Lys	Thr	Ser	Gly	Ser	Arg	Thr	Pro	Gly	
			420					425					430			
cgc	tac	tcc	aca	ggc	tca	cag	gta	aac	aat							1326
Arg	Tyr	Ser	Thr	Gly	Ser	Gln	Val	Asn	Asn							
		435					440									

<210> 62
 <211> 442
 <212> PRT

72/160

<213> Homo sapiens

<400> 62

```

Thr His Leu Pro Ser Ala Ser Ser Gln Ile Pro Ala Leu Glu Glu Ser
 1      5      10      15
Cys Glu Ala Val Glu Ala Arg Glu Ile Met Trp Phe Lys Thr Arg Gln
      20      25      30
Gly Gln Ile Ala Lys Gln Pro Cys Pro Ala Gly Thr Ile Gly Val Ser
      35      40      45
Thr Tyr Leu Cys Leu Ala Pro Asp Gly Ile Trp Asp Pro Gln Gly Pro
 50      55      60
Asp Leu Ser Asn Cys Ser Ser Pro Trp Val Asn His Ile Thr Gln Lys
65      70      75      80
Arg Ser Cys Arg Ala Tyr Val Gln Ser Glu Glu Asn Phe Asn Pro Asn
      85      90      95
Cys Ser Phe Trp Ser Tyr Ser Lys Arg Thr Met Thr Gly Tyr Trp Ser
      100      105      110
Thr Gln Gly Cys Arg Leu Leu Thr Thr Asn Lys Thr His Thr Thr Cys
      115      120      125
Ser Cys Asn His Leu Thr Asn Phe Ala Val Leu Met Ala His Val Glu
130      135      140
His Ser Asp Ala Val His Asp Leu Leu Leu Asp Val Ile Thr Trp Val
145      150      155      160
Gly Ile Leu Leu Ser Leu Val Cys Leu Leu Ile Cys Ile Phe Thr Phe
      165      170      175
Cys Phe Phe Arg Gly Leu Gln Ser Asp Arg Asn Thr Ile His Lys Asn
      180      185      190
Leu Cys Ile Ser Leu Phe Val Ala Glu Leu Leu Phe Leu Ile Gly Ile
195      200      205
Asn Arg Thr Asp Gln Pro Ile Ala Cys Ala Val Phe Ala Ala Leu Leu
210      215      220
His Phe Phe Phe Leu Ala Ala Phe Thr Trp Met Phe Leu Glu Gly Val
225      230      235      240
Gln Leu Tyr Ile Met Leu Val Glu Val Phe Glu Ser Glu His Ser Arg
      245      250      255
Arg Lys Tyr Phe Tyr Leu Val Gly Tyr Gly Met Pro Ala Leu Ile Val
260      265      270
Ala Val Ser Ala Ala Val Asp Tyr Arg Ser Tyr Gly Thr Asp Lys Val
275      280      285
Cys Trp Leu Arg Leu Asp Thr Tyr Phe Ile Trp Ser Phe Ile Gly Pro
290      295      300
Ala Thr Leu Ile Ile Met Leu Asn Val Ile Phe Leu Gly Ile Ala Leu
305      310      315      320
Tyr Lys Met Phe His His Thr Ala Ile Leu Lys Pro Glu Ser Gly Cys
      325      330      335
Leu Asp Asn Ile Lys Ser Trp Val Ile Gly Ala Ile Ala Leu Leu Cys
340      345      350
Leu Leu Gly Leu Thr Trp Ala Phe Gly Leu Met Tyr Ile Asn Glu Ser
355      360      365
Thr Val Ile Met Ala Tyr Leu Phe Thr Ile Phe Asn Ser Leu Gln Gly
370      375      380
Met Phe Ile Phe Ile Phe His Cys Val Leu Gln Lys Lys Val Arg Lys
385      390      395      400
Glu Tyr Gly Lys Cys Leu Arg Thr His Cys Cys Ser Gly Lys Ser Thr
405      410      415
Glu Ser Ser Ile Gly Ser Gly Lys Thr Ser Gly Ser Arg Thr Pro Gly
420      425      430
Arg Tyr Ser Thr Gly Ser Gln Val Asn Asn
435      440

```

<210> 63

<211> 1275

73/160

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1275)

<400> 63

cac	agg	agg	ctg	aag	cag	gag	aat	cac	ttg	aac	ccg	gga	ggc	aga	ggc	48
His	Arg	Arg	Leu	Lys	Gln	Glu	Asn	His	Leu	Asn	Pro	Gly	Gly	Arg	Gly	
1				5					10					15		
tgc	atg	ggg	ctt	tgg	ggc	ggg	ggc	ctt	tgc	tgg	gtg	ccc	acc	gcg	cca	96
Cys	Met	Gly	Leu	Trp	Gly	Gly	Gly	Leu	Cys	Trp	Val	Pro	Thr	Ala	Pro	
			20					25					30			
ggg	agc	tgc	ggc	gct	ccc	ccg	ggc	cgc	ctg	cgg	tgc	ccc	gac	tgg	ttc	144
Gly	Ser	Cys	Gly	Ala	Pro	Pro	Gly	Arg	Leu	Arg	Cys	Pro	Asp	Trp	Phe	
		35					40					45				
tct	gcc	ctg	tcc	tca	act	agc	atg	atg	tca	ggc	cct	tca	ctc	tcc	ctc	192
Ser	Ala	Leu	Ser	Ser	Thr	Ser	Met	Met	Ser	Gly	Pro	Ser	Leu	Ser	Leu	
	50					55					60					
tgc	tgt	cct	cac	gga	ccc	agg	tgt	ctg	cag	aca	gga	cac	tgg	agc	ccc	240
Cys	Cys	Pro	His	Gly	Pro	Arg	Cys	Leu	Gln	Thr	Gly	His	Trp	Ser	Pro	
65					70				75						80	
agg	atg	cag	gcc	act	gtc	tcc	gga	gaa	ggg	gtc	tgg	tgc	aac	cac	ggc	288
Arg	Met	Gln	Ala	Thr	Val	Ser	Gly	Glu	Gly	Val	Trp	Ser	Asn	His	Gly	
				85				90						95		
tgt	gcg	ctc	acg	aga	gga	aac	ctc	acc	tac	tcc	gtc	tgc	cgc	tgc	act	336
Cys	Ala	Leu	Thr	Arg	Gly	Asn	Leu	Thr	Tyr	Ser	Val	Cys	Arg	Cys	Thr	
		100					105						110			
cac	ctc	acc	aac	ttt	gcc	atc	ctc	atg	cag	ctt	gca	cgc	gga	cac	cag	384
His	Leu	Thr	Asn	Phe	Ala	Ile	Leu	Met	Gln	Leu	Ala	Arg	Gly	His	Gln	
		115					120					125				
gtg	gcg	ctg	tgc	tct	atc	agc	tat	gtg	ggc	tgc	tcc	ctc	tcc	gtg	ctc	432
Val	Ala	Leu	Ser	Ser	Ile	Ser	Tyr	Val	Gly	Cys	Ser	Leu	Ser	Val	Leu	
	130					135					140					
tgc	ctg	gtg	gcc	acg	ctg	gtc	acc	ttc	gcc	gtg	ctg	tcc	acc	atc	cgg	480
Cys	Leu	Val	Ala	Thr	Leu	Val	Thr	Phe	Ala	Val	Leu	Ser	Thr	Ile	Arg	
145					150				155						160	
aac	cag	cgc	tac	cac	atc	cac	gcc	aac	ctg	tcc	ttc	gcc	gtg	ctg	gtg	528
Asn	Gln	Arg	Tyr	His	Ile	His	Ala	Asn	Leu	Ser	Phe	Ala	Val	Leu	Val	
				165				170						175		
gcc	cag	gtc	ctg	ctg	ctc	att	agt	ttc	cgc	ctc	gag	ccg	ggc	acg	gtg	576
Ala	Gln	Val	Leu	Leu	Leu	Ile	Ser	Phe	Arg	Leu	Glu	Pro	Gly	Thr	Val	
		180					185						190			
agt	ggg	cgc	agc	tcc	acc	ccc	tgc	caa	gtg	atg	gcc	gtg	ctc	cta	cac	624
Ser	Gly	Arg	Ser	Ser	Thr	Pro	Cys	Gln	Val	Met	Ala	Val	Leu	Leu	His	
	195					200						205				
tac	ttc	ttc	ctg	agt	gcc	ttc	gca	tgg	atg	ctg	gtg	gag	ggg	ctg	cac	672
Tyr	Phe	Phe	Leu	Ser	Ala	Phe	Ala	Trp	Met	Leu	Val	Glu	Gly	Leu	His	
	210					215					220					

74/160

```

ctc tac agc atg gtg atc aag gtc ttt ggg tcg gag gac agc aag cac 720
Leu Tyr Ser Met Val Ile Lys Val Phe Gly Ser Glu Asp Ser Lys His
225                230                235                240

cgt tac tac tat ggg atg gga tgg ggt ttt cct ctt ctg atc tgc atc 768
Arg Tyr Tyr Tyr Gly Met Gly Trp Gly Phe Pro Leu Leu Ile Cys Ile
245                250                255

att tca ctg tca ttt gcc atg gac agt tac gga aca agc aac aat tgc 816
Ile Ser Leu Ser Phe Ala Met Asp Ser Tyr Gly Thr Ser Asn Asn Cys
260                265                270

tgg ctg tcg ttg gcg agt ggc gcc atc tgg gcc ttt gta gcc cct gcc 864
Trp Leu Ser Leu Ala Ser Gly Ala Ile Trp Ala Phe Val Ala Pro Ala
275                280                285

ctg ttt gtc atc gtg gta cct aat ttt gta ttt tta gta gag acg ggt 912
Leu Phe Val Ile Val Val Pro Asn Phe Val Phe Leu Val Glu Thr Gly
290                295                300

cca gtt ttg ctt act gga cta gcg agc caa gac cct tct gtg cgc tcc 960
Pro Val Leu Leu Thr Gly Leu Ala Ser Gln Asp Pro Ser Val Arg Ser
305                310                315                320

acc cag ttg acg gcc aag gca gcg gcc gtg ctg ctg ccc atc ctg ggt 1008
Thr Gln Leu Thr Ala Lys Ala Ala Ala Val Leu Leu Pro Ile Leu Gly
325                330                335

acc tcg tgg gtc ttt ggc gtg ctt gct gtc aac ggt tgt gct gtg gtt 1056
Thr Ser Trp Val Phe Gly Val Leu Ala Val Asn Gly Cys Ala Val Val
340                345                350

ttc cag tac atg ttt gcc acg ctc aac tcc ctg cag gga ctg ttc ata 1104
Phe Gln Tyr Met Phe Ala Thr Leu Asn Ser Leu Gln Gly Leu Phe Ile
355                360                365

ttc ctc ttt cat tgt ctc ctg aat tca gag gta cag ggg ctg gag gag 1152
Phe Leu Phe His Cys Leu Leu Asn Ser Glu Val Gln Gly Leu Glu Glu
370                375                380

ctg cag aag aaa tgg tgg ggc ggt gac cct gag tta ggc atc agc agg 1200
Leu Gln Lys Lys Trp Trp Gly Gly Asp Pro Glu Leu Gly Ile Ser Arg
385                390                395                400

aag cca ctg cca tcc ggg gct gca ggg gcc ggg aag ggt gag cac agc 1248
Lys Pro Leu Pro Ser Gly Ala Ala Gly Ala Gly Lys Gly Glu His Ser
405                410                415

cag ggc ctg ggt ggc aag tcc agg gca 1275
Gln Gly Leu Gly Gly Lys Ser Arg Ala
420                425

```

<210> 64

<211> 425

<212> PRT

<213> Homo sapiens

<400> 64

```

His Arg Arg Leu Lys Gln Glu Asn His Leu Asn Pro Gly Gly Arg Gly
1          5          10          15
Cys Met Gly Leu Trp Gly Gly Gly Leu Cys Trp Val Pro Thr Ala Pro

```

75/160

20							25					30				
Gly	Ser	Cys	Gly	Ala	Pro	Pro	Gly	Arg	Leu	Arg	Cys	Pro	Asp	Trp	Phe	
		35					40					45				
Ser	Ala	Leu	Ser	Ser	Thr	Ser	Met	Met	Ser	Gly	Pro	Ser	Leu	Ser	Leu	
50						55					60					
Cys	Cys	Pro	His	Gly	Pro	Arg	Cys	Leu	Gln	Thr	Gly	His	Trp	Ser	Pro	
65					70					75						
Arg	Met	Gln	Ala	Thr	Val	Ser	Gly	Glu	Gly	Val	Trp	Ser	Asn	His	Gly	
				85					90							
Cys	Ala	Leu	Thr	Arg	Gly	Asn	Leu	Thr	Tyr	Ser	Val	Cys	Arg	Cys	Thr	
		100						105								
His	Leu	Thr	Asn	Phe	Ala	Ile	Leu	Met	Gln	Leu	Ala	Arg	Gly	His	Gln	
		115				120										
Val	Ala	Leu	Ser	Ser	Ile	Ser	Tyr	Val	Gly	Cys	Ser	Leu	Ser	Val	Leu	
130						135										
Cys	Leu	Val	Ala	Thr	Leu	Val	Thr	Phe	Ala	Val	Leu	Ser	Thr	Ile	Arg	
145					150					155						
Asn	Gln	Arg	Tyr	His	Ile	His	Ala	Asn	Leu	Ser	Phe	Ala	Val	Leu	Val	
				165					170							
Ala	Gln	Val	Leu	Leu	Leu	Ile	Ser	Phe	Arg	Leu	Glu	Pro	Gly	Thr	Val	
		180						185								
Ser	Gly	Arg	Ser	Ser	Thr	Pro	Cys	Gln	Val	Met	Ala	Val	Leu	Leu	His	
195						200										
Tyr	Phe	Phe	Leu	Ser	Ala	Phe	Ala	Trp	Met	Leu	Val	Glu	Gly	Leu	His	
210						215										
Leu	Tyr	Ser	Met	Val	Ile	Lys	Val	Phe	Gly	Ser	Glu	Asp	Ser	Lys	His	
225					230					235						
Arg	Tyr	Tyr	Tyr	Gly	Met	Gly	Trp	Gly	Phe	Pro	Leu	Leu	Ile	Cys	Ile	
				245					250							
Ile	Ser	Leu	Ser	Phe	Ala	Met	Asp	Ser	Tyr	Gly	Thr	Ser	Asn	Asn	Cys	
		260						265								
Trp	Leu	Ser	Leu	Ala	Ser	Gly	Ala	Ile	Trp	Ala	Phe	Val	Ala	Pro	Ala	
275						280										
Leu	Phe	Val	Ile	Val	Val	Pro	Asn	Phe	Val	Phe	Leu	Val	Glu	Thr	Gly	
290						295					300					
Pro	Val	Leu	Leu	Thr	Gly	Leu	Ala	Ser	Gln	Asp	Pro	Ser	Val	Arg	Ser	
305					310					315						
Thr	Gln	Leu	Thr	Ala	Lys	Ala	Ala	Ala	Val	Leu	Leu	Pro	Ile	Leu	Gly	
				325					330							
Thr	Ser	Trp	Val	Phe	Gly	Val	Leu	Ala	Val	Asn	Gly	Cys	Ala	Val	Val	
		340						345								
Phe	Gln	Tyr	Met	Phe	Ala	Thr	Leu	Asn	Ser	Leu	Gln	Gly	Leu	Phe	Ile	
355						360										
Phe	Leu	Phe	His	Cys	Leu	Leu	Asn	Ser	Glu	Val	Gln	Gly	Leu	Glu	Glu	
370						375					380					
Leu	Gln	Lys	Lys	Trp	Trp	Gly	Gly	Asp	Pro	Glu	Leu	Gly	Ile	Ser	Arg	
385					390					395						
Lys	Pro	Leu	Pro	Ser	Gly	Ala	Ala	Gly	Ala	Gly	Lys	Gly	Glu	His	Ser	
				405					410							
Gln	Gly	Leu	Gly	Gly	Lys	Ser	Arg	Ala								
		420						425								

```
<210> 65
<211> 1275
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> CDS  
<222> (1) ... (1275)
```

<400> 65

76/160

tat	tat	cag	gaa	caa	ttg	gca	cag	aaa	gac	cct	ttg	acg	tac	tta	aat	48
Tyr	Tyr	Gln	Glu	Gln	Leu	Ala	Gln	Lys	Asp	Pro	Leu	Thr	Tyr	Leu	Asn	
1				5					10					15		
gat	aat	tgc	ttt	att	ctt	cct	gat	att	ttc	act	tgt	aga	ttc	acc	tgc	96
Asp	Asn	Cys	Phe	Ile	Leu	Pro	Asp	Ile	Phe	Thr	Cys	Arg	Phe	Thr	Cys	
		20						25					30			
cca	tgg	ggc	caa	tct	tgt	agt	ctt	tgc	cca	tac	cta	tgt	cct	gaa	tgg	144
Pro	Trp	Gly	Gln	Ser	Cys	Ser	Leu	Cys	Pro	Tyr	Leu	Cys	Pro	Glu	Trp	
		35					40					45				
ttc	cag	ttg	ttt	cct	tct	gct	cag	gtt	atc	aga	agc	tgc	aca	aag	tgg	192
Phe	Gln	Leu	Phe	Pro	Ser	Ala	Gln	Val	Ile	Arg	Ser	Cys	Thr	Lys	Trp	
	50					55					60					
tct	ggg	act	tgg	gac	act	ttt	ttt	gga	gga	tgg	aac	acg	tca	gga	tgt	240
Ser	Gly	Thr	Trp	Asp	Thr	Phe	Phe	Gly	Gly	Trp	Asn	Thr	Ser	Gly	Cys	
65					70					75				80		
gtt	gca	cac	aga	gat	tca	gat	gca	agt	gag	aca	gtc	tgc	ctg	tgt	aac	288
Val	Ala	His	Arg	Asp	Ser	Asp	Ala	Ser	Glu	Thr	Val	Cys	Leu	Cys	Asn	
				85					90					95		
cac	ttc	aca	cac	ttt	gga	gtt	ctg	atg	tta	gat	gca	aga	aac	act	aaa	336
His	Phe	Thr	His	Phe	Gly	Val	Leu	Met	Leu	Asp	Ala	Arg	Asn	Thr	Lys	
			100					105					110			
gtc	ctc	act	ttc	atc	agc	tat	att	ggg	tgt	gga	ata	tct	gct	att	ttt	384
Val	Leu	Thr	Phe	Ile	Ser	Tyr	Ile	Gly	Cys	Gly	Ile	Ser	Ala	Ile	Phe	
		115					120					125				
tca	gca	gca	act	ctc	ctg	aca	tat	gtt	gct	ttt	gaa	ttc	ctt	ttt	tca	432
Ser	Ala	Ala	Thr	Leu	Leu	Thr	Tyr	Val	Ala	Phe	Glu	Phe	Leu	Phe	Ser	
	130					135					140					
ttt	ttt	agg	aaa	ttg	cga	agg	gat	tat	ccc	tcc	aaa	atc	ttg	atg	aac	480
Phe	Phe	Arg	Lys	Leu	Arg	Arg	Asp	Tyr	Pro	Ser	Lys	Ile	Leu	Met	Asn	
145					150					155				160		
ctg	agc	aca	gcc	ctg	ctg	ttc	ctg	aat	ctc	ctc	ttc	ctc	cta	gat	ggc	528
Leu	Ser	Thr	Ala	Leu	Leu	Phe	Leu	Asn	Leu	Leu	Phe	Leu	Leu	Asp	Gly	
				165					170					175		
tgg	atc	acc	tcc	ttc	aat	gtg	gat	gga	ctt	tgc	att	gct	gtt	gca	gtc	576
Trp	Ile	Thr	Ser	Phe	Asn	Val	Asp	Gly	Leu	Cys	Ile	Ala	Val	Ala	Val	
			180					185					190			
ctg	ttg	cat	ttc	ttc	ctt	ctg	gca	acc	ttt	acc	tgg	atg	ggg	cta	gaa	624
Leu	Leu	His	Phe	Phe	Leu	Leu	Ala	Thr	Phe	Thr	Trp	Met	Gly	Leu	Glu	
		195					200					205				
gca	att	cac	atg	tac	att	gct	cta	gtt	aaa	gta	ttt	aac	act	tac	att	672
Ala	Ile	His	Met	Tyr	Ile	Ala	Leu	Val	Lys	Val	Phe	Asn	Thr	Tyr	Ile	
	210					215					220					
cgc	cga	tac	att	cta	aaa	ttc	tgc	atc	att	ggc	tgg	ggt	ttg	cct	gcc	720
Arg	Arg	Tyr	Ile	Leu	Lys	Phe	Cys	Ile	Ile	Gly	Trp	Gly	Leu	Pro	Ala	
225					230					235				240		
tta	gtg	gtg	tca	gtt	gtt	cta	gcg	agc	aga	aac	aac	aat	gaa	gtc	tat	768
Leu	Val	Val	Ser	Val	Val	Leu	Ala	Ser	Arg	Asn	Asn	Asn	Glu	Val	Tyr	

77/160

245										250										255										
gga	aaa	gaa	agt	tat	ggg	aaa	gaa	aaa	ggg	gat	gaa	ttc	tgt	tgg	att	816														
Gly	Lys	Glu	Ser	Tyr	Gly	Lys	Glu	Lys	Gly	Asp	Glu	Phe	Cys	Trp	Ile															
			260					265					270																	
caa	gat	cca	gtc	ata	ttt	tat	gtg	acc	tgt	gct	ggg	tat	ttt	gga	gtc	864														
Gln	Asp	Pro	Val	Ile	Phe	Tyr	Val	Thr	Cys	Ala	Gly	Tyr	Phe	Gly	Val															
		275					280					285																		
atg	ttt	ttt	ctg	aac	att	gcc	atg	ttc	att	gtg	gta	atg	gtg	cag	atc	912														
Met	Phe	Phe	Leu	Asn	Ile	Ala	Met	Phe	Ile	Val	Val	Met	Val	Gln	Ile															
	290					295				300																				
tgt	ggg	agg	aat	ggc	aag	aga	agc	aac	cgg	acc	ctg	aga	gaa	gaa	gtg	960														
Cys	Gly	Arg	Asn	Gly	Lys	Arg	Ser	Asn	Arg	Thr	Leu	Arg	Glu	Glu	Val															
305				310					315					320																
tta	agg	aac	ctg	cgc	agt	gtg	gtt	agc	ttg	acc	ttt	ctg	ttg	ggc	atg	1008														
Leu	Arg	Asn	Leu	Arg	Ser	Val	Val	Ser	Leu	Thr	Phe	Leu	Leu	Gly	Met															
			325					330					335																	
aca	tgg	ggg	ttt	gca	ttc	ttt	gcc	tgg	gga	ccc	tta	aat	atc	ccc	ttc	1056														
Thr	Trp	Gly	Phe	Ala	Phe	Phe	Ala	Trp	Gly	Pro	Leu	Asn	Ile	Pro	Phe															
			340					345					350																	
atg	tac	ctc	ttc	tcc	atc	ttc	aat	tca	tta	caa	ggc	tta	ttt	ata	ttc	1104														
Met	Tyr	Leu	Phe	Ser	Ile	Phe	Asn	Ser	Leu	Gln	Gly	Leu	Phe	Ile	Phe															
		355					360					365																		
atc	ttc	cac	tgt	gct	atg	aag	gag	aat	gtt	cag	aaa	cag	tgg	cgg	cag	1152														
Ile	Phe	His	Cys	Ala	Met	Lys	Glu	Asn	Val	Gln	Lys	Gln	Trp	Arg	Gln															
	370					375					380																			
cat	ctc	tgc	tgt	ggg	aga	ttt	cgt	ggc	acg	atc	tgc	gct	cac	tgc	aag	1200														
His	Leu	Cys	Cys	Gly	Arg	Phe	Arg	Gly	Thr	Ile	Ser	Ala	His	Cys	Lys															
385				390					395					400																
ctc	cgc	ctc	ccc	ggg	tca	cgc	cat	tct	cct	gcc	tca	gcc	tcc	caa	gta	1248														
Leu	Arg	Leu	Pro	Gly	Ser	Arg	His	Ser	Pro	Ala	Ser	Ala	Ser	Gln	Val															
				405				410						415																
gct	ggg	act	aca	ggc	acc	agc	cac	cat								1275														
Ala	Gly	Thr	Thr	Gly	Thr	Ser	His	His																						
			420				425																							

<210> 66

<211> 425

<212> PRT

<213> Homo sapiens

<400> 66

Tyr	Tyr	Gln	Glu	Gln	Leu	Ala	Gln	Lys	Asp	Pro	Leu	Thr	Tyr	Leu	Asn
1				5					10					15	
Asp	Asn	Cys	Phe	Ile	Leu	Pro	Asp	Ile	Phe	Thr	Cys	Arg	Phe	Thr	Cys
			20					25					30		
Pro	Trp	Gly	Gln	Ser	Cys	Ser	Leu	Cys	Pro	Tyr	Leu	Cys	Pro	Glu	Trp
		35					40					45			
Phe	Gln	Leu	Phe	Pro	Ser	Ala	Gln	Val	Ile	Arg	Ser	Cys	Thr	Lys	Trp
	50					55				60					
Ser	Gly	Thr	Trp	Asp	Thr	Phe	Phe	Gly	Gly	Trp	Asn	Thr	Ser	Gly	Cys

78/160

65					70					75				80
Val	Ala	His	Arg	Asp	Ser	Asp	Ala	Ser	Glu	Thr	Val	Cys	Leu	Cys
				85					90					95
His	Phe	Thr	His	Phe	Gly	Val	Leu	Met	Leu	Asp	Ala	Arg	Asn	Thr
			100					105					110	
Val	Leu	Thr	Phe	Ile	Ser	Tyr	Ile	Gly	Cys	Gly	Ile	Ser	Ala	Ile
			115				120					125		
Ser	Ala	Ala	Thr	Leu	Leu	Thr	Tyr	Val	Ala	Phe	Glu	Phe	Leu	Phe
	130					135					140			
Phe	Phe	Arg	Lys	Leu	Arg	Arg	Asp	Tyr	Pro	Ser	Lys	Ile	Leu	Met
145					150					155				160
Leu	Ser	Thr	Ala	Leu	Leu	Phe	Leu	Asn	Leu	Leu	Phe	Leu	Leu	Asp
				165				170						175
Trp	Ile	Thr	Ser	Phe	Asn	Val	Asp	Gly	Leu	Cys	Ile	Ala	Val	Ala
			180					185					190	
Leu	Leu	His	Phe	Phe	Leu	Leu	Ala	Thr	Phe	Thr	Trp	Met	Gly	Leu
		195					200					205		
Ala	Ile	His	Met	Tyr	Ile	Ala	Leu	Val	Lys	Val	Phe	Asn	Thr	Tyr
	210					215					220			
Arg	Arg	Tyr	Ile	Leu	Lys	Phe	Cys	Ile	Ile	Gly	Trp	Gly	Leu	Pro
225					230					235				240
Leu	Val	Val	Ser	Val	Val	Leu	Ala	Ser	Arg	Asn	Asn	Asn	Glu	Val
				245					250					255
Gly	Lys	Glu	Ser	Tyr	Gly	Lys	Glu	Lys	Gly	Asp	Glu	Phe	Cys	Trp
			260					265					270	
Gln	Asp	Pro	Val	Ile	Phe	Tyr	Val	Thr	Cys	Ala	Gly	Tyr	Phe	Gly
	275						280					285		
Met	Phe	Phe	Leu	Asn	Ile	Ala	Met	Phe	Ile	Val	Val	Met	Val	Gln
	290					295					300			
Cys	Gly	Arg	Asn	Gly	Lys	Arg	Ser	Asn	Arg	Thr	Leu	Arg	Glu	Glu
305					310					315				320
Leu	Arg	Asn	Leu	Arg	Ser	Val	Val	Ser	Leu	Thr	Phe	Leu	Leu	Gly
				325					330					335
Thr	Trp	Gly	Phe	Ala	Phe	Phe	Ala	Trp	Gly	Pro	Leu	Asn	Ile	Pro
			340					345					350	
Met	Tyr	Leu	Phe	Ser	Ile	Phe	Asn	Ser	Leu	Gln	Gly	Leu	Phe	Ile
	355						360					365		
Ile	Phe	His	Cys	Ala	Met	Lys	Glu	Asn	Val	Gln	Lys	Gln	Trp	Arg
	370					375					380			
His	Leu	Cys	Cys	Gly	Arg	Phe	Arg	Gly	Thr	Ile	Ser	Ala	His	Cys
385					390					395				400
Leu	Arg	Leu	Pro	Gly	Ser	Arg	His	Ser	Pro	Ala	Ser	Ala	Ser	Gln
				405					410					415
Ala	Gly	Thr	Thr	Gly	Thr	Ser	His	His						
			420					425						

<210> 67
 <211> 2454
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)... (2454)

<400> 67
 gga cat atc ata att gga ggt ttg ttt gct att cat gaa aaa atg ttg 48
 Gly His Ile Ile Ile Gly Gly Leu Phe Ala Ile His Glu Lys Met Leu
 1 5 10 15

tcc tca gaa gac tct ccc aga cga cca caa atc cag gag tgt gtt ggc 96
 Ser Ser Glu Asp Ser Pro Arg Arg Pro Gln Ile Gln Glu Cys Val Gly

79/160

20	25	30	
ttt gaa ata tca gtt ttt ctt caa act ctt gcc atg ata cac agc att Phe Glu Ile Ser Val Phe Leu Gln Thr Leu Ala Met Ile His Ser Ile 35 40 45			144
gag atg atc aac aat tca aca ctc tta cct gga gtc aaa ctg ggg tat Glu Met Ile Asn Asn Ser Thr Leu Leu Pro Gly Val Lys Leu Gly Tyr 50 55 60			192
gaa atc tat gac act tgt aca gaa gtc aca gtg gca atg gca gcc act Glu Ile Tyr Asp Thr Cys Thr Glu Val Thr Val Ala Met Ala Ala Thr 65 70 75 80			240
ctg agg ttt ctt tct aaa ttc aac tgc tcc aga gaa act gtg gag ttt Leu Arg Phe Leu Ser Lys Phe Asn Cys Ser Arg Glu Thr Val Glu Phe 85 90 95			288
aag tgt gac tat tcc agc tac atg cca aga gtt aag gct gtc ata ggt Lys Cys Asp Tyr Ser Ser Tyr Met Pro Arg Val Lys Ala Val Ile Gly 100 105 110			336
tct ggg tac tca gaa ata act atg gct gtc tcc agg atg ttg aat tta Ser Gly Tyr Ser Glu Ile Thr Met Ala Val Ser Arg Met Leu Asn Leu 115 120 125			384
cag ctc atg cca cag gtg ggt tat gaa tca act gca gaa atc ctg agt Gln Leu Met Pro Gln Val Gly Tyr Glu Ser Thr Ala Glu Ile Leu Ser 130 135 140			432
gac aaa att cgc ttt cct tca ttt tta cgg act gtg ccc agt gac ttc Asp Lys Ile Arg Phe Pro Ser Phe Leu Arg Thr Val Pro Ser Asp Phe 145 150 155 160			480
cat caa att aaa gca atg gct cac ctg att cag aaa tct ggt tgg aac His Gln Ile Lys Ala Met Ala His Leu Ile Gln Lys Ser Gly Trp Asn 165 170 175			528
tgg att ggc atc ata acc aca gat gat gac tat gga cga ttg gct ctt Trp Ile Gly Ile Ile Thr Thr Asp Asp Asp Tyr Gly Arg Leu Ala Leu 180 185 190			576
aac act ttt ata att cag gct gaa gca aat aac gtg tgc ata gcc ttc Asn Thr Phe Ile Ile Gln Ala Glu Ala Asn Asn Val Cys Ile Ala Phe 195 200 205			624
aaa gag gtt ctt cca gcc ttt ctt tca gat aat acc att gaa gtc aga Lys Glu Val Leu Pro Ala Phe Leu Ser Asp Asn Thr Ile Glu Val Arg 210 215 220			672
atc aat cgg aca ctg aag aaa atc att tta gaa gcc cag gtt aat gtc Ile Asn Arg Thr Leu Lys Lys Ile Ile Leu Glu Ala Gln Val Asn Val 225 230 235 240			720
att gtg gta ttt ctg agg caa ttc cat gtt ttt gat ctc ttc aat aaa Ile Val Val Phe Leu Arg Gln Phe His Val Phe Asp Leu Phe Asn Lys 245 250 255			768
gcc att gaa atg aat ata aat aag atg tgg att gct agt gat aat tgg Ala Ile Glu Met Asn Ile Asn Lys Met Trp Ile Ala Ser Asp Asn Trp 260 265 270			816

80/160

tca act gcc acc aag att acc acc att cct aat gtt aaa aag att ggc	864
Ser Thr Ala Thr Lys Ile Thr Thr Ile Pro Asn Val Lys Lys Ile Gly	
275 280 285	
aaa gtt gta ggg ttt gcc ttt aga aga ggg aat ata tcc tct ttc cat	912
Lys Val Val Gly Phe Ala Phe Arg Arg Gly Asn Ile Ser Ser Phe His	
290 295 300	
tcc ttt ctt caa aat ctg cac ttg ctt ccc agt gac agt cac aaa ctc	960
Ser Phe Leu Gln Asn Leu His Leu Leu Pro Ser Asp Ser His Lys Leu	
305 310 315 320	
tta cat gaa tat gcc atg cat tta tct gcc tgc gca tat gtc aag gac	1008
Leu His Glu Tyr Ala Met His Leu Ser Ala Cys Ala Tyr Val Lys Asp	
325 330 335	
act gat ttg agt caa tgc ata ttc aat cat tct caa agg act ttg gcc	1056
Thr Asp Leu Ser Gln Cys Ile Phe Asn His Ser Gln Arg Thr Leu Ala	
340 345 350	
tac aag gct aac aag gct ata gaa agg aac ttc gtc atg aga aat gac	1104
Tyr Lys Ala Asn Lys Ala Ile Glu Arg Asn Phe Val Met Arg Asn Asp	
355 360 365	
ttc ctc tgg gac tat gct gag cca gga ctc att cat agt att cag ctt	1152
Phe Leu Trp Asp Tyr Ala Glu Pro Gly Leu Ile His Ser Ile Gln Leu	
370 375 380	
gca gtg ttt gcc ctt ggt tat gcc att cgg gat ctg tgt caa gct cgt	1200
Ala Val Phe Ala Leu Gly Tyr Ala Ile Arg Asp Leu Cys Gln Ala Arg	
385 390 395 400	
gac tgt cag aac ccc aac gcc ttt caa cca tgg gag tta ctt ggt gtg	1248
Asp Cys Gln Asn Pro Asn Ala Phe Gln Pro Trp Glu Leu Leu Gly Val	
405 410 415	
cta aaa aat gtg aca ttc act gat gga tgg aat tca ttt cat ttt gat	1296
Leu Lys Asn Val Thr Phe Thr Asp Gly Trp Asn Ser Phe His Phe Asp	
420 425 430	
gct cac ggg gat tta aat act gga tat gat gtt gtg ctc tgg aag gag	1344
Ala His Gly Asp Leu Asn Thr Gly Tyr Asp Val Val Leu Trp Lys Glu	
435 440 445	
atc aat gga cac atg act gtc act aag atg gca gaa tat gac cta cag	1392
Ile Asn Gly His Met Thr Val Thr Lys Met Ala Glu Tyr Asp Leu Gln	
450 455 460	
aat gat gtc ttc atc atc cca gat cag gaa aca aaa aat gag ttc agg	1440
Asn Asp Val Phe Ile Ile Pro Asp Gln Glu Thr Lys Asn Glu Phe Arg	
465 470 475 480	
aat ctt aag caa att caa tct aaa tgc tcc aag gaa tgc agt cct ggg	1488
Asn Leu Lys Gln Ile Gln Ser Lys Cys Ser Lys Glu Cys Ser Pro Gly	
485 490 495	
caa atg aag aaa act aca aga agt caa cac atc tgt tgc tat gaa tgt	1536
Gln Met Lys Lys Thr Thr Arg Ser Gln His Ile Cys Cys Tyr Glu Cys	
500 505 510	
cag aac tgt cct gaa aat cat tac act aat cag aca gat atg cct cac	1584

81/160

Gln	Asn	Cys	Pro	Glu	Asn	His	Tyr	Thr	Asn	Gln	Thr	Asp	Met	Pro	His	
		515					520					525				
tgc	ctt	tta	tgc	aac	aac	aaa	act	cac	tgg	gcc	cct	gtt	agg	agc	act	1632
Cys	Leu	Leu	Cys	Asn	Asn	Lys	Thr	His	Trp	Ala	Pro	Val	Arg	Ser	Thr	
	530					535					540					
atg	tgc	ttt	gaa	aag	gaa	gtg	gaa	tat	ctc	aac	tgg	aat	gac	tcc	ttg	1680
Met	Cys	Phe	Glu	Lys	Glu	Val	Glu	Tyr	Leu	Asn	Trp	Asn	Asp	Ser	Leu	
545					550					555					560	
gcc	atc	cta	ctc	ctg	att	ctc	tcc	cta	ctg	gga	atc	ata	ttt	gtt	ctg	1728
Ala	Ile	Leu	Leu	Leu	Ile	Leu	Ser	Leu	Leu	Gly	Ile	Ile	Phe	Val	Leu	
				565					570					575		
gtt	gtt	ggc	ata	ata	ttt	aca	aga	aac	ctg	aac	aca	cct	gtt	gtg	aaa	1776
Val	Val	Gly	Ile	Ile	Phe	Thr	Arg	Asn	Leu	Asn	Thr	Pro	Val	Val	Lys	
			580					585					590			
tca	tcc	ggg	gga	tta	aga	gtc	tgc	tat	gtg	atc	ctt	ctc	tgt	cat	ttc	1824
Ser	Ser	Gly	Gly	Leu	Arg	Val	Cys	Tyr	Val	Ile	Leu	Leu	Cys	His	Phe	
		595					600					605				
ctc	aat	ttt	gcc	agc	acg	agc	ttt	ttc	att	gga	gaa	cca	caa	gac	ttc	1872
Leu	Asn	Phe	Ala	Ser	Thr	Ser	Phe	Phe	Ile	Gly	Glu	Pro	Gln	Asp	Phe	
	610					615					620					
aca	tgt	aaa	acc	agg	cag	aca	atg	ttt	gga	gtg	agc	ttt	act	ctt	tgc	1920
Thr	Cys	Lys	Thr	Arg	Gln	Thr	Met	Phe	Gly	Val	Ser	Phe	Thr	Leu	Cys	
625					630					635					640	
atc	tcc	tgc	att	ttg	acg	aag	tct	ctg	aaa	att	ttg	cta	gcc	ttc	agc	1968
Ile	Ser	Cys	Ile	Leu	Thr	Lys	Ser	Leu	Lys	Ile	Leu	Leu	Ala	Phe	Ser	
				645					650					655		
ttt	gat	ccc	aaa	tta	cag	aaa	ttt	ctg	aag	tgc	ctc	tat	aga	ccg	atc	2016
Phe	Asp	Pro	Lys	Leu	Gln	Lys	Phe	Leu	Lys	Cys	Leu	Tyr	Arg	Pro	Ile	
		660					665						670			
ctt	att	atc	ttc	act	tgc	acg	ggc	atc	cag	gtt	gtc	att	tgc	aca	ctc	2064
Leu	Ile	Ile	Phe	Thr	Cys	Thr	Gly	Ile	Gln	Val	Val	Ile	Cys	Thr	Leu	
		675					680					685				
tgg	cta	atc	ttt	gca	gca	cct	act	gta	gag	gtg	aat	gtc	tcc	ttg	ccc	2112
Trp	Leu	Ile	Phe	Ala	Ala	Pro	Thr	Val	Glu	Val	Asn	Val	Ser	Leu	Pro	
	690					695					700					
aga	gtc	atc	atc	ctg	gag	tgt	gag	gag	gga	tcc	ata	ctt	gca	ttt	ggc	2160
Arg	Val	Ile	Ile	Leu	Glu	Cys	Glu	Glu	Gly	Ser	Ile	Leu	Ala	Phe	Gly	
705					710				715						720	
acc	atg	ctg	ggc	tac	att	gcc	atc	ctg	gcc	ttc	att	tgc	ttc	ata	ttt	2208
Thr	Met	Leu	Gly	Tyr	Ile	Ala	Ile	Leu	Ala	Phe	Ile	Cys	Phe	Ile	Phe	
				725					730					735		
gct	ttc	aaa	ggc	aaa	tat	gag	aat	tac	aat	gaa	gcc	aaa	ttc	att	aca	2256
Ala	Phe	Lys	Gly	Lys	Tyr	Glu	Asn	Tyr	Asn	Glu	Ala	Lys	Phe	Ile	Thr	
			740					745					750			
ttt	ggc	atg	ctc	att	tac	ttc	ata	gct	tgg	atc	aca	ttc	atc	cct	atc	2304
Phe	Gly	Met	Leu	Ile	Tyr	Phe	Ile	Ala	Trp	Ile	Thr	Phe	Ile	Pro	Ile	

82/160

755	760	765	
tat gct acc aca ttt ggc aaa tat gta cca gct gtg gag att att gtc			2352
Tyr Ala Thr Thr Phe Gly Lys Tyr Val Pro Ala Val Glu Ile Ile Val			
770	775	780	
ata tta ata tct aac tat gga atc ctg tat tgc aca ttc atc ccc aaa			2400
Ile Leu Ile Ser Asn Tyr Gly Ile Leu Tyr Cys Thr Phe Ile Pro Lys			
785	790	795	800
tgc tat gtt att att tgt aag caa gag att aac aca aag tct gcc ttt			2448
Cys Tyr Val Ile Ile Cys Lys Gln Glu Ile Asn Thr Lys Ser Ala Phe			
805	810	815	
ctc aag			2454
Leu Lys			

<210> 68

<211> 818

<212> PRT

<213> Homo sapiens

<400> 68

Gly His Ile Ile Ile Gly Gly Leu Phe Ala Ile His Glu Lys Met Leu			
1	5	10	15
Ser Ser Glu Asp Ser Pro Arg Arg Pro Gln Ile Gln Glu Cys Val Gly			
20	25	30	
Phe Glu Ile Ser Val Phe Leu Gln Thr Leu Ala Met Ile His Ser Ile			
35	40	45	
Glu Met Ile Asn Asn Ser Thr Leu Leu Pro Gly Val Lys Leu Gly Tyr			
50	55	60	
Glu Ile Tyr Asp Thr Cys Thr Glu Val Thr Val Ala Met Ala Ala Thr			
65	70	75	80
Leu Arg Phe Leu Ser Lys Phe Asn Cys Ser Arg Glu Thr Val Glu Phe			
85	90	95	
Lys Cys Asp Tyr Ser Ser Tyr Met Pro Arg Val Lys Ala Val Ile Gly			
100	105	110	
Ser Gly Tyr Ser Glu Ile Thr Met Ala Val Ser Arg Met Leu Asn Leu			
115	120	125	
Gln Leu Met Pro Gln Val Gly Tyr Glu Ser Thr Ala Glu Ile Leu Ser			
130	135	140	
Asp Lys Ile Arg Phe Pro Ser Phe Leu Arg Thr Val Pro Ser Asp Phe			
145	150	155	160
His Gln Ile Lys Ala Met Ala His Leu Ile Gln Lys Ser Gly Trp Asn			
165	170	175	
Trp Ile Gly Ile Ile Thr Thr Asp Asp Asp Tyr Gly Arg Leu Ala Leu			
180	185	190	
Asn Thr Phe Ile Ile Gln Ala Glu Ala Asn Asn Val Cys Ile Ala Phe			
195	200	205	
Lys Glu Val Leu Pro Ala Phe Leu Ser Asp Asn Thr Ile Glu Val Arg			
210	215	220	
Ile Asn Arg Thr Leu Lys Lys Ile Ile Leu Glu Ala Gln Val Asn Val			
225	230	235	240
Ile Val Val Phe Leu Arg Gln Phe His Val Phe Asp Leu Phe Asn Lys			
245	250	255	
Ala Ile Glu Met Asn Ile Asn Lys Met Trp Ile Ala Ser Asp Asn Trp			
260	265	270	
Ser Thr Ala Thr Lys Ile Thr Thr Ile Pro Asn Val Lys Lys Ile Gly			
275	280	285	
Lys Val Val Gly Phe Ala Phe Arg Arg Gly Asn Ile Ser Ser Phe His			

83/160

290	295	300
Ser Phe Leu Gln Asn Leu His Leu Leu Pro Ser Asp Ser His Lys Leu		
305	310	315
Leu His Glu Tyr Ala Met His Leu Ser Ala Cys Ala Tyr Val Lys Asp		
	325	330
Thr Asp Leu Ser Gln Cys Ile Phe Asn His Ser Gln Arg Thr Leu Ala		
	340	345
Tyr Lys Ala Asn Lys Ala Ile Glu Arg Asn Phe Val Met Arg Asn Asp		
	355	360
Phe Leu Trp Asp Tyr Ala Glu Pro Gly Leu Ile His Ser Ile Gln Leu		
	370	375
Ala Val Phe Ala Leu Gly Tyr Ala Ile Arg Asp Leu Cys Gln Ala Arg		
385	390	395
Asp Cys Gln Asn Pro Asn Ala Phe Gln Pro Trp Glu Leu Leu Gly Val		
	405	410
Leu Lys Asn Val Thr Phe Thr Asp Gly Trp Asn Ser Phe His Phe Asp		
	420	425
Ala His Gly Asp Leu Asn Thr Gly Tyr Asp Val Val Leu Trp Lys Glu		
	435	440
Ile Asn Gly His Met Thr Val Thr Lys Met Ala Glu Tyr Asp Leu Gln		
	450	455
Asn Asp Val Phe Ile Ile Pro Asp Gln Glu Thr Lys Asn Glu Phe Arg		
465	470	475
Asn Leu Lys Gln Ile Gln Ser Lys Cys Ser Lys Glu Cys Ser Pro Gly		
	485	490
Gln Met Lys Lys Thr Thr Arg Ser Gln His Ile Cys Cys Tyr Glu Cys		
	500	505
Gln Asn Cys Pro Glu Asn His Tyr Thr Asn Gln Thr Asp Met Pro His		
	515	520
Cys Leu Leu Cys Asn Asn Lys Thr His Trp Ala Pro Val Arg Ser Thr		
	530	535
Met Cys Phe Glu Lys Glu Val Glu Tyr Leu Asn Trp Asn Asp Ser Leu		
545	550	555
Ala Ile Leu Leu Leu Ile Leu Ser Leu Leu Gly Ile Ile Phe Val Leu		
	565	570
Val Val Gly Ile Ile Phe Thr Arg Asn Leu Asn Thr Pro Val Val Lys		
	580	585
Ser Ser Gly Gly Leu Arg Val Cys Tyr Val Ile Leu Leu Cys His Phe		
	595	600
Leu Asn Phe Ala Ser Thr Ser Phe Phe Ile Gly Glu Pro Gln Asp Phe		
	610	615
Thr Cys Lys Thr Arg Gln Thr Met Phe Gly Val Ser Phe Thr Leu Cys		
625	630	635
Ile Ser Cys Ile Leu Thr Lys Ser Leu Lys Ile Leu Leu Ala Phe Ser		
	645	650
Phe Asp Pro Lys Leu Gln Lys Phe Leu Lys Cys Leu Tyr Arg Pro Ile		
	660	665
Leu Ile Ile Phe Thr Cys Thr Gly Ile Gln Val Val Ile Cys Thr Leu		
	675	680
Trp Leu Ile Phe Ala Ala Pro Thr Val Glu Val Asn Val Ser Leu Pro		
	690	695
Arg Val Ile Ile Leu Glu Cys Glu Glu Gly Ser Ile Leu Ala Phe Gly		
705	710	715
Thr Met Leu Gly Tyr Ile Ala Ile Leu Ala Phe Ile Cys Phe Ile Phe		
	725	730
Ala Phe Lys Gly Lys Tyr Glu Asn Tyr Asn Glu Ala Lys Phe Ile Thr		
	740	745
Phe Gly Met Leu Ile Tyr Phe Ile Ala Trp Ile Thr Phe Ile Pro Ile		
	755	760
Tyr Ala Thr Thr Phe Gly Lys Tyr Val Pro Ala Val Glu Ile Ile Val		
	770	775
Ile Leu Ile Ser Asn Tyr Gly Ile Leu Tyr Cys Thr Phe Ile Pro Lys		
785	790	795
		800

84/160

Cys Tyr Val Ile Ile Cys Lys Gln Glu Ile Asn Thr Lys Ser Ala Phe
 805 810 815
 Leu Lys

<210> 69

<211> 2376

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(2376)

<400> 69

ggc aga cta gtc gta gga gcc ctt ttt aat cta gaa agt tgg tac caa	48
Gly Arg Leu Val Val Gly Ala Leu Phe Asn Leu Glu Ser Trp Tyr Gln	
1 5 10 15	
gaa gca tgt cct gag att tat tgt ttt cat cct ccc acc tgc cta ggc	96
Glu Ala Cys Pro Glu Ile Tyr Cys Phe His Pro Pro Thr Cys Leu Gly	
20 25 30	
ttc aat gag cat ggc tac cac ctc ttc cag gct atg cgg ctt ggg gtt	144
Phe Asn Glu His Gly Tyr His Leu Phe Gln Ala Met Arg Leu Gly Val	
35 40 45	
gag gag ata aac aac tcc acg gcc ctg ctg ccc aac atc acc ctg ggg	192
Glu Glu Ile Asn Asn Ser Thr Ala Leu Leu Pro Asn Ile Thr Leu Gly	
50 55 60	
tac cag ctg tat gat gtg tgt tct gac tct gcc aat gtg tat gcc acg	240
Tyr Gln Leu Tyr Asp Val Cys Ser Asp Ser Ala Asn Val Tyr Ala Thr	
65 70 75 80	
ctg aga gtg ctc tcc ctg cca ggg caa cac cac ata gag ctc caa gga	288
Leu Arg Val Leu Ser Leu Pro Gly Gln His His Ile Glu Leu Gln Gly	
85 90 95	
gac ctt ctc cac tat tcc cct acg gtg ctg gca gtg att ggg cct gac	336
Asp Leu Leu His Tyr Ser Pro Thr Val Leu Ala Val Ile Gly Pro Asp	
100 105 110	
agc acc aac cgt gct gcc acc aca gcc gcc ctg ctg agc cct ttc ctg	384
Ser Thr Asn Arg Ala Ala Thr Thr Ala Ala Leu Leu Ser Pro Phe Leu	
115 120 125	
gtg ccc atg att agc tat gcg gcc agc agc gag acg ctc agc gtg aag	432
Val Pro Met Ile Ser Tyr Ala Ala Ser Ser Glu Thr Leu Ser Val Lys	
130 135 140	
cgg cag tat ccc tct ttc ctg cgc acc atc ccc aat gac aag tac cag	480
Arg Gln Tyr Pro Ser Phe Leu Arg Thr Ile Pro Asn Asp Lys Tyr Gln	
145 150 155 160	
gtg gag acc atg gtg ctg ctg ctg cag aag ttc ggg tgg acc tgg atc	528
Val Glu Thr Met Val Leu Leu Leu Gln Lys Phe Gly Trp Thr Trp Ile	
165 170 175	
tct ctg gtt ggc agc agt gac gac tat ggg cag cta ggg gtg cag gca	576

85/160

Ser	Leu	Val	Gly	Ser	Ser	Asp	Asp	Tyr	Gly	Gln	Leu	Gly	Val	Gln	Ala		
			180					185					190				
ctg	gag	aac	cag	gcc	act	ggg	cag	ggg	atc	tgc	att	gct	ttc	aag	gac	624	
Leu	Glu	Asn	Gln	Ala	Thr	Gly	Gln	Gly	Ile	Cys	Ile	Ala	Phe	Lys	Asp		
		195				200					205						
atc	atg	ccc	ttc	tct	gcc	cag	gtg	ggc	gat	gag	agg	atg	cag	tgc	ctc	672	
Ile	Met	Pro	Phe	Ser	Ala	Gln	Val	Gly	Asp	Glu	Arg	Met	Gln	Cys	Leu		
	210				215					220							
atg	cgc	cac	ctg	gcc	cag	gcc	ggg	gcc	acc	gtc	gtg	ggt	ggt	ttt	tcc	720	
Met	Arg	His	Leu	Ala	Gln	Ala	Gly	Ala	Thr	Val	Val	Val	Val	Phe	Ser		
225				230				235						240			
agc	cgg	cag	ttg	gcc	agg	gtg	ttt	ttc	gag	tcc	gtg	gtg	ctg	acc	aac	768	
Ser	Arg	Gln	Leu	Ala	Arg	Val	Phe	Phe	Glu	Ser	Val	Val	Leu	Thr	Asn		
			245					250					255				
ctg	act	ggc	aag	gtg	tgg	gtc	gcc	tca	gaa	gcc	tgg	gcc	ctc	tcc	agg	816	
Leu	Thr	Gly	Lys	Val	Trp	Val	Ala	Ser	Glu	Ala	Trp	Ala	Leu	Ser	Arg		
		260					265					270					
cac	atc	act	ggg	gtg	ccc	ggg	atc	cag	cgc	att	ggg	atg	gtg	ctg	ggc	864	
His	Ile	Thr	Gly	Val	Pro	Gly	Ile	Gln	Arg	Ile	Gly	Met	Val	Leu	Gly		
	275					280					285						
gtg	gcc	atc	cag	aag	agg	gct	gtc	cct	ggc	ctg	aag	gcg	ttt	gaa	gaa	912	
Val	Ala	Ile	Gln	Lys	Arg	Ala	Val	Pro	Gly	Leu	Lys	Ala	Phe	Glu	Glu		
	290					295				300							
gcc	tat	gcc	cgg	gca	gac	aag	aag	gcc	cct	agg	cct	tgc	cac	aag	ggc	960	
Ala	Tyr	Ala	Arg	Ala	Asp	Lys	Lys	Ala	Pro	Arg	Pro	Cys	His	Lys	Gly		
305				310				315						320			
tcc	tgg	tgc	agc	agc	aat	cag	ctc	tgc	aga	gaa	tgc	caa	gct	ttc	atg	1008	
Ser	Trp	Cys	Ser	Ser	Asn	Gln	Leu	Cys	Arg	Glu	Cys	Gln	Ala	Phe	Met		
			325					330					335				
gca	cac	acg	atg	ccc	aag	ctc	aaa	gcc	ttc	tcc	atg	agt	tct	gcc	tac	1056	
Ala	His	Thr	Met	Pro	Lys	Leu	Lys	Ala	Phe	Ser	Met	Ser	Ser	Ala	Tyr		
			340					345					350				
aac	gca	tac	cgg	gct	gtg	tat	gcg	gtg	gcc	cat	ggc	ctc	cac	cag	ctc	1104	
Asn	Ala	Tyr	Arg	Ala	Val	Tyr	Ala	Val	Ala	His	Gly	Leu	His	Gln	Leu		
	355					360					365						
ctg	ggc	tgt	gcc	tct	gga	gct	tgt	tcc	agg	ggc	cga	gtc	tac	ccc	tgg	1152	
Leu	Gly	Cys	Ala	Ser	Gly	Ala	Cys	Ser	Arg	Gly	Arg	Val	Tyr	Pro	Trp		
	370				375					380							
cag	ctt	ttg	gag	cag	atc	cac	aag	gtg	cat	ttc	ctt	cta	cac	aag	gac	1200	
Gln	Leu	Leu	Glu	Gln	Ile	His	Lys	Val	His	Phe	Leu	Leu	His	Lys	Asp		
385					390			395						400			
act	gtg	gcg	ttt	aat	gac	aac	aga	gat	ccc	ctc	agt	agc	tat	aac	ata	1248	
Thr	Val	Ala	Phe	Asn	Asp	Asn	Arg	Asp	Pro	Leu	Ser	Ser	Tyr	Asn	Ile		
			405					410					415				
att	gcc	tgg	gac	tgg	aat	gga	ccc	aag	tgg	acc	ttc	acg	gtc	ctc	ggg	1296	
Ile	Ala	Trp	Asp	Trp	Asn	Gly	Pro	Lys	Trp	Thr	Phe	Thr	Val	Leu	Gly		

86/160

420					425					430						
tcc	tcc	aca	tgg	tct	cca	gtt	cag	cta	aac	ata	aat	gag	acc	aaa	atc	1344
Ser	Ser	Thr	Trp	Ser	Pro	Val	Gln	Leu	Asn	Ile	Asn	Glu	Thr	Lys	Ile	
		435				440						445				
cag	tgg	cac	gga	aag	gac	aac	cag	gtg	cct	aag	tct	gtg	tgt	tcc	agc	1392
Gln	Trp	His	Gly	Lys	Asp	Asn	Gln	Val	Pro	Lys	Ser	Val	Cys	Ser	Ser	
		450				455						460				
gac	tgt	ctt	gaa	ggg	cac	cag	cga	gtg	gtt	acg	ggg	ttc	cat	cac	tgc	1440
Asp	Cys	Leu	Glu	Gly	His	Gln	Arg	Val	Val	Thr	Gly	Phe	His	His	Cys	
		465				470						475				480
tgc	ttt	gag	tgt	gtg	ccc	tgt	ggg	gct	ggg	acc	ttc	ctc	aac	aag	agt	1488
Cys	Phe	Glu	Cys	Val	Pro	Cys	Gly	Ala	Gly	Thr	Phe	Leu	Asn	Lys	Ser	
				485				490						495		
ggg	gaa	tgc	cag	cct	tgt	ggg	aaa	gaa	gag	tgg	gca	cct	gag	gga	agc	1536
Gly	Glu	Cys	Gln	Pro	Cys	Gly	Lys	Glu	Glu	Trp	Ala	Pro	Glu	Gly	Ser	
		500						505				510				
cag	acc	tgc	ttc	ccg	cgc	act	gtg	gtg	ttt	ttg	gct	ttg	cgt	gag	cac	1584
Gln	Thr	Cys	Phe	Pro	Arg	Thr	Val	Val	Phe	Leu	Ala	Leu	Arg	Glu	His	
		515						520				525				
acc	tct	tgg	gtg	ctg	ctg	gca	gct	aac	acg	ctg	ctg	ctg	ctg	ctg	ctg	1632
Thr	Ser	Trp	Val	Leu	Leu	Ala	Ala	Asn	Thr	Leu	Leu	Leu	Leu	Leu	Leu	
		530				535						540				
ctt	ggg	act	gct	ggc	ctg	ttt	gcc	tgg	cac	cta	gac	acc	cct	gtg	gtg	1680
Leu	Gly	Thr	Ala	Gly	Leu	Phe	Ala	Trp	His	Leu	Asp	Thr	Pro	Val	Val	
		545				550						555				560
agg	tca	gca	ggg	ggc	cgc	ctg	tgc	ttt	ctt	atg	ctg	ggc	tcc	ctg	gca	1728
Arg	Ser	Ala	Gly	Gly	Arg	Leu	Cys	Phe	Leu	Met	Leu	Gly	Ser	Leu	Ala	
				565				570						575		
gca	ggg	agt	ggc	agc	ctc	tat	ggc	ttc	ttt	ggg	gaa	ccc	aca	agg	cct	1776
Ala	Gly	Ser	Gly	Ser	Leu	Tyr	Gly	Phe	Phe	Gly	Glu	Pro	Thr	Arg	Pro	
		580						585				590				
gcg	tgc	ttg	cta	cgc	cag	gcc	ctc	ttt	gcc	ctt	ggg	ttc	acc	atc	ttc	1824
Ala	Cys	Leu	Leu	Arg	Gln	Ala	Leu	Phe	Ala	Leu	Gly	Phe	Thr	Ile	Phe	
		595				600						605				
ctg	tcc	tgc	ctg	aca	gtt	cgc	tca	ttc	caa	cta	atc	atc	atc	ttc	aag	1872
Leu	Ser	Cys	Leu	Thr	Val	Arg	Ser	Phe	Gln	Leu	Ile	Ile	Ile	Phe	Lys	
		610				615						620				
ttt	tcc	acc	aag	gta	cct	aca	ttc	tac	cac	gcc	tgg	gtc	caa	aac	cac	1920
Phe	Ser	Thr	Lys	Val	Pro	Thr	Phe	Tyr	His	Ala	Trp	Val	Gln	Asn	His	
		625				630						635				640
ggg	gct	ggc	ctg	ttt	gtg	atg	atc	agc	tca	gcg	gcc	cag	ctg	ctt	atc	1968
Gly	Ala	Gly	Leu	Phe	Val	Met	Ile	Ser	Ser	Ala	Ala	Gln	Leu	Leu	Ile	
				645				650						655		
tgt	cta	act	tgg	ctg	gtg	gtg	tgg	acc	cca	ctg	cct	gct	agg	gaa	tac	2016
Cys	Leu	Thr	Trp	Leu	Val	Val	Trp	Thr	Pro	Leu	Pro	Ala	Arg	Glu	Tyr	
		660						665				670				

87/160

cag cgc ttc ccc cat ctg gtg atg ctt gag tgc aca gag acc aac tcc 2064
 Gln Arg Phe Pro His Leu Val Met Leu Glu Cys Thr Glu Thr Asn Ser
 675 680 685

ctg ggc ttc ata ctg gcc ttc ctc tac aat ggc ctc ctc tcc atc agt 2112
 Leu Gly Phe Ile Leu Ala Phe Leu Tyr Asn Gly Leu Leu Ser Ile Ser
 690 695 700

gcc ttt gcc tgc agc tac ctg ggt aag gac ttg cca gag aac tac aac 2160
 Ala Phe Ala Cys Ser Tyr Leu Gly Lys Asp Leu Pro Glu Asn Tyr Asn
 705 710 715 720

gag gcc aaa tgt gtc acc ttc agc ctg ctc ttc aac ttc gtg tcc tgg 2208
 Glu Ala Lys Cys Val Thr Phe Ser Leu Leu Phe Asn Phe Val Ser Trp
 725 730 735

atc gcc ttc ttc acc acg gcc agc gtc tac gac ggc aag tac ctg cct 2256
 Ile Ala Phe Phe Thr Thr Ala Ser Val Tyr Asp Gly Lys Tyr Leu Pro
 740 745 750

gcg gcc aac atg atg gct ggg ctg agc agc ctg agc agc ggc ttc ggt 2304
 Ala Ala Asn Met Met Ala Gly Leu Ser Ser Leu Ser Ser Gly Phe Gly
 755 760 765

ggg tat ttt ctg cct aag tgc tac gtg atc ctc tgc cgc cca gac ctc 2352
 Gly Tyr Phe Leu Pro Lys Cys Tyr Val Ile Leu Cys Arg Pro Asp Leu
 770 775 780

aac agc aca gag cac ttc cag gcc 2376
 Asn Ser Thr Glu His Phe Gln Ala
 785 790

<210> 70

<211> 792

<212> PRT

<213> Homo sapiens

<400> 70

Gly Arg Leu Val Val Gly Ala Leu Phe Asn Leu Glu Ser Trp Tyr Gln
 1 5 10 15
 Glu Ala Cys Pro Glu Ile Tyr Cys Phe His Pro Pro Thr Cys Leu Gly
 20 25 30
 Phe Asn Glu His Gly Tyr His Leu Phe Gln Ala Met Arg Leu Gly Val
 35 40 45

Glu Glu Ile Asn Asn Ser Thr Ala Leu Leu Pro Asn Ile Thr Leu Gly
 50 55 60
 Tyr Gln Leu Tyr Asp Val Cys Ser Asp Ser Ala Asn Val Tyr Ala Thr
 65 70 75 80
 Leu Arg Val Leu Ser Leu Pro Gly Gln His His Ile Glu Leu Gln Gly
 85 90 95
 Asp Leu Leu His Tyr Ser Pro Thr Val Leu Ala Val Ile Gly Pro Asp
 100 105 110
 Ser Thr Asn Arg Ala Ala Thr Thr Ala Ala Leu Leu Ser Pro Phe Leu
 115 120 125
 Val Pro Met Ile Ser Tyr Ala Ala Ser Ser Glu Thr Leu Ser Val Lys
 130 135 140
 Arg Gln Tyr Pro Ser Phe Leu Arg Thr Ile Pro Asn Asp Lys Tyr Gln
 145 150 155 160
 Val Glu Thr Met Val Leu Leu Leu Gln Lys Phe Gly Trp Thr Trp Ile
 165 170 175

88/160

Ser Leu Val Gly Ser Ser Asp Asp Tyr Gly Gln Leu Gly Val Gln Ala
 180 185 190
 Leu Glu Asn Gln Ala Thr Gly Gln Gly Ile Cys Ile Ala Phe Lys Asp
 195 200 205
 Ile Met Pro Phe Ser Ala Gln Val Gly Asp Glu Arg Met Gln Cys Leu
 210 215 220
 Met Arg His Leu Ala Gln Ala Gly Ala Thr Val Val Val Phe Ser
 225 230 235 240
 Ser Arg Gln Leu Ala Arg Val Phe Phe Glu Ser Val Val Leu Thr Asn
 245 250 255
 Leu Thr Gly Lys Val Trp Val Ala Ser Glu Ala Trp Ala Leu Ser Arg
 260 265 270
 His Ile Thr Gly Val Pro Gly Ile Gln Arg Ile Gly Met Val Leu Gly
 275 280 285
 Val Ala Ile Gln Lys Arg Ala Val Pro Gly Leu Lys Ala Phe Glu Glu
 290 295 300
 Ala Tyr Ala Arg Ala Asp Lys Lys Ala Pro Arg Pro Cys His Lys Gly
 305 310 315 320
 Ser Trp Cys Ser Ser Asn Gln Leu Cys Arg Glu Cys Gln Ala Phe Met
 325 330 335
 Ala His Thr Met Pro Lys Leu Lys Ala Phe Ser Met Ser Ser Ala Tyr
 340 345 350
 Asn Ala Tyr Arg Ala Val Tyr Ala Val Ala His Gly Leu His Gln Leu
 355 360 365
 Leu Gly Cys Ala Ser Gly Ala Cys Ser Arg Gly Arg Val Tyr Pro Trp
 370 375 380
 Gln Leu Leu Glu Gln Ile His Lys Val His Phe Leu Leu His Lys Asp
 385 390 395 400
 Thr Val Ala Phe Asn Asp Asn Arg Asp Pro Leu Ser Ser Tyr Asn Ile
 405 410 415
 Ile Ala Trp Asp Trp Asn Gly Pro Lys Trp Thr Phe Thr Val Leu Gly
 420 425 430
 Ser Ser Thr Trp Ser Pro Val Gln Leu Asn Ile Asn Glu Thr Lys Ile
 435 440 445
 Gln Trp His Gly Lys Asp Asn Gln Val Pro Lys Ser Val Cys Ser Ser
 450 455 460
 Asp Cys Leu Glu Gly His Gln Arg Val Val Thr Gly Phe His His Cys
 465 470 475 480
 Cys Phe Glu Cys Val Pro Cys Gly Ala Gly Thr Phe Leu Asn Lys Ser
 485 490 495
 Gly Glu Cys Gln Pro Cys Gly Lys Glu Glu Trp Ala Pro Glu Gly Ser
 500 505 510
 Gln Thr Cys Phe Pro Arg Thr Val Val Phe Leu Ala Leu Arg Glu His
 515 520 525
 Thr Ser Trp Val Leu Leu Ala Asn Thr Leu Leu Leu Leu Leu
 530 535 540
 Leu Gly Thr Ala Gly Leu Phe Ala Trp His Leu Asp Thr Pro Val Val
 545 550 555 560
 Arg Ser Ala Gly Gly Arg Leu Cys Phe Leu Met Leu Gly Ser Leu Ala
 565 570 575
 Ala Gly Ser Gly Ser Leu Tyr Gly Phe Phe Gly Glu Pro Thr Arg Pro
 580 585 590
 Ala Cys Leu Leu Arg Gln Ala Leu Phe Ala Leu Gly Phe Thr Ile Phe
 595 600 605
 Leu Ser Cys Leu Thr Val Arg Ser Phe Gln Leu Ile Ile Ile Phe Lys
 610 615 620
 Phe Ser Thr Lys Val Pro Thr Phe Tyr His Ala Trp Val Gln Asn His
 625 630 635 640
 Gly Ala Gly Leu Phe Val Met Ile Ser Ser Ala Ala Gln Leu Leu Ile
 645 650 655
 Cys Leu Thr Trp Leu Val Val Trp Thr Pro Leu Pro Ala Arg Glu Tyr
 660 665 670
 Gln Arg Phe Pro His Leu Val Met Leu Glu Cys Thr Glu Thr Asn Ser

[illegible]

```
<220>  
<221> CDS  
<222> (1)...(2415)
```

<400> 71																	
ggg	gac	tac	gtg	ctg	ggg	ggg	ctg	ttc	ccc	ctg	ggc	gag	gcc	gag	gag	48	
Gly	Asp	Tyr	Val	Leu	Gly	Gly	Leu	Phe	Pro	Leu	Gly	Glu	Ala	Glu	Glu		
1				5					10					15			
gct ggc ctc cgc agc cgg aca cgg ccc agc agc cct gtg tgc acc agg 96																	
Ala	Gly	Leu	Arg	Ser	Arg	Thr	Arg	Pro	Ser	Ser	Pro	Val	Cys	Thr	Arg		
			20					25					30				
ttc tcc tca aac ggc ctg ctc tgg gca ctg gcc atg aaa atg gcc gtg 144																	
Phe	Ser	Ser	Asn	Gly	Leu	Leu	Trp	Ala	Leu	Ala	Met	Lys	Met	Ala	Val		
			35				40					45					
gag gag atc aac aac aag tgc gat ctg ctg ccc ggg ctg cgc ctg ggc 192																	
Glu	Glu	Ile	Asn	Asn	Lys	Ser	Asp	Leu	Leu	Pro	Gly	Leu	Arg	Leu	Gly		
		50				55					60						
tac gac ctc ttt gat acg tgc tgc gag cct gtg gtg gcc atg aag ccc 240																	
Tyr	Asp	Leu	Phe	Asp	Thr	Cys	Ser	Glu	Pro	Val	Val	Ala	Met	Lys	Pro		
65				70					75					80			
agc ctc atg ttc ctg gcc aag gca ggc agc cgc gac atc gcc gcc tac 288																	
Ser	Leu	Met	Phe	Leu	Ala	Lys	Ala	Gly	Ser	Arg	Asp	Ile	Ala	Ala	Tyr		
				85					90					95			
tgc aac tac acg cag tac cag ccc cgt gtg ctg gct gtc atc ggg ccc 336																	
Cys	Asn	Tyr	Thr	Gln	Tyr	Gln	Pro	Arg	Val	Leu	Ala	Val	Ile	Gly	Pro		
			100				105					110					
cac tgc tca gag ctc gcc atg gtc acc ggg aag ttc ttc agc ttc ttc 384																	
His	Ser	Ser	Glu	Leu	Ala	Met	Val	Thr	Gly	Lys	Phe	Phe	Ser	Phe	Phe		
			115				120					125					
ctc atg ccc caa tgc ctc ttg gcc ttg cag gtc agc tac ggt gct agc 432																	
Leu	Met	Pro	Gln	Cys	Leu	Leu	Ala	Leu	Gln	Val	Ser	Tyr	Gly	Ala	Ser		

90/160

130	135	140	
atg gag ctg ctg agc gcc cgg gag acc ttc ccc tcc ttc ttc cgc acc			480
Met Glu Leu Leu Ser Ala Arg Glu Thr Phe Pro Ser Phe Phe Arg Thr			
145	150	155	160
gtg ccc agc gac cgt gtg cag ctg acg gcc gcc gcg gag ctg ctg cag			528
Val Pro Ser Asp Arg Val Gln Leu Thr Ala Ala Ala Glu Leu Leu Gln			
	165	170	175
gag ttc ggc tgg aac tgg gtg gcc gcc ctg ggc agc gac gac gag tac			576
Glu Phe Gly Trp Asn Trp Val Ala Ala Leu Gly Ser Asp Asp Glu Tyr			
	180	185	190
ggc cgg cag ggc ctg agc atc ttc tgc gcc ctg gcc gcg gca cgc ggc			624
Gly Arg Gln Gly Leu Ser Ile Phe Ser Ala Leu Ala Ala Ala Arg Gly			
	195	200	205
atc tgc atc gcg cac gag ggc ctg gtg ccg ctg ccc cgt gcc gat gac			672
Ile Cys Ile Ala His Glu Gln Leu Val Pro Leu Pro Arg Ala Asp Asp			
	210	215	220
tcg cgg ctg ggg aag gtg cag gac gtc ctg cac cag gtg aac cag agc			720
Ser Arg Leu Gly Lys Val Gln Asp Val Leu His Gln Val Asn Gln Ser			
	225	230	235
agc gtg cag gtg gtg ctg ctg ttc gcc tcc gtg cac gcc gcc cac gcc			768
Ser Val Gln Val Val Leu Leu Phe Ala Ser Val His Ala Ala His Ala			
	245	250	255
ctc ttc aac tac agc atc agc agc agg ctc tcg ccc aag gtg tgg gtg			816
Leu Phe Asn Tyr Ser Ile Ser Ser Arg Leu Ser Pro Lys Val Trp Val			
	260	265	270
gcc agc gag gcc tgg ctg acc tct gac ctg gtc atg ggg ctg ccc ggc			864
Ala Ser Glu Ala Trp Leu Thr Ser Asp Leu Val Met Gly Leu Pro Gly			
	275	280	285
atg gcc cag atg ggc acg gtg ctt ggc ttc ctc cag agg ggt gcc cag			912
Met Ala Gln Met Gly Thr Val Leu Gly Phe Leu Gln Arg Gly Ala Gln			
	290	295	300
ctg cac gag ttc ccc cag tac gtg aag acg cac ctg gcc ctg gcc acc			960
Leu His Glu Phe Pro Gln Tyr Val Lys Thr His Leu Ala Leu Ala Thr			
	305	310	315
gac ccg gcc ttc tgc tct gcc ctg ggc gag agg gag cag ggt ctg gag			1008
Asp Pro Ala Phe Cys Ser Ala Leu Gly Glu Arg Glu Gln Gly Leu Glu			
	325	330	335
gag gac gtg gtg ggc cag cgc tgc ccg cag tgt gac tgc atc acg ctg			1056
Glu Asp Val Val Gly Gln Arg Cys Pro Gln Cys Asp Cys Ile Thr Leu			
	340	345	350
cag aac gtg agc gca ggg cta aat cac cac cag acg ttc tct gtc tac			1104
Gln Asn Val Ser Ala Gly Leu Asn His His Gln Thr Phe Ser Val Tyr			
	355	360	365
gca gct gtg tat agc gtg gcc cag gcc ctg cac aac act ctt cag tgc			1152
Ala Ala Val Tyr Ser Val Ala Gln Ala Leu His Asn Thr Leu Gln Cys			
	370	375	380

91/160

aac gcc tca ggc tgc ccc gcg cag gac ccc gtg aag ccc tgg cag ctc	1200
Asn Ala Ser Gly Cys Pro Ala Gln Asp Pro Val Lys Pro Trp Gln Leu	
385 390 395 400	
ctg gag aac atg tac aac ctg acc ttc cac gtg ggc ggg ctg ccg ctg	1248
Leu Glu Asn Met Tyr Asn Leu Thr Phe His Val Gly Gly Leu Pro Leu	
405 410 415	
cgg ttc gac agc agc gga aac gtg gac atg gag tac gac ctg aag ctg	1296
Arg Phe Asp Ser Ser Gly Asn Val Asp Met Glu Tyr Asp Leu Lys Leu	
420 425 430	
tgg gtg tgg cag ggc tca gtg ccc agg ctc cac gac gtg ggc agg ttc	1344
Trp Val Trp Gln Gly Ser Val Pro Arg Leu His Asp Val Gly Arg Phe	
435 440 445	
aac ggc agc ctc agg aca gag cgc ctg aag atc cgc tgg cac acg tct	1392
Asn Gly Ser Leu Arg Thr Glu Arg Leu Lys Ile Arg Trp His Thr Ser	
450 455 460	
gac aac cag aag ccc gtg tcc cgg tgc tgc cgg cag tgc cag gag ggc	1440
Asp Asn Gln Lys Pro Val Ser Arg Cys Ser Arg Gln Cys Gln Glu Gly	
465 470 475 480	
cag gtg cgc cgg gtc aag ggg ttc cac tcc tgc tgc tac gac tgt gtg	1488
Gln Val Arg Arg Val Lys Gly Phe His Ser Cys Cys Tyr Asp Cys Val	
485 490 495	
gac tgc gag gcg ggc agc tac cgg caa aac cca gac gac atc gcc tgc	1536
Asp Cys Glu Ala Gly Ser Tyr Arg Gln Asn Pro Asp Asp Ile Ala Cys	
500 505 510	
acc ttt tgt ggc cag gat gag tgg tcc ccg gag cga agc aca cgc tgc	1584
Thr Phe Cys Gly Gln Asp Glu Trp Ser Pro Glu Arg Ser Thr Arg Cys	
515 520 525	
ttc cgc cgc agg tct cgg ttc ctg gca tgg ggc gag ccg gct gtg ctg	1632
Phe Arg Arg Arg Ser Arg Phe Leu Ala Trp Gly Glu Pro Ala Val Leu	
530 535 540	
ctg ctg ctc ctg ctg ctg agc ctg gcg ctg ggc ctt gtg ctg gct gct	1680
Leu Leu Leu Leu Leu Leu Ser Leu Ala Leu Gly Leu Val Leu Ala Ala	
545 550 555 560	
ttg ggg ctg ttc gtt cac cat cgg gac agc cca ctg gtt cag gcc tcg	1728
Leu Gly Leu Phe Val His His Arg Asp Ser Pro Leu Val Gln Ala Ser	
565 570 575	
ggg ggg ccc ctg gcc tgc ttt ggc ctg gtg tgc ctg ggc ctg gtc tgc	1776
Gly Gly Pro Leu Ala Cys Phe Gly Leu Val Cys Leu Gly Leu Val Cys	
580 585 590	
ctc agc gtc ctc ctg ttc cct ggc cag ccc agc cct gcc cga tgc ctg	1824
Leu Ser Val Leu Leu Phe Pro Gly Gln Pro Ser Pro Ala Arg Cys Leu	
595 600 605	
gcc cag cag ccc ttg tcc cac ctc ccg ctc acg ggc tgc ctg agc aca	1872
Ala Gln Gln Pro Leu Ser His Leu Pro Leu Thr Gly Cys Leu Ser Thr	
610 615 620	

92/160

ctg ttc ctg cag gcg gcc gag atc ttc gtg gag tca gaa ctg cct ctg 1920
 Leu Phe Leu Gln Ala Ala Glu Ile Phe Val Glu Ser Glu Leu Pro Leu
 625 630 635 640

agc tgg gca gac cgg ctg agt ggc tgc ctg cgg ggg ccc tgg gcc tgg 1968
 Ser Trp Ala Asp Arg Leu Ser Gly Cys Leu Arg Gly Pro Trp Ala Trp
 645 650 655

ctg gtg gtg ctg ctg gcc atg ctg gtg gag gtc gca ctg tgc acc tgg 2016
 Leu Val Val Leu Leu Ala Met Leu Val Glu Val Ala Leu Cys Thr Trp
 660 665 670

tac ctg gtg gcc ttc ccg ccg gag gtg gtg acg gac tgg cac atg ctg 2064
 Tyr Leu Val Ala Phe Pro Pro Glu Val Val Thr Asp Trp His Met Leu
 675 680 685

ccc acg gag gcg ctg gtg cac tgc cgc aca cgc tcc tgg gtc agc ttc 2112
 Pro Thr Glu Ala Leu Val His Cys Arg Thr Arg Ser Trp Val Ser Phe
 690 695 700

ggc cta gcg cac gcc acc aat gcc acg ctg gcc ttt ctc tgc ttc ctg 2160
 Gly Leu Ala His Ala Thr Asn Ala Thr Leu Ala Phe Leu Cys Phe Leu
 705 710 715 720

ggc act ttc ctg gtg cgg agc cag ccg ggc tgc tac aac cgt gcc cgt 2208
 Gly Thr Phe Leu Val Arg Ser Gln Pro Gly Cys Tyr Asn Arg Ala Arg
 725 730 735

ggc ctc acc ttt gcc atg ctg gcc tac ttc atc acc tgg gtc tcc ttt 2256
 Gly Leu Thr Phe Ala Met Leu Ala Tyr Phe Ile Thr Trp Val Ser Phe
 740 745 750

gtg ccc ctc ctg gcc aat gtg cag gtg gtc ctc agg ccc gcc gtg cag 2304
 Val Pro Leu Leu Ala Asn Val Gln Val Val Leu Arg Pro Ala Val Gln
 755 760 765

atg ggc gcc ctc ctg ctc tgt gtc ctg ggc atc ctg gct gcc ttc cac 2352
 Met Gly Ala Leu Leu Leu Cys Val Leu Gly Ile Leu Ala Ala Phe His
 770 775 780

ctg ccc agg tgt tac ctg ctc atg cgg cag cca ggg ctc aac acc ccc 2400
 Leu Pro Arg Cys Tyr Leu Leu Met Arg Gln Pro Gly Leu Asn Thr Pro
 785 790 795 800

gag ttc ttc ctg gga 2415
 Glu Phe Phe Leu Gly
 805

<210> 72

<211> 805

<212> PRT

<213> Homo sapiens

<400> 72

Gly Asp Tyr Val Leu Gly Gly Leu Phe Pro Leu Gly Glu Ala Glu Glu
 1 5 10 15
 Ala Gly Leu Arg Ser Arg Thr Arg Pro Ser Ser Pro Val Cys Thr Arg
 20 25 30
 Phe Ser Ser Asn Gly Leu Leu Trp Ala Leu Ala Met Lys Met Ala Val
 35 40 45

93/160

Glu Glu Ile Asn Asn Lys Ser Asp Leu Leu Pro Gly Leu Arg Leu Gly
 50 55 60
 Tyr Asp Leu Phe Asp Thr Cys Ser Glu Pro Val Val Ala Met Lys Pro
 65 70 75 80
 Ser Leu Met Phe Leu Ala Lys Ala Gly Ser Arg Asp Ile Ala Ala Tyr
 85 90 95
 Cys Asn Tyr Thr Gln Tyr Gln Pro Arg Val Leu Ala Val Ile Gly Pro
 100 105 110
 His Ser Ser Glu Leu Ala Met Val Thr Gly Lys Phe Phe Ser Phe Phe
 115 120 125
 Leu Met Pro Gln Cys Leu Leu Ala Leu Gln Val Ser Tyr Gly Ala Ser
 130 135 140
 Met Glu Leu Leu Ser Ala Arg Glu Thr Phe Pro Ser Phe Phe Arg Thr
 145 150 155 160
 Val Pro Ser Asp Arg Val Gln Leu Thr Ala Ala Ala Glu Leu Leu Gln
 165 170 175
 Glu Phe Gly Trp Asn Trp Val Ala Ala Leu Gly Ser Asp Asp Glu Tyr
 180 185 190
 Gly Arg Gln Gly Leu Ser Ile Phe Ser Ala Leu Ala Ala Arg Gly
 195 200 205
 Ile Cys Ile Ala His Glu Gly Leu Val Pro Leu Pro Arg Ala Asp Asp
 210 215 220
 Ser Arg Leu Gly Lys Val Gln Asp Val Leu His Gln Val Asn Gln Ser
 225 230 235 240
 Ser Val Gln Val Val Leu Leu Phe Ala Ser Val His Ala Ala His Ala
 245 250 255
 Leu Phe Asn Tyr Ser Ile Ser Ser Arg Leu Ser Pro Lys Val Trp Val
 260 265 270
 Ala Ser Glu Ala Trp Leu Thr Ser Asp Leu Val Met Gly Leu Pro Gly
 275 280 285
 Met Ala Gln Met Gly Thr Val Leu Gly Phe Leu Gln Arg Gly Ala Gln
 290 295 300
 Leu His Glu Phe Pro Gln Tyr Val Lys Thr His Leu Ala Leu Ala Thr
 305 310 315 320
 Asp Pro Ala Phe Cys Ser Ala Leu Gly Glu Arg Glu Gln Gly Leu Glu
 325 330 335
 Glu Asp Val Val Gly Gln Arg Cys Pro Gln Cys Asp Cys Ile Thr Leu
 340 345 350
 Gln Asn Val Ser Ala Gly Leu Asn His His Gln Thr Phe Ser Val Tyr
 355 360 365

 Ala Ala Val Tyr Ser Val Ala Gln Ala Leu His Asn Thr Leu Gln Cys
 370 375 380
 Asn Ala Ser Gly Cys Pro Ala Gln Asp Pro Val Lys Pro Trp Gln Leu
 385 390 395 400
 Leu Glu Asn Met Tyr Asn Leu Thr Phe His Val Gly Gly Leu Pro Leu
 405 410 415
 Arg Phe Asp Ser Ser Gly Asn Val Asp Met Glu Tyr Asp Leu Lys Leu
 420 425 430
 Trp Val Trp Gln Gly Ser Val Pro Arg Leu His Asp Val Gly Arg Phe
 435 440 445
 Asn Gly Ser Leu Arg Thr Glu Arg Leu Lys Ile Arg Trp His Thr Ser
 450 455 460
 Asp Asn Gln Lys Pro Val Ser Arg Cys Ser Arg Gln Cys Gln Glu Gly
 465 470 475 480
 Gln Val Arg Arg Val Lys Gly Phe His Ser Cys Cys Tyr Asp Cys Val
 485 490 495
 Asp Cys Glu Ala Gly Ser Tyr Arg Gln Asn Pro Asp Asp Ile Ala Cys
 500 505 510
 Thr Phe Cys Gly Gln Asp Glu Trp Ser Pro Glu Arg Ser Thr Arg Cys
 515 520 525
 Phe Arg Arg Arg Ser Arg Phe Leu Ala Trp Gly Glu Pro Ala Val Leu
 530 535 540

94/160

Leu Leu Leu Leu Leu Leu Ser Leu Ala Leu Gly Leu Val Leu Ala Ala
 545 550 555 560
 Leu Gly Leu Phe Val His His Arg Asp Ser Pro Leu Val Gln Ala Ser
 565 570 575
 Gly Gly Pro Leu Ala Cys Phe Gly Leu Val Cys Leu Gly Leu Val Cys
 580 585 590
 Leu Ser Val Leu Leu Phe Pro Gly Gln Pro Ser Pro Ala Arg Cys Leu
 595 600 605
 Ala Gln Gln Pro Leu Ser His Leu Pro Leu Thr Gly Cys Leu Ser Thr
 610 615 620
 Leu Phe Leu Gln Ala Ala Glu Ile Phe Val Glu Ser Glu Leu Pro Leu
 625 630 635 640
 Ser Trp Ala Asp Arg Leu Ser Gly Cys Leu Arg Gly Pro Trp Ala Trp
 645 650 655
 Leu Val Val Leu Leu Ala Met Leu Val Glu Val Ala Leu Cys Thr Trp
 660 665 670
 Tyr Leu Val Ala Phe Pro Pro Glu Val Val Thr Asp Trp His Met Leu
 675 680 685
 Pro Thr Glu Ala Leu Val His Cys Arg Thr Arg Ser Trp Val Ser Phe
 690 695 700
 Gly Leu Ala His Ala Thr Asn Ala Thr Leu Ala Phe Leu Cys Phe Leu
 705 710 715 720
 Gly Thr Phe Leu Val Arg Ser Gln Pro Gly Cys Tyr Asn Arg Ala Arg
 725 730 735
 Gly Leu Thr Phe Ala Met Leu Ala Tyr Phe Ile Thr Trp Val Ser Phe
 740 745 750
 Val Pro Leu Leu Ala Asn Val Gln Val Val Leu Arg Pro Ala Val Gln
 755 760 765
 Met Gly Ala Leu Leu Leu Cys Val Leu Gly Ile Leu Ala Ala Phe His
 770 775 780
 Leu Pro Arg Cys Tyr Leu Leu Met Arg Gln Pro Gly Leu Asn Thr Pro
 785 790 795 800
 Glu Phe Phe Leu Gly
 805

<210> 73

<211> 1857

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1857)

<400> 73

gcc ttg gcg ctg ctg cag cgc tct agc ggc gct gcg gcc gcc tcg gcc	48
Ala Leu Ala Leu Leu Gln Arg Ser Ser Gly Ala Ala Ala Ala Ser Ala	
1 5 10 15	
aag gag ctg gca tgc caa gag atc acc gtg ccg ctg tgt aag ggc atc	96
Lys Glu Leu Ala Cys Gln Glu Ile Thr Val Pro Leu Cys Lys Gly Ile	
20 25 30	
ggc tac aac tac acc tac atg ccc aat cag ttc aac cac gac acg caa	144
Gly Tyr Asn Tyr Thr Tyr Met Pro Asn Gln Phe Asn His Asp Thr Gln	
35 40 45	
gac gag gcg ggc ctg gag gtg cac cag ttc tgg ccg ctg gtg gag atc	192
Asp Glu Ala Gly Leu Glu Val His Gln Phe Trp Pro Leu Val Glu Ile	
50 55 60	
cag tgc tcg ccc gat ctc aag ttc ttc ctg tgc agc atg tac acg ccc	240

95/160

Gln 65	Cys	Ser	Pro	Asp	Leu 70	Lys	Phe	Phe	Leu	Cys 75	Ser	Met	Tyr	Thr	Pro 80	
atc	tgc	cta	gag	gac	tac	aag	aag	ccg	ctg	ccg	ccc	tgc	cgc	tcg	gtg	288
Ile	Cys	Leu	Glu	Asp	Tyr	Lys	Lys	Pro	Leu	Pro	Pro	Cys	Arg	Ser	Val	
				85					90					95		
tgc	gag	cgc	gcc	aag	gcc	ggc	tgc	gcg	ccg	ctc	atg	cgc	cag	tac	ggc	336
Cys	Glu	Arg	Ala	Lys	Ala	Gly	Cys	Ala	Pro	Leu	Met	Arg	Gln	Tyr	Gly	
			100					105					110			
ttc	gcc	tgg	ccc	gac	cgc	atg	cgc	tgc	gac	cgg	ctg	ccc	gag	caa	ggc	384
Phe	Ala	Trp	Pro	Asp	Arg	Met	Arg	Cys	Asp	Arg	Leu	Pro	Glu	Gln	Gly	
		115					120					125				
aac	cct	gac	acg	ctg	tgc	atg	gac	tac	aac	cgc	acc	gac	cta	acc	acc	432
Asn	Pro	Asp	Thr	Leu	Cys	Met	Asp	Tyr	Asn	Arg	Thr	Asp	Leu	Thr	Thr	
	130					135					140					
gcc	gcg	ccc	agc	ccg	ccg	cgc	cgc	ctg	ccg	ccg	ccg	ccg	ccc	ggc	gag	480
Ala	Ala	Pro	Ser	Pro	Pro	Arg	Arg	Leu	Pro	Pro	Pro	Pro	Pro	Gly	Glu	
145					150				155					160		
cag	ccg	cct	tcg	ggc	agc	ggc	cac	ggc	cgc	ccg	ccg	ggg	gcc	agg	ccc	528
Gln	Pro	Pro	Ser	Gly	Ser	Gly	His	Gly	Arg	Pro	Pro	Gly	Ala	Arg	Pro	
				165				170						175		
ccg	cac	cgc	ggc	ggc	ggc	agg	ggc	ggt	ggc	ggc	ggg	gac	gcg	gcg	gcg	576
Pro	His	Arg	Gly	Gly	Gly	Arg	Gly	Gly	Gly	Gly	Gly	Asp	Ala	Ala	Ala	
			180					185					190			
ccc	cca	gct	cgc	ggc	ggc	ggc	ggt	ggc	ggg	aag	gcg	cgg	ccc	cct	ggc	624
Pro	Pro	Ala	Arg	Gly	Gly	Gly	Gly	Gly	Gly	Lys	Ala	Arg	Pro	Pro	Gly	
		195					200					205				
ggc	ggc	gcg	gct	ccc	tgc	gag	ccc	ggg	tgc	cag	tgc	cgc	gcg	cct	atg	672
Gly	Gly	Ala	Ala	Pro	Cys	Glu	Pro	Gly	Cys	Gln	Cys	Arg	Ala	Pro	Met	
	210					215					220					
gtg	agc	gtg	tcc	agc	gag	cgc	cac	ccg	ctc	tac	aac	cgc	gtc	aag	aca	720
Val	Ser	Val	Ser	Ser	Glu	Arg	His	Pro	Leu	Tyr	Asn	Arg	Val	Lys	Thr	
225					230					235				240		
ggc	cag	atc	gct	aac	tgc	gcg	ctg	ccc	tgc	cac	aac	ccc	ttt	ttc	agc	768
Gly	Gln	Ile	Ala	Asn	Cys	Ala	Leu	Pro	Cys	His	Asn	Pro	Phe	Phe	Ser	
				245				250						255		
cag	gac	gag	cgc	gcc	ttc	acc	gtc	ttc	tgg	atc	ggc	ctg	tgg	tcg	gtg	816
Gln	Asp	Glu	Arg	Ala	Phe	Thr	Val	Phe	Trp	Ile	Gly	Leu	Trp	Ser	Val	
				260				265					270			
ctc	tgc	ttc	gtg	tcc	acc	ttc	gcc	acc	gtc	tcc	acc	ttc	ctt	atc	gac	864
Leu	Cys	Phe	Val	Ser	Thr	Phe	Ala	Thr	Val	Ser	Thr	Phe	Leu	Ile	Asp	
		275					280					285				
atg	gag	cgc	ttc	aag	tac	ccg	gag	cgg	ccc	att	atc	ttc	ctc	tcg	gcc	912
Met	Glu	Arg	Phe	Lys	Tyr	Pro	Glu	Arg	Pro	Ile	Ile	Phe	Leu	Ser	Ala	
	290					295					300					
tgc	tac	ctc	ttc	gtg	tcg	gtg	ggc	tac	cta	gtg	cgc	ctg	gtg	gcg	ggc	960
Cys	Tyr	Leu	Phe	Val	Ser	Val	Gly	Tyr	Leu	Val	Arg	Leu	Val	Ala	Gly	
305					310					315					320	

96/160

cac gag aag gtg gcg tgc agc ggt ggc gcg ccg ggc gcg ggg ggc gct	1008
His Glu Lys Val Ala Cys Ser Gly Gly Ala Pro Gly Ala Gly Gly Ala	
325 330 335	
ggg ggc gcg ggc ggc gcg gcg gcg ggc gcg ggc gcg gcg ggc gcg ggc	1056
Gly Gly Ala Gly Gly Ala Ala Ala Gly Ala Gly Ala Ala Gly Ala Gly	
340 345 350	
gcg ggc ggc ccg ggc ggg cgc ggc gag tac gag gag ctg ggc gcg gtg	1104
Ala Gly Gly Pro Gly Gly Arg Gly Glu Tyr Glu Glu Leu Gly Ala Val	
355 360 365	
gag cag cac gtg cgc tac gag acc acc ggc ccc gcg ctg tgc acc gtg	1152
Glu Gln His Val Arg Tyr Glu Thr Thr Gly Pro Ala Leu Cys Thr Val	
370 375 380	
gtc ttc ttg ctg gtc tac ttc ttc ggc atg gcc agc tcc atc tgg tgg	1200
Val Phe Leu Leu Val Tyr Phe Phe Gly Met Ala Ser Ser Ile Trp Trp	
385 390 395 400	
gtg atc ttg tgc ctc aca tgg ttc ctg gcg gcc ggt atg aag tgg ggc	1248
Val Ile Leu Ser Leu Thr Trp Phe Leu Ala Ala Gly Met Lys Trp Gly	
405 410 415	
aac gaa gcc atc gcc ggc tac tgc cag tac ttc cac ctg gcc gcg tgg	1296
Asn Glu Ala Ile Ala Gly Tyr Ser Gln Tyr Phe His Leu Ala Ala Trp	
420 425 430	
ctt gtg ccc agc gtc aag tcc atc gcg gtg ctg gcg ctc agc tgc gtg	1344
Leu Val Pro Ser Val Lys Ser Ile Ala Val Leu Ala Leu Ser Ser Val	
435 440 445	
gac ggc gac ccg gtg gcg ggc atc tgc tac gtg ggc aac cag agc ctg	1392
Asp Gly Asp Pro Val Ala Gly Ile Cys Tyr Val Gly Asn Gln Ser Leu	
450 455 460	
gac aac ctg cgc ggc ttc gtg ctg gcg ccg ctg gtc atc tac ctc ttc	1440
Asp Asn Leu Arg Gly Phe Val Leu Ala Pro Leu Val Ile Tyr Leu Phe	
465 470 475 480	
atc ggc acc atg ttc ctg ctg gcc ggc ttc gtg tcc ctc ttc cgc atc	1488
Ile Gly Thr Met Phe Leu Leu Ala Gly Phe Val Ser Leu Phe Arg Ile	
485 490 495	
cgc tgc gtc atc aag caa cag gac ggc ccc acc aag acg cac aag ctg	1536
Arg Ser Val Ile Lys Gln Gln Asp Gly Pro Thr Lys Thr His Lys Leu	
500 505 510	
gag aag ctg atg atc cgc ctg ggc ctg ttc acc gtg ctc tac acc gtg	1584
Glu Lys Leu Met Ile Arg Leu Gly Leu Phe Thr Val Leu Tyr Thr Val	
515 520 525	
ccc gcc gcg gtg gtg gtc gcc tgc ctc ttc tac gag cag cac aac cgc	1632
Pro Ala Ala Val Val Val Cys Leu Phe Tyr Glu Gln His Asn Arg	
530 535 540	
ccg cgc tgg gag gcc acg cac aac tgc ccg tgc ctg cgg gac ctg cag	1680
Pro Arg Trp Glu Ala Thr His Asn Cys Pro Cys Leu Arg Asp Leu Gln	
545 550 555 560	

97/160

ccc gac cag gca cgc agg ccc gac tac gcc gtc ttc atg ctc aag tac 1728
 Pro Asp Gln Ala Arg Arg Pro Asp Tyr Ala Val Phe Met Leu Lys Tyr
 565 570 575

ttc atg tgc cta gtg gtg ggc atc acc tcg ggc gtg tgg gtc tgg tcc 1776
 Phe Met Cys Leu Val Val Gly Ile Thr Ser Gly Val Trp Val Trp Ser
 580 585 590

ggc aag acg ctg gag tcc tgg cgc tcc ctg tgc acc cgc tgc tgc tgg 1824
 Gly Lys Thr Leu Glu Ser Trp Arg Ser Leu Cys Thr Arg Cys Cys Trp
 595 600 605

gcc agc aag ggc gcc gcg gtg ggc ggg ggc gcg 1857
 Ala Ser Lys Gly Ala Ala Val Gly Gly Gly Ala
 610 615

<210> 74

<211> 619

<212> PRT

<213> Homo sapiens

<400> 74

Ala Leu Ala Leu Leu Gln Arg Ser Ser Gly Ala Ala Ala Ala Ser Ala
 1 5 10 15
 Lys Glu Leu Ala Cys Gln Glu Ile Thr Val Pro Leu Cys Lys Gly Ile
 20 25 30
 Gly Tyr Asn Tyr Thr Tyr Met Pro Asn Gln Phe Asn His Asp Thr Gln
 35 40 45
 Asp Glu Ala Gly Leu Glu Val His Gln Phe Trp Pro Leu Val Glu Ile
 50 55 60
 Gln Cys Ser Pro Asp Leu Lys Phe Phe Leu Cys Ser Met Tyr Thr Pro
 65 70 75 80
 Ile Cys Leu Glu Asp Tyr Lys Lys Pro Leu Pro Pro Cys Arg Ser Val
 85 90 95
 Cys Glu Arg Ala Lys Ala Gly Cys Ala Pro Leu Met Arg Gln Tyr Gly
 100 105 110

Phe Ala Trp Pro Asp Arg Met Arg Cys Asp Arg Leu Pro Glu Gln Gly
 115 120 125
 Asn Pro Asp Thr Leu Cys Met Asp Tyr Asn Arg Thr Asp Leu Thr Thr
 130 135 140
 Ala Ala Pro Ser Pro Pro Arg Arg Leu Pro Pro Pro Pro Gly Glu
 145 150 155 160
 Gln Pro Pro Ser Gly Ser Gly His Gly Arg Pro Pro Gly Ala Arg Pro
 165 170 175
 Pro His Arg Gly Gly Gly Arg Gly Gly Gly Gly Gly Asp Ala Ala Ala
 180 185 190
 Pro Pro Ala Arg Gly Gly Gly Gly Gly Gly Lys Ala Arg Pro Pro Gly
 195 200 205
 Gly Gly Ala Ala Pro Cys Glu Pro Gly Cys Gln Cys Arg Ala Pro Met
 210 215 220
 Val Ser Val Ser Ser Glu Arg His Pro Leu Tyr Asn Arg Val Lys Thr
 225 230 235 240
 Gly Gln Ile Ala Asn Cys Ala Leu Pro Cys His Asn Pro Phe Phe Ser
 245 250 255
 Gln Asp Glu Arg Ala Phe Thr Val Phe Trp Ile Gly Leu Trp Ser Val
 260 265 270
 Leu Cys Phe Val Ser Thr Phe Ala Thr Val Ser Thr Phe Leu Ile Asp
 275 280 285
 Met Glu Arg Phe Lys Tyr Pro Glu Arg Pro Ile Ile Phe Leu Ser Ala
 290 295 300
 Cys Tyr Leu Phe Val Ser Val Gly Tyr Leu Val Arg Leu Val Ala Gly

98/160

305					310					315					320	
His	Glu	Lys	Val	Ala	Cys	Ser	Gly	Gly	Ala	Pro	Gly	Ala	Gly	Gly	Ala	
				325					330					335		
Gly	Gly	Ala	Gly	Gly	Ala	Ala	Ala	Gly	Ala	Gly	Ala	Ala	Gly	Ala	Gly	
				340					345					350		
Ala	Gly	Gly	Pro	Gly	Gly	Arg	Gly	Glu	Tyr	Glu	Glu	Leu	Gly	Ala	Val	
				355					360					365		
Glu	Gln	His	Val	Arg	Tyr	Glu	Thr	Thr	Gly	Pro	Ala	Leu	Cys	Thr	Val	
				370					375					380		
Val	Phe	Leu	Leu	Val	Tyr	Phe	Phe	Gly	Met	Ala	Ser	Ser	Ile	Trp	Trp	
385					390					395					400	
Val	Ile	Leu	Ser	Leu	Thr	Trp	Phe	Leu	Ala	Ala	Gly	Met	Lys	Trp	Gly	
				405					410					415		
Asn	Glu	Ala	Ile	Ala	Gly	Tyr	Ser	Gln	Tyr	Phe	His	Leu	Ala	Ala	Trp	
				420					425					430		
Leu	Val	Pro	Ser	Val	Lys	Ser	Ile	Ala	Val	Leu	Ala	Leu	Ser	Ser	Val	
				435					440					445		
Asp	Gly	Asp	Pro	Val	Ala	Gly	Ile	Cys	Tyr	Val	Gly	Asn	Gln	Ser	Leu	
				450					455					460		
Asp	Asn	Leu	Arg	Gly	Phe	Val	Leu	Ala	Pro	Leu	Val	Ile	Tyr	Leu	Phe	
465					470					475					480	
Ile	Gly	Thr	Met	Phe	Leu	Leu	Ala	Gly	Phe	Val	Ser	Leu	Phe	Arg	Ile	
				485					490					495		
Arg	Ser	Val	Ile	Lys	Gln	Gln	Asp	Gly	Pro	Thr	Lys	Thr	His	Lys	Leu	
				500					505					510		
Glu	Lys	Leu	Met	Ile	Arg	Leu	Gly	Leu	Phe	Thr	Val	Leu	Tyr	Thr	Val	
				515					520					525		
Pro	Ala	Ala	Val	Val	Val	Ala	Cys	Leu	Phe	Tyr	Glu	Gln	His	Asn	Arg	
				530					535					540		
Pro	Arg	Trp	Glu	Ala	Thr	His	Asn	Cys	Pro	Cys	Leu	Arg	Asp	Leu	Gln	
545					550					555					560	
Pro	Asp	Gln	Ala	Arg	Arg	Pro	Asp	Tyr	Ala	Val	Phe	Met	Leu	Lys	Tyr	
				565					570					575		
Phe	Met	Cys	Leu	Val	Val	Gly	Ile	Thr	Ser	Gly	Val	Trp	Val	Trp	Ser	
				580					585					590		
Gly	Lys	Thr	Leu	Glu	Ser	Trp	Arg	Ser	Leu	Cys	Thr	Arg	Cys	Cys	Trp	
				595					600					605		
Ala	Ser	Lys	Gly	Ala	Ala	Val	Gly	Gly	Gly	Ala						
				610					615							

```
<210> 75
<211> 966
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> CDS
<222> (1) ... (966)
```

<400> 75																
ctg	gca	agg	agc	agc	aat	cct	ttt	gag	gag	aag	agg	cac	tct	ggt	ttt	48
Leu	Ala	Arg	Ser	Ser	Asn	Pro	Phe	Glu	Glu	Lys	Arg	His	Ser	Gly	Phe	
1				5					10					15		
ttg	aat	ttt	cag	ctt	ttc	tgc	tct	ggt	ttc	tcc	cca	tct	ttg	tgc	tgt	96
Leu	Asn	Phe	Gln	Leu	Phe	Cys	Ser	Gly	Phe	Ser	Pro	Ser	Leu	Cys	Cys	
			20					25					30			
cag	aca	ggg	aca	ttt	agg	tct	gca	gaa	gtt	ttc	tat	tgc	ctt	ttg	ttc	144
Gln	Thr	Gly	Thr	Phe	Arg	Ser	Ala	Glu	Val	Phe	Tyr	Cys	Leu	Leu	Phe	
		35					40					45				

99/160

agc tgt gcc ctg ctc aca gac cag aag gag aag atg gct tta cat ttt	192
Ser Cys Ala Leu Leu Thr Asp Gln Lys Glu Lys Met Ala Leu His Phe	
50 55 60	
ctt ttc cat cag aca ctt caa ctc ata cat ttg gag ctg gaa aag atg	240
Leu Phe His Gln Thr Leu Gln Leu Ile His Leu Glu Leu Glu Lys Met	
65 70 75 80	
att tta aaa aat ctt ttc atg ccc tat tgg gat gtg tgg cat cat cag	288
Ile Leu Lys Asn Leu Phe Met Pro Tyr Trp Asp Val Trp His His Gln	
85 90 95	
ttt caa tat gca aat caa att ttg ggt aag ggt cta tac tgc ttc ttc	336
Phe Gln Tyr Ala Asn Gln Ile Leu Gly Lys Gly Leu Tyr Cys Phe Phe	
100 105 110	
agg gta ttt gtt ttc tat tcc tgt agc ttt gtg gag ctt gca gtg agc	384
Arg Val Phe Val Phe Tyr Ser Cys Ser Phe Val Glu Leu Ala Val Ser	
115 120 125	
cga gat cgt gcc act gca ctc cag cct ggg cga cag agc gag act ctg	432
Arg Asp Arg Ala Thr Ala Leu Gln Pro Gly Arg Gln Ser Glu Thr Leu	
130 135 140	
tct caa aaa aaa aaa aaa aga aat gca act gat ttt tgc atg ttg tct	480
Ser Gln Lys Lys Lys Lys Arg Asn Ala Thr Asp Phe Cys Met Leu Ser	
145 150 155 160	
ttg tgt att gaa gga aca tac ctc caa ata ata aga gcc att tgt tgc	528
Leu Cys Ile Glu Gly Thr Tyr Leu Gln Ile Ile Arg Ala Ile Cys Cys	
165 170 175	
aaa ccc aca gcc act ggc cca gtc cct ttc act cag tgt gtc acc aaa	576
Lys Pro Thr Ala Thr Gly Pro Val Pro Phe Thr Gln Cys Val Thr Lys	
180 185 190	
ggc agc ttc aag gct caa tgg caa gag acc acc tat aac ctc ttc acc	624
Gly Ser Phe Lys Ala Gln Trp Gln Glu Thr Thr Tyr Asn Leu Phe Thr	
195 200 205	
ttc tgc tgc ctc ttt ctg ctg cca ctg act gcc atg gtc atc tgc tat	672
Phe Cys Cys Leu Phe Leu Leu Pro Leu Thr Ala Met Val Ile Cys Tyr	
210 215 220	
agc cgc att gtc ctc agt gtt ata ttt tct aaa ttc cta gcc cct gct	720
Ser Arg Ile Val Leu Ser Val Ile Phe Ser Lys Phe Leu Ala Pro Ala	
225 230 235 240	
ggg gaa ttt gcc ctc ccc cgc tcc ttt gac aat tgt ccc cgt gtt cgt	768
Gly Glu Phe Ala Leu Pro Arg Ser Phe Asp Asn Cys Pro Arg Val Arg	
245 250 255	
ctc cgg gcc ctg aga ctg gcc ctg ctt atc ttg ctg acc ttc atc ctc	816
Leu Arg Ala Leu Arg Leu Ala Leu Leu Ile Leu Leu Thr Phe Ile Leu	
260 265 270	
tgc tgg aca cct tat tac cta ctg ggt atg tgg tac tgg ttc tcc ccc	864
Cys Trp Thr Pro Tyr Tyr Leu Leu Gly Met Trp Tyr Trp Phe Ser Pro	
275 280 285	
acc atg cta act gaa gtc cct ccc agc ctg agc cac atc ctt ttc ctc	912
Thr Met Leu Thr Glu Val Pro Pro Ser Leu Ser His Ile Leu Phe Leu	
290 295 300	

100/160

ttg ggc ctc ctc aat gct cct ttg gat cct ctc ctc tat ggg gcc ttc 960
 Leu Gly Leu Leu Asn Ala Pro Leu Asp Pro Leu Leu Tyr Gly Ala Phe
 305 310 315 320

acc ctt 966
 Thr Leu

<210> 76
 <211> 322
 <212> PRT
 <213> Homo sapiens

<400> 76
 Leu Ala Arg Ser Ser Asn Pro Phe Glu Glu Lys Arg His Ser Gly Phe
 1 5 10 15
 Leu Asn Phe Gln Leu Phe Cys Ser Gly Phe Ser Pro Ser Leu Cys Cys
 20 25 30
 Gln Thr Gly Thr Phe Arg Ser Ala Glu Val Phe Tyr Cys Leu Leu Phe
 35 40 45
 Ser Cys Ala Leu Leu Thr Asp Gln Lys Glu Lys Met Ala Leu His Phe
 50 55 60
 Leu Phe His Gln Thr Leu Gln Leu Ile His Leu Glu Leu Glu Lys Met
 65 70 75 80
 Ile Leu Lys Asn Leu Phe Met Pro Tyr Trp Asp Val Trp His His Gln
 85 90 95
 Phe Gln Tyr Ala Asn Gln Ile Leu Gly Lys Gly Leu Tyr Cys Phe Phe
 100 105 110
 Arg Val Phe Val Phe Tyr Ser Cys Ser Phe Val Glu Leu Ala Val Ser
 115 120 125
 Arg Asp Arg Ala Thr Ala Leu Gln Pro Gly Arg Gln Ser Glu Thr Leu
 130 135 140
 Ser Gln Lys Lys Lys Lys Arg Asn Ala Thr Asp Phe Cys Met Leu Ser
 145 150 155 160
 Leu Cys Ile Glu Gly Thr Tyr Leu Gln Ile Ile Arg Ala Ile Cys Cys
 165 170 175
 Lys Pro Thr Ala Thr Gly Pro Val Pro Phe Thr Gln Cys Val Thr Lys
 180 185 190
 Gly Ser Phe Lys Ala Gln Trp Gln Glu Thr Thr Tyr Asn Leu Phe Thr
 195 200 205
 Phe Cys Cys Leu Phe Leu Leu Pro Leu Thr Ala Met Val Ile Cys Tyr
 210 215 220
 Ser Arg Ile Val Leu Ser Val Ile Phe Ser Lys Phe Leu Ala Pro Ala
 225 230 235 240
 Gly Glu Phe Ala Leu Pro Arg Ser Phe Asp Asn Cys Pro Arg Val Arg
 245 250 255
 Leu Arg Ala Leu Arg Leu Ala Leu Leu Ile Leu Leu Thr Phe Ile Leu
 260 265 270
 Cys Trp Thr Pro Tyr Tyr Leu Leu Gly Met Trp Tyr Trp Phe Ser Pro
 275 280 285
 Thr Met Leu Thr Glu Val Pro Pro Ser Leu Ser His Ile Leu Phe Leu
 290 295 300
 Leu Gly Leu Leu Asn Ala Pro Leu Asp Pro Leu Leu Tyr Gly Ala Phe
 305 310 315 320
 Thr Leu

<210> 77
 <211> 1212

101/160

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1212)

<400> 77

ctg ggc gca gtg act acg cct gta atc cca gca ctt ggg gac gcc gag	48
Leu Gly Ala Val Thr Thr Pro Val Ile Pro Ala Leu Gly Asp Ala Glu	
1 5 10 15	
gca ggc agg tca tct gag gtc atc gtc ctg cat tac aac tac acc ggc	96
Ala Gly Arg Ser Ser Glu Val Ile Val Leu His Tyr Asn Tyr Thr Gly	
20 25 30	
aag ctc cgc ggt gcg cgc tac cag ccg ggt gcc ggc ctg cgc gcc gac	144
Lys Leu Arg Gly Ala Arg Tyr Gln Pro Gly Ala Gly Leu Arg Ala Asp	
35 40 45	
gcc gtg gtg tgc ctg gcg gtg tgc gcc ttc atc gtg cta gag aat cta	192
Ala Val Val Cys Leu Ala Val Cys Ala Phe Ile Val Leu Glu Asn Leu	
50 55 60	
gcc gtg ttg ttg gtg ctc gga cgc cac ccg cgc ttc cac gct ccc atg	240
Ala Val Leu Leu Val Leu Gly Arg His Pro Arg Phe His Ala Pro Met	
65 70 75 80	
ttc ctg ctc ctg ggc agc ctc acg ttg tcg gat ctg ctg gca ggc gcc	288
Phe Leu Leu Leu Gly Ser Leu Thr Leu Ser Asp Leu Leu Ala Gly Ala	
85 90 95	
gcc tac gcc gcc aac atc cta ctg tcg ggg ccg ctc acg ctg aaa ctg	336
Ala Tyr Ala Ala Asn Ile Leu Leu Ser Gly Pro Leu Thr Leu Lys Leu	
100 105 110	
tcc ccc gcg ctc tgg ttc gca cgg gag gga ggc gtc ttc gtg gca ctc	384
Ser Pro Ala Leu Trp Phe Ala Arg Glu Gly Gly Val Phe Val Ala Leu	
115 120 125	
act gcg tcc gtg ctg agc ctc ctg gcc atc gcg ctg gag cgc agc ctc	432
Thr Ala Ser Val Leu Ser Leu Leu Ala Ile Ala Leu Glu Arg Ser Leu	
130 135 140	
acc atg gcg cgc agg ggg ccc gcg ccc gtc tcc agt cgg ggg cgc acg	480
Thr Met Ala Arg Arg Gly Pro Ala Pro Val Ser Ser Arg Gly Arg Thr	
145 150 155 160	
ctg gcg atg gca gcc gcg gcc tgg ggc gtg tcg ctg ctc ctc ggg ctc	528
Leu Ala Met Ala Ala Ala Ala Trp Gly Val Ser Leu Leu Leu Gly Leu	
165 170 175	
ctg cca gcg ctg ggc tgg aat tgc ctg ggt cgc ctg gac gct tgc tcc	576
Leu Pro Ala Leu Gly Trp Asn Cys Leu Gly Arg Leu Asp Ala Cys Ser	
180 185 190	
act gtc ttg ccg ctc tac gcc aag gcc tac gtg ctc ttc tgc gtg ctc	624
Thr Val Leu Pro Leu Tyr Ala Lys Ala Tyr Val Leu Phe Cys Val Leu	
195 200 205	
gcc ttc gtg ggc atc ctg gcc gct atc tgt gca ctc tac gcg cgc atc	672

102/160

Ala Phe Val Gly Ile Leu Ala Ala Ile Cys Ala Leu Tyr Ala Arg Ile	
210 215 220	
tac tgc cag gta cgc gcc aac gcg cgg cgc ctg ccg gca cgg ccc ggg	720
Tyr Cys Gln Val Arg Ala Asn Ala Arg Arg Leu Pro Ala Arg Pro Gly	
225 230 235 240	
act gcg ggg acc acc tcg acc cgg gcg cgt cgc aag ccg cgc tcg ctg	768
Thr Ala Gly Thr Thr Ser Thr Arg Ala Arg Arg Lys Pro Arg Ser Leu	
245 250 255	
gcc ttg ctg cgc acg ctc agc gtg gtg ctc ctg gcc ttt gtg gca tgt	816
Ala Leu Leu Arg Thr Leu Ser Val Val Leu Leu Ala Phe Val Ala Cys	
260 265 270	
tgg ggc ccc ctc ttc ctg ctg ctg ttg ctc gac gtg gcg tgc ccg gcg	864
Trp Gly Pro Leu Phe Leu Leu Leu Leu Leu Asp Val Ala Cys Pro Ala	
275 280 285	
cgc acc tgt cct gta ctc ctg cag gcc gat ccc ttc ctg gga ctg gcc	912
Arg Thr Cys Pro Val Leu Leu Gln Ala Asp Pro Phe Leu Gly Leu Ala	
290 295 300	
atg gcc aac tca ctt ctg aac ccc atc atc tac acg ctc acc aac cgc	960
Met Ala Asn Ser Leu Leu Asn Pro Ile Ile Tyr Thr Leu Thr Asn Arg	
305 310 315 320	
gac ctg cgc cac gcg ctc ctg cgc ctg gtc tgc tgc gga cgc cac tcc	1008
Asp Leu Arg His Ala Leu Leu Arg Leu Val Cys Cys Gly Arg His Ser	
325 330 335	
tgc ggc aga gac ccg agt ggc tcc cag cag tcg gcg agc gcg gct gag	1056
Cys Gly Arg Asp Pro Ser Gly Ser Gln Gln Ser Ala Ser Ala Ala Glu	
340 345 350	
gct tcc ggg ggc ctg cgc cgc tgc ctg ccc ccg ggc ctt gat ggg agc	1104
Ala Ser Gly Gly Leu Arg Arg Cys Leu Pro Pro Gly Leu Asp Gly Ser	
355 360 365	
ttc agc ggc tcg gag cgc tca tcg ccc cag cgc gac ggg ctg gac acc	1152
Phe Ser Gly Ser Glu Arg Ser Ser Pro Gln Arg Asp Gly Leu Asp Thr	
370 375 380	
agc ggc tcc aca ggc agc ccc gcc tgt gtg atg aaa tca tgt ctt tta	1200
Ser Gly Ser Thr Gly Ser Pro Ala Cys Val Met Lys Ser Cys Leu Leu	
385 390 395 400	
gga aaa cat aag	1212
Gly Lys His Lys	

<210> 78

<211> 404

<212> PRT

<213> Homo sapiens

<400> 78

Leu Gly Ala Val Thr Thr Pro Val Ile Pro Ala Leu Gly Asp Ala Glu

1

5

10

15

Ala Gly Arg Ser Ser Glu Val Ile Val Leu His Tyr Asn Tyr Thr Gly

104/160

Ser 1	Pro	Gln	Ala	Pro 5	Gly	Thr	Trp	Ala	Ala 10	Ala	Trp	Val	Pro	Leu 15	Pro		
acg	ggt	gat	ggt	cca	gac	cat	gcc	cac	tat	acc	ctg	ggc	aca	gtg	atc		96
Thr	Val	Asp	Val	Pro	Asp	His	Ala	His	Tyr	Thr	Leu	Gly	Thr	Val	Ile		
			20				25						30				
ttg	ctg	gtg	gga	ctc	acg	ggg	atg	ctg	ggc	aac	ctg	acg	gtc	atc	tat		144
Leu	Leu	Val	Gly	Leu	Thr	Gly	Met	Leu	Gly	Asn	Leu	Thr	Val	Ile	Tyr		
		35					40					45					
acc	ttc	tgc	agg	agc	aga	agc	ctc	cgg	aca	cct	gcc	aac	atg	ttc	att		192
Thr	Phe	Cys	Arg	Ser	Arg	Ser	Leu	Arg	Thr	Pro	Ala	Asn	Met	Phe	Ile		
	50					55					60						
atc	aac	ctc	gcg	gtc	agc	gac	ttc	ctc	atg	tcc	ttc	acc	cag	gcc	cct		240
Ile	Asn	Leu	Ala	Val	Ser	Asp	Phe	Leu	Met	Ser	Phe	Thr	Gln	Ala	Pro		
	65					70				75					80		
gtc	ttc	ttc	acc	agt	agc	ctc	tat	aag	cag	tgg	ctc	ttt	ggg	gag	aca		288
Val	Phe	Phe	Thr	Ser	Ser	Leu	Tyr	Lys	Gln	Trp	Leu	Phe	Gly	Glu	Thr		
				85					90					95			
ggc	tgc	gag	ttc	tat	gcc	ttc	tgt	gga	gct	ctc	ttt	ggc	att	tcc	tcc		336
Gly	Cys	Glu	Phe	Tyr	Ala	Phe	Cys	Gly	Ala	Leu	Phe	Gly	Ile	Ser	Ser		
			100					105					110				
atg	atc	acc	ctg	acg	gcc	atc	gcc	ctg	gac	cgc	tac	ctg	gta	atc	aca		384
Met	Ile	Thr	Leu	Thr	Ala	Ile	Ala	Leu	Asp	Arg	Tyr	Leu	Val	Ile	Thr		
		115					120					125					
cgc	ccg	ctg	gcc	acc	ttt	ggt	gtg	gcg	tcc	aag	agg	cgt	gcg	gca	ttt		432
Arg	Pro	Leu	Ala	Thr	Phe	Gly	Val	Ala	Ser	Lys	Arg	Arg	Ala	Ala	Phe		
	130					135					140						
gtc	ctg	ctg	ggc	gtt	tgg	ctc	tat	gcc	ctg	gcc	tgg	agt	ctg	cca	ccc		480
Val	Leu	Leu	Gly	Val	Trp	Leu	Tyr	Ala	Leu	Ala	Trp	Ser	Leu	Pro	Pro		
	145				150					155					160		
ttc	ttc	ggc	tgg	agc	gcc	tac	gtg	ccc	gag	ggg	ttg	ctg	aca	tcc	tgc		528
Phe	Phe	Gly	Trp	Ser	Ala	Tyr	Val	Pro	Glu	Gly	Leu	Leu	Thr	Ser	Cys		
				165					170					175			
tcc	tgg	gac	tac	atg	agc	ttc	acg	ccg	gcc	gtg	cgt	gcc	tac	acc	atg		576
Ser	Trp	Asp	Tyr	Met	Ser	Phe	Thr	Pro	Ala	Val	Arg	Ala	Tyr	Thr	Met		
			180					185					190				
ctt	ctc	tgc	tgc	ttc	gtg	ttc	ttc	ctc	cct	ctg	ctt	atc	atc	atc	tac		624
Leu	Leu	Cys	Cys	Phe	Val	Phe	Phe	Leu	Pro	Leu	Leu	Ile	Ile	Ile	Tyr		
		195					200					205					
tgc	tac	atc	ttc	atc	ttc	agg	gcc	atc	cgg	gag	aca	gga	cgg	gct	ctc		672
Cys	Tyr	Ile	Phe	Ile	Phe	Arg	Ala	Ile	Arg	Glu	Thr	Gly	Arg	Ala	Leu		
	210					215					220						
cag	acc	ttc	ggg	gcc	tgc	aag	ggc	aat	ggc	gag	tcc	ctg	tgg	cag	cgg		720
Gln	Thr	Phe	Gly	Ala	Cys	Lys	Gly	Asn	Gly	Glu	Ser	Leu	Trp	Gln	Arg		
	225				230				235						240		
cag	cgg	ctg	cag	agc	gag	tgc	aag	atg	gcc	aag	atc	atg	ctg	ctg	gtc		768
Gln	Arg	Leu	Gln	Ser	Glu	Cys	Lys	Met	Ala	Lys	Ile	Met	Leu	Leu	Val		
				245					250					255			

105/160

atc ctc ctc ttc gtg ctc tcc tgg gct ccc tat tcc gct gtg gcc ctg 816
 Ile Leu Leu Phe Val Leu Ser Trp Ala Pro Tyr Ser Ala Val Ala Leu
 260 265 270

gtg gcc ttt gct ggg tac gca cac gtc ctg aca ccc tac atg agc tcg 864
 Val Ala Phe Ala Gly Tyr Ala His Val Leu Thr Pro Tyr Met Ser Ser
 275 280 285

gtg cca gcc gtc atc gcc aag gcc tct gca atc cac aac ccc atc att 912
 Val Pro Ala Val Ile Ala Lys Ala Ser Ala Ile His Asn Pro Ile Ile
 290 295 300

tac gcc atc acc cac ccc aag tac agg tca gat gct gtg gct tcc tgg 960
 Tyr Ala Ile Thr His Pro Lys Tyr Arg Ser Asp Ala Val Ala Ser Trp
 305 310 315 320

cag tcc aga cgt ctt ggg gta cac ttg tac ccc tgg tcc ctg gtg ttc 1008
 Gln Ser Arg Arg Leu Gly Val His Leu Tyr Pro Trp Ser Leu Val Phe
 325 330 335

tgc cac cct agc gag ttt gaa aac cac aac tgg agc acc agg gat gtt 1056
 Cys His Pro Ser Glu Phe Glu Asn His Asn Trp Ser Thr Arg Asp Val
 340 345 350

gcc cca ggc cac ctg atg aca gaa atg gag act aga gtg ttg tct ata 1104
 Ala Pro Gly His Leu Met Thr Glu Met Glu Thr Arg Val Leu Ser Ile
 355 360 365

cta agc caa 1113
 Leu Ser Gln
 370

<210> 80
 <211> 371
 <212> PRT
 <213> Homo sapiens

<400> 80
 Ser Pro Gln Ala Pro Gly Thr Trp Ala Ala Ala Trp Val Pro Leu Pro
 1 5 10 15
 Thr Val Asp Val Pro Asp His Ala His Tyr Thr Leu Gly Thr Val Ile
 20 25 30
 Leu Leu Val Gly Leu Thr Gly Met Leu Gly Asn Leu Thr Val Ile Tyr
 35 40 45
 Thr Phe Cys Arg Ser Arg Ser Leu Arg Thr Pro Ala Asn Met Phe Ile
 50 55 60
 Ile Asn Leu Ala Val Ser Asp Phe Leu Met Ser Phe Thr Gln Ala Pro
 65 70 75 80
 Val Phe Phe Thr Ser Ser Leu Tyr Lys Gln Trp Leu Phe Gly Glu Thr
 85 90 95
 Gly Cys Glu Phe Tyr Ala Phe Cys Gly Ala Leu Phe Gly Ile Ser Ser
 100 105 110
 Met Ile Thr Leu Thr Ala Ile Ala Leu Asp Arg Tyr Leu Val Ile Thr
 115 120 125
 Arg Pro Leu Ala Thr Phe Gly Val Ala Ser Lys Arg Arg Ala Ala Phe
 130 135 140
 Val Leu Leu Gly Val Trp Leu Tyr Ala Leu Ala Trp Ser Leu Pro Pro
 145 150 155 160
 Phe Phe Gly Trp Ser Ala Tyr Val Pro Glu Gly Leu Leu Thr Ser Cys
 165 170 175

106/160

Ser Trp Asp Tyr Met Ser Phe Thr Pro Ala Val Arg Ala Tyr Thr Met
 180 185 190
 Leu Leu Cys Cys Phe Val Phe Phe Leu Pro Leu Leu Ile Ile Ile Tyr
 195 200 205
 Cys Tyr Ile Phe Ile Phe Arg Ala Ile Arg Glu Thr Gly Arg Ala Leu
 210 215 220
 Gln Thr Phe Gly Ala Cys Lys Gly Asn Gly Glu Ser Leu Trp Gln Arg
 225 230 235 240
 Gln Arg Leu Gln Ser Glu Cys Lys Met Ala Lys Ile Met Leu Leu Val
 245 250 255
 Ile Leu Leu Phe Val Leu Ser Trp Ala Pro Tyr Ser Ala Val Ala Leu
 260 265 270
 Val Ala Phe Ala Gly Tyr Ala His Val Leu Thr Pro Tyr Met Ser Ser
 275 280 285
 Val Pro Ala Val Ile Ala Lys Ala Ser Ala Ile His Asn Pro Ile Ile
 290 295 300
 Tyr Ala Ile Thr His Pro Lys Tyr Arg Ser Asp Ala Val Ala Ser Trp
 305 310 315 320
 Gln Ser Arg Arg Leu Gly Val His Leu Tyr Pro Trp Ser Leu Val Phe
 325 330 335
 Cys His Pro Ser Glu Phe Glu Asn His Asn Trp Ser Thr Arg Asp Val
 340 345 350
 Ala Pro Gly His Leu Met Thr Glu Met Glu Thr Arg Val Leu Ser Ile
 355 360 365
 Leu Ser Gln
 370

<210> 81

<211> 1119 -

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1119)

<400> 81

tct cta cta aaa ata caa aaa att agt cgg acg tgg tgg cgg gtg cct 48
 Ser Leu Leu Lys Ile Gln Lys Ile Ser Arg Thr Trp Trp Arg Val Pro
 1 5 10 15
 agc aca gat gtg agc tgc tta cct atg tgg gga gac ttc agg gct gtg 96
 Ser Thr Asp Val Ser Cys Leu Pro Met Trp Gly Asp Phe Arg Ala Val
 20 25 30
 agt agt gaa ctc gaa atc tta gtt tta acg att gga att ttt att ttt 144
 Ser Ser Glu Leu Glu Ile Leu Val Leu Thr Ile Gly Ile Phe Ile Phe
 35 40 45
 ttc ctt gta ggg att ctg tcc aca ttt gga aat gga tat gtc ctt tac 192
 Phe Leu Val Gly Ile Leu Ser Thr Phe Gly Asn Gly Tyr Val Leu Tyr
 50 55 60
 atg tct tct aga cga aag aag aag ctg aga ccc gct gaa ata atg act 240
 Met Ser Ser Arg Arg Lys Lys Lys Leu Arg Pro Ala Glu Ile Met Thr
 65 70 75 80
 atc aat tta gca gtc tgt gat ctg ggg att tca gtt gta ggc aag ccg 288
 Ile Asn Leu Ala Val Cys Asp Leu Gly Ile Ser Val Val Gly Lys Pro
 85 90 95
 ttc acc atc atc tct tgc ttt tgt cac cgc tgg gtg ttt ggc tgg atc 336

107/160

Phe Thr Ile Ile Ser Cys Phe Cys His Arg Trp Val Phe Gly Trp Ile	
100 105 110	
ggc tgc cgc tgg tat gga tgg gct gga ttt ttc ttt ggc tgt gga agc	384
Gly Cys Arg Trp Tyr Gly Trp Ala Gly Phe Phe Phe Gly Cys Gly Ser	
115 120 125	
ctt atc acc atg act gct gtc agc ctg gat cga tat ttg aaa atc tgc	432
Leu Ile Thr Met Thr Ala Val Ser Leu Asp Arg Tyr Leu Lys Ile Cys	
130 135 140	
tat tta tct tat ggg gtt tgg ctg aaa aga aag cac gcc tac atc tgc	480
Tyr Leu Ser Tyr Gly Val Trp Leu Lys Arg Lys His Ala Tyr Ile Cys	
145 150 155 160	
ctg gca gcc atc tgg gcc tat gct tcc ttc tgg acc acc atg ccc ttg	528
Leu Ala Ala Ile Trp Ala Tyr Ala Ser Phe Trp Thr Thr Met Pro Leu	
165 170 175	
gta ggt ctg ggg gac tac gta cct gag ccc ttc gga acc tcg tgc acc	576
Val Gly Leu Gly Asp Tyr Val Pro Glu Pro Phe Gly Thr Ser Cys Thr	
180 185 190	
ctg gac tgg tgg ctg gcc cag gcc tcg gta ggg ggc cag gtt ttc atc	624
Leu Asp Trp Trp Leu Ala Gln Ala Ser Val Gly Gly Gln Val Phe Ile	
195 200 205	
ctg aac atc ctc ttc ttc tgc ctc ttg ctc cca acg gct gtg atc gtg	672
Leu Asn Ile Leu Phe Phe Cys Leu Leu Leu Pro Thr Ala Val Ile Val	
210 215 220	
ttc tcc tac gta aag atc att gcc aag gtt aag tcc tct tcc aaa gaa	720
Phe Ser Tyr Val Lys Ile Ile Ala Lys Val Lys Ser Ser Ser Lys Glu	
225 230 235 240	
gta gct cat ttc gac agt cgg atc cat agc agc cat gtg ctg gaa atg	768
Val Ala His Phe Asp Ser Arg Ile His Ser Ser His Val Leu Glu Met	
245 250 255	
aaa ctg aca aag gta gcg atg ttg att tgt gct gga ttc ctg att gcc	816
Lys Leu Thr Lys Val Ala Met Leu Ile Cys Ala Gly Phe Leu Ile Ala	
260 265 270	
tgg att cct tat gca gtg gtg tct gtg tgg tca gct ttt gga agg cca	864
Trp Ile Pro Tyr Ala Val Val Ser Val Trp Ser Ala Phe Gly Arg Pro	
275 280 285	
gac tcc att ccc ata cag ctc tct gtg gtg cca acc cta ctt gca aaa	912
Asp Ser Ile Pro Ile Gln Leu Ser Val Val Pro Thr Leu Leu Ala Lys	
290 295 300	
tct gca gcg atg tac aat ccc atc att tac caa caa aac ttc tca ata	960
Ser Ala Ala Met Tyr Asn Pro Ile Ile Tyr Gln Gln Asn Phe Ser Ile	
305 310 315 320	
tca aat ttt cgt gat tcc cta gct cag agc tca gtc cct tgg att cag	1008
Ser Asn Phe Arg Asp Ser Leu Ala Gln Ser Ser Val Pro Trp Ile Gln	
325 330 335	
tgc tgt tat tat cct caa gag agc agg gga cag cta gaa agg gtt gta	1056
Cys Cys Tyr Tyr Pro Gln Glu Ser Arg Gly Gln Leu Glu Arg Val Val	
340 345 350	

108/160

gaa tcg aga gat ttt gtg agg atg tca gca gtt agc gca gat cta caa 1104
 Glu Ser Arg Asp Phe Val Arg Met Ser Ala Val Ser Ala Asp Leu Gln
 355 360 365

aaa ttc cag agg aat 1119
 Lys Phe Gln Arg Asn
 370

<210> 82
 <211> 373
 <212> PRT
 <213> Homo sapiens

<400> 82
 Ser Leu Leu Lys Ile Gln Lys Ile Ser Arg Thr Trp Trp Arg Val Pro
 1 5 10 15
 Ser Thr Asp Val Ser Cys Leu Pro Met Trp Gly Asp Phe Arg Ala Val
 20 25 30
 Ser Ser Glu Leu Glu Ile Leu Val Leu Thr Ile Gly Ile Phe Ile Phe
 35 40 45
 Phe Leu Val Gly Ile Leu Ser Thr Phe Gly Asn Gly Tyr Val Leu Tyr
 50 55 60
 Met Ser Ser Arg Arg Lys Lys Lys Leu Arg Pro Ala Glu Ile Met Thr
 65 70 75 80

 Ile Asn Leu Ala Val Cys Asp Leu Gly Ile Ser Val Val Gly Lys Pro
 85 90 95
 Phe Thr Ile Ile Ser Cys Phe Cys His Arg Trp Val Phe Gly Trp Ile
 100 105 110
 Gly Cys Arg Trp Tyr Gly Trp Ala Gly Phe Phe Phe Gly Cys Gly Ser
 115 120 125
 Leu Ile Thr Met Thr Ala Val Ser Leu Asp Arg Tyr Leu Lys Ile Cys
 130 135 140
 Tyr Leu Ser Tyr Gly Val Trp Leu Lys Arg Lys His Ala Tyr Ile Cys
 145 150 155 160
 Leu Ala Ala Ile Trp Ala Tyr Ala Ser Phe Trp Thr Thr Met Pro Leu
 165 170 175
 Val Gly Leu Gly Asp Tyr Val Pro Glu Pro Phe Gly Thr Ser Cys Thr
 180 185 190
 Leu Asp Trp Trp Leu Ala Gln Ala Ser Val Gly Gly Gln Val Phe Ile
 195 200 205
 Leu Asn Ile Leu Phe Phe Cys Leu Leu Leu Pro Thr Ala Val Ile Val
 210 215 220
 Phe Ser Tyr Val Lys Ile Ile Ala Lys Val Lys Ser Ser Ser Lys Glu
 225 230 235 240
 Val Ala His Phe Asp Ser Arg Ile His Ser Ser His Val Leu Glu Met
 245 250 255
 Lys Leu Thr Lys Val Ala Met Leu Ile Cys Ala Gly Phe Leu Ile Ala
 260 265 270
 Trp Ile Pro Tyr Ala Val Val Ser Val Trp Ser Ala Phe Gly Arg Pro
 275 280 285
 Asp Ser Ile Pro Ile Gln Leu Ser Val Val Pro Thr Leu Leu Ala Lys
 290 295 300
 Ser Ala Ala Met Tyr Asn Pro Ile Ile Tyr Gln Gln Asn Phe Ser Ile
 305 310 315 320
 Ser Asn Phe Arg Asp Ser Leu Ala Gln Ser Ser Val Pro Trp Ile Gln
 325 330 335
 Cys Cys Tyr Tyr Pro Gln Glu Ser Arg Gly Gln Leu Glu Arg Val Val
 340 345 350
 Glu Ser Arg Asp Phe Val Arg Met Ser Ala Val Ser Ala Asp Leu Gln
 355 360 365

109/160

Lys Phe Gln Arg Asn
370

<210> 83

<211> 1533

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (1533)

<400> 83

atg agt gtt gtt ctg cag gat act cag acg tta aca ata gac tca aac 48
Met Ser Val Val Leu Gln Asp Thr Gln Thr Leu Thr Ile Asp Ser Asn
1 5 10 15

att aac agc ctg ctc ata gtt gcc ctg ctg gta act ggg att aca ggc 96
Ile Asn Ser Leu Leu Ile Val Ala Leu Leu Val Thr Gly Ile Thr Gly
20 25 30

atg cac cac cac gcc cgg cta att tta aaa tta ttt gta agt aaa agt 144
Met His His His Ala Arg Leu Ile Leu Lys Leu Phe Val Ser Lys Ser
35 40 45

agc ata aac ttt gct gat ttc atc tct cag agc tcc tct gcc agt ccc 192
Ser Ile Asn Phe Ala Asp Phe Ile Ser Gln Ser Ser Ser Ala Ser Pro
50 55 60

gga ggt gtt gat tac att ttg cat ggc agt aca gtc acc ttt cag cat 240
Gly Gly Val Asp Tyr Ile Leu His Gly Ser Thr Val Thr Phe Gln His
65 70 75 80

ggg caa aac tta agt ttt ata aat atc tcc atc att gat gac aat gaa 288
Gly Gln Asn Leu Ser Phe Ile Asn Ile Ser Ile Ile Asp Asp Asn Glu
85 90 95

agt gaa ttt gag gag ccc att gaa att cta ctc act gga gct act gga 336
Ser Glu Phe Glu Glu Pro Ile Glu Ile Leu Leu Thr Gly Ala Thr Gly
100 105 110

gga gcg gtc ctt ggg cgc cac cta gtg agc aga atc ata ata gct aag 384
Gly Ala Val Leu Gly Arg His Leu Val Ser Arg Ile Ile Ile Ala Lys
115 120 125

agt gac tct ccc ttt gga gtt ata agg ttt ctc aat caa agc aaa att 432
Ser Asp Ser Pro Phe Gly Val Ile Arg Phe Leu Asn Gln Ser Lys Ile
130 135 140

tct att gct aat ccc aat tcc aca atg att tta tca ctg gtg ctg gag 480
Ser Ile Ala Asn Pro Asn Ser Thr Met Ile Leu Ser Leu Val Leu Glu
145 150 155 160

cgg act gga gga ctc ttg gga gag att cag gtg aac tgg gag aca gta 528
Arg Thr Gly Gly Leu Leu Gly Glu Ile Gln Val Asn Trp Glu Thr Val
165 170 175

gga ccc aac tct caa gaa gcc tta ctg cca cag aat aga gac att gca 576
Gly Pro Asn Ser Gln Glu Ala Leu Leu Pro Gln Asn Arg Asp Ile Ala
180 185 190

gac cca gtg agc ggg ttg ttc tat ttt gga gaa gga gaa gga gga gtg 624

110/160

Asp	Pro	Val	Ser	Gly	Leu	Phe	Tyr	Phe	Gly	Glu	Gly	Glu	Gly	Gly	Val		
		195					200					205					
aga	acc	ata	att	ctg	aca	atc	tat	cct	cat	gaa	gaa	att	gaa	gtt	gaa	672	
Arg	Thr	Ile	Ile	Leu	Thr	Ile	Tyr	Pro	His	Glu	Glu	Ile	Glu	Val	Glu		
	210					215				220							
gag	aca	ttc	att	att	aaa	ctt	cat	ctt	gtg	aaa	gga	gaa	gct	aaa	tta	720	
Glu	Thr	Phe	Ile	Ile	Lys	Leu	His	Leu	Val	Lys	Gly	Glu	Ala	Lys	Leu		
225					230					235					240		
gac	tcc	aga	gct	aaa	gat	gtt	aca	tta	acc	ata	caa	gag	ttt	ggg	gac	768	
Asp	Ser	Arg	Ala	Lys	Asp	Val	Thr	Leu	Thr	Ile	Gln	Glu	Phe	Gly	Asp		
				245				250						255			
cca	aat	gga	gtt	gtt	cag	ttt	gct	cct	gaa	act	ttg	tct	aag	aag	act	816	
Pro	Asn	Gly	Val	Val	Gln	Phe	Ala	Pro	Glu	Thr	Leu	Ser	Lys	Lys	Thr		
			260					265					270				
tat	tca	gag	cct	ctg	gct	ctg	gaa	ggg	ccc	ctg	ctc	att	acc	ttc	ttt	864	
Tyr	Ser	Glu	Pro	Leu	Ala	Leu	Glu	Gly	Pro	Leu	Leu	Ile	Thr	Phe	Phe		
		275					280					285					
gtc	aga	aga	gtc	aag	ggc	acc	ttt	gga	gag	att	atg	gtt	tac	tgg	gaa	912	
Val	Arg	Arg	Val	Lys	Gly	Thr	Phe	Gly	Glu	Ile	Met	Val	Tyr	Trp	Glu		
	290					295					300						
tta	agt	agt	gag	ttt	gac	att	act	gaa	gac	ttt	ctt	tcc	acc	agt	gga	960	
Leu	Ser	Ser	Glu	Phe	Asp	Ile	Thr	Glu	Asp	Phe	Leu	Ser	Thr	Ser	Gly		
305					310					315					320		
ttt	ttc	acc	att	gct	gat	gga	gag	agt	gaa	gct	agc	ttt	gat	gtt	cat	1008	
Phe	Phe	Thr	Ile	Ala	Asp	Gly	Glu	Ser	Glu	Ala	Ser	Phe	Asp	Val	His		
				325				330						335			
ttg	cta	cca	gat	gag	gta	cct	gag	ata	gag	gaa	gat	tat	gtg	atc	cag	1056	
Leu	Leu	Pro	Asp	Glu	Val	Pro	Glu	Ile	Glu	Glu	Asp	Tyr	Val	Ile	Gln		
			340					345					350				
ctt	gtt	tct	gta	gag	gga	gga	gcc	gaa	ctg	gat	ctg	gag	aag	agt	atc	1104	
Leu	Val	Ser	Val	Glu	Gly	Gly	Ala	Glu	Leu	Asp	Leu	Glu	Lys	Ser	Ile		
			355				360					365					
aca	tgg	ttc	tct	gtt	tat	gca	aat	gat	gac	cca	cat	gga	gta	ttt	gcc	1152	
Thr	Trp	Phe	Ser	Val	Tyr	Ala	Asn	Asp	Asp	Pro	His	Gly	Val	Phe	Ala		
	370					375					380						
ctg	tat	tcg	gat	cgc	cag	tca	ata	ctt	att	ggg	cag	aac	ctt	att	aga	1200	
Leu	Tyr	Ser	Asp	Arg	Gln	Ser	Ile	Leu	Ile	Gly	Gln	Asn	Leu	Ile	Arg		
385					390					395					400		
tcc	atc	caa	att	aac	ata	acc	cgg	ctt	gct	gga	aca	ttt	gga	gat	gtg	1248	
Ser	Ile	Gln	Ile	Asn	Ile	Thr	Arg	Leu	Ala	Gly	Thr	Phe	Gly	Asp	Val		
				405				410						415			
gct	gtt	ggg	ctt	cga	ata	tca	tcg	gat	cat	aaa	gaa	cag	ccg	att	gtt	1296	
Ala	Val	Gly	Leu	Arg	Ile	Ser	Ser	Asp	His	Lys	Glu	Gln	Pro	Ile	Val		
			420					425					430				
acc	gaa	aat	gca	gag	agg	cag	ctg	gtg	gtc	aaa	gat	ggg	gcc	aca	tat	1344	
Thr	Glu	Asn	Ala	Glu	Arg	Gln	Leu	Val	Val	Lys	Asp	Gly	Ala	Thr	Tyr		

111/160

435					440					445						
aaa	gtg	gac	gtg	ttt	gga	acc	ttt	tat	tac	agc	ttc	atc	tcc	tgt	act	1392
Lys	Val	Asp	Val	Phe	Gly	Thr	Phe	Tyr	Tyr	Ser	Phe	Ile	Ser	Cys	Thr	
	450					455					460					
gat	gga	gct	gta	aat	cta	aca	tac	atc	cag	atc	att	tca	aag	cct	att	1440
Asp	Gly	Ala	Val	Asn	Leu	Thr	Tyr	Ile	Gln	Ile	Ile	Ser	Lys	Pro	Ile	
	465					470					475				480	
ttt	tct	cac	tac	aca	gat	gcc	tat	ata	ttt	ctt	cat	tac	agc	ctt	tta	1488
Phe	Ser	His	Tyr	Thr	Asp	Ala	Tyr	Ile	Phe	Leu	His	Tyr	Ser	Leu	Leu	
				485					490					495		
aat	act	ttt	ctc	tgt	gat	aat	tcc	cac	ttt	aaa	att	tcg	aga	aag		1533
Asn	Thr	Phe	Leu	Cys	Asp	Asn	Ser	His	Phe	Lys	Ile	Ser	Arg	Lys		
			500					505					510			

<210> 84

<211> 511

<212> PRT

<213> Homo sapiens

<400> 84

Met	Ser	Val	Val	Leu	Gln	Asp	Thr	Gln	Thr	Leu	Thr	Ile	Asp	Ser	Asn	
1				5					10				15			
Ile	Asn	Ser	Leu	Leu	Ile	Val	Ala	Leu	Leu	Val	Thr	Gly	Ile	Thr	Gly	
			20					25					30			
Met	His	His	His	Ala	Arg	Leu	Ile	Leu	Lys	Leu	Phe	Val	Ser	Lys	Ser	
		35					40					45				
Ser	Ile	Asn	Phe	Ala	Asp	Phe	Ile	Ser	Gln	Ser	Ser	Ser	Ala	Ser	Pro	
	50					55					60					
Gly	Gly	Val	Asp	Tyr	Ile	Leu	His	Gly	Ser	Thr	Val	Thr	Phe	Gln	His	
65					70					75				80		
Gly	Gln	Asn	Leu	Ser	Phe	Ile	Asn	Ile	Ser	Ile	Ile	Asp	Asp	Asn	Glu	
			85						90					95		
Ser	Glu	Phe	Glu	Glu	Pro	Ile	Glu	Ile	Leu	Leu	Thr	Gly	Ala	Thr	Gly	
			100					105					110			
Gly	Ala	Val	Leu	Gly	Arg	His	Leu	Val	Ser	Arg	Ile	Ile	Ile	Ala	Lys	
		115					120					125				
Ser	Asp	Ser	Pro	Phe	Gly	Val	Ile	Arg	Phe	Leu	Asn	Gln	Ser	Lys	Ile	
	130					135					140					
Ser	Ile	Ala	Asn	Pro	Asn	Ser	Thr	Met	Ile	Leu	Ser	Leu	Val	Leu	Glu	
145					150					155					160	
Arg	Thr	Gly	Gly	Leu	Leu	Gly	Glu	Ile	Gln	Val	Asn	Trp	Glu	Thr	Val	
			165						170					175		
Gly	Pro	Asn	Ser	Gln	Glu	Ala	Leu	Leu	Pro	Gln	Asn	Arg	Asp	Ile	Ala	
		180					185						190			
Asp	Pro	Val	Ser	Gly	Leu	Phe	Tyr	Phe	Gly	Glu	Gly	Glu	Gly	Gly	Val	
		195					200					205				
Arg	Thr	Ile	Ile	Leu	Thr	Ile	Tyr	Pro	His	Glu	Glu	Ile	Glu	Val	Glu	
	210					215					220					
Glu	Thr	Phe	Ile	Ile	Lys	Leu	His	Leu	Val	Lys	Gly	Glu	Ala	Lys	Leu	
225					230					235					240	
Asp	Ser	Arg	Ala	Lys	Asp	Val	Thr	Leu	Thr	Ile	Gln	Glu	Phe	Gly	Asp	
			245						250					255		
Pro	Asn	Gly	Val	Val	Gln	Phe	Ala	Pro	Glu	Thr	Leu	Ser	Lys	Lys	Thr	
		260					265						270			
Tyr	Ser	Glu	Pro	Leu	Ala	Leu	Glu	Gly	Pro	Leu	Leu	Ile	Thr	Phe	Phe	
		275					280					285				
Val	Arg	Arg	Val	Lys	Gly	Thr	Phe	Gly	Glu	Ile	Met	Val	Tyr	Trp	Glu	

112/160

290 295 300
 Leu Ser Ser Glu Phe Asp Ile Thr Glu Asp Phe Leu Ser Thr Ser Gly
 305 310 315 320
 Phe Phe Thr Ile Ala Asp Gly Glu Ser Glu Ala Ser Phe Asp Val His
 325 330 335
 Leu Leu Pro Asp Glu Val Pro Glu Ile Glu Glu Asp Tyr Val Ile Gln
 340 345 350
 Leu Val Ser Val Glu Gly Gly Ala Glu Leu Asp Leu Glu Lys Ser Ile
 355 360 365
 Thr Trp Phe Ser Val Tyr Ala Asn Asp Asp Pro His Gly Val Phe Ala
 370 375 380
 Leu Tyr Ser Asp Arg Gln Ser Ile Leu Ile Gly Gln Asn Leu Ile Arg
 385 390 395 400
 Ser Ile Gln Ile Asn Ile Thr Arg Leu Ala Gly Thr Phe Gly Asp Val
 405 410 415
 Ala Val Gly Leu Arg Ile Ser Ser Asp His Lys Glu Gln Pro Ile Val
 420 425 430
 Thr Glu Asn Ala Glu Arg Gln Leu Val Val Lys Asp Gly Ala Thr Tyr
 435 440 445
 Lys Val Asp Val Phe Gly Thr Phe Tyr Tyr Ser Phe Ile Ser Cys Thr
 450 455 460
 Asp Gly Ala Val Asn Leu Thr Tyr Ile Gln Ile Ile Ser Lys Pro Ile
 465 470 475 480

 Phe Ser His Tyr Thr Asp Ala Tyr Ile Phe Leu His Tyr Ser Leu Leu
 485 490 495
 Asn Thr Phe Leu Cys Asp Asn Ser His Phe Lys Ile Ser Arg Lys
 500 505 510

<210> 85
 <211> 2160
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(2160)

<400> 85
 ggg gga ggt att tta ttt atg ctg ctt ttc ccc tca aag atc cac cta 48
 Gly Gly Gly Ile Leu Phe Met Leu Leu Phe Pro Ser Lys Ile His Leu
 1 5 10 15

 atc acc tac aaa gtc tat ttc ttt ttc agg ttt aac ttt cag aga ttc 96
 Ile Thr Tyr Lys Val Tyr Phe Phe Phe Arg Phe Asn Phe Gln Arg Phe
 20 25 30

 cgc tgg atg aaa gcc atg atc cac atg atc aag gag att aat aag agg 144
 Arg Trp Met Lys Ala Met Ile His Met Ile Lys Glu Ile Asn Lys Arg
 35 40 45

 aag gat att ttg ccc aac atc act ctg ggc tat cag atc ttt gat acc 192
 Lys Asp Ile Leu Pro Asn Ile Thr Leu Gly Tyr Gln Ile Phe Asp Thr
 50 55 60

 tgt ttt acc atc tcc aaa tca gtg gaa gca gtc ttg gta ttt ctt aca 240
 Cys Phe Thr Ile Ser Lys Ser Val Glu Ala Val Leu Val Phe Leu Thr
 65 70 75 80

 ggg cag gaa gaa aac agg ccc aat ttt aga aac agc act gga gca ttt 288
 Gly Gln Glu Glu Asn Arg Pro Asn Phe Arg Asn Ser Thr Gly Ala Phe
 85 90 95

113/160

ccg gca gga att gtt gga gca ggt gga tca ttc tta tca gtt cct gct	336
Pro Ala Gly Ile Val Gly Ala Gly Gly Ser Phe Leu Ser Val Pro Ala	
100 105 110	
tca aga att cta ggg tta tat tat ttg cct cag gtg ggc tat acc tct	384
Ser Arg Ile Leu Gly Leu Tyr Tyr Leu Pro Gln Val Gly Tyr Thr Ser	
115 120 125	
acc tgc gtg att ctt agt gac aaa tac cag ttt cca tct tat ctt cgt	432
Thr Cys Val Ile Leu Ser Asp Lys Tyr Gln Phe Pro Ser Tyr Leu Arg	
130 135 140	
gta ata gcc agc gat aag atc cag tgc aag gct gtg gta aaa cgt atc	480
Val Ile Ala Ser Asp Lys Ile Gln Ser Lys Ala Val Val Lys Arg Ile	
145 150 155 160	
caa cac ttt cac ttt ctc act ctg tgc ccc agg ctg gag tgc agt ggc	528
Gln His Phe His Phe Leu Thr Leu Ser Pro Arg Leu Glu Cys Ser Gly	
165 170 175	
gcc atc ctg gct cat ggc aac ctc tgc ctc cca gta gct ggg att aca	576
Ala Ile Leu Ala His Gly Asn Leu Cys Leu Pro Val Ala Gly Ile Thr	
180 185 190	
ggg gtg tgc cac cat gcc aga cta att ttt gta ttt tta gta gag aca	624
Gly Val Cys His His Ala Arg Leu Ile Phe Val Phe Leu Val Glu Thr	
195 200 205	
ggg ttt tgc cat gtt gcc cag gct gac gga gtc tgc ctc tgt tgc cat	672
Gly Phe Cys His Val Ala Gln Ala Asp Gly Val Ser Leu Cys Cys His	
210 215 220	
gct gga gta tac aat tct cct gcc tca gcc ccc cta gta gct ggg act	720
Ala Gly Val Tyr Asn Ser Pro Ala Ser Ala Pro Leu Val Ala Gly Thr	
225 230 235 240	
aca ggc gca cac cac cac gct cag cta att ttt gta ttt tta aga tat	768
Thr Gly Ala His His His Ala Gln Leu Ile Phe Val Phe Leu Arg Tyr	
245 250 255	
gta aca ctt ctg tca ttg cag aaa gga cag agc tgc cct aat gtg ttc	816
Val Thr Leu Leu Ser Leu Gln Lys Gly Gln Ser Cys Pro Asn Val Phe	
260 265 270	
atg cat tat cta ggg gaa gaa tat ttc cag cac agg gaa cag cac ctt	864
Met His Tyr Leu Gly Glu Glu Tyr Phe Gln His Arg Glu Gln His Leu	
275 280 285	
cta aac cct gag gcg cgt gtg gct ggc act ttg gag gaa cag aaa aga	912
Leu Asn Pro Glu Ala Arg Val Ala Gly Thr Leu Glu Glu Gln Lys Arg	
290 295 300	
agt caa tgt ggc tgg aaa gac tta tct att gtg tat aca tac ttc tgt	960
Ser Gln Cys Gly Trp Lys Asp Leu Ser Ile Val Tyr Thr Tyr Phe Cys	
305 310 315 320	
aat gtt atg tac cat aac cta gct cag aga ttg gta ata ttt tct atg	1008
Asn Val Met Tyr His Asn Leu Ala Gln Arg Leu Val Ile Phe Ser Met	
325 330 335	

114/160

tta ttt aat tca gat tta ctc tgg aaa act caa cat atg aaa att ctg	1056
Leu Phe Asn Ser Asp Leu Leu Trp Lys Thr Gln His Met Lys Ile Leu	
340 345 350	
att tct aaa ata aat ata aag gga aaa tat ttt tta ggc ttt caa gat	1104
Ile Ser Lys Ile Asn Ile Lys Gly Lys Tyr Phe Leu Gly Phe Gln Asp	
355 360 365	
gat tct tgg aat cat agg tcc ttc aca agc agg aac aga cct ctt ccc	1152
Asp Ser Trp Asn His Arg Ser Phe Thr Ser Arg Asn Arg Pro Leu Pro	
370 375 380	
cat tca gtg tgt act gat gtg tgt cct cct ggg act cgg aag ggg att	1200
His Ser Val Cys Thr Asp Val Cys Pro Pro Gly Thr Arg Lys Gly Ile	
385 390 395 400	
cgt tca gag gga gaa cca ata tgc tgc ttt gac tcc atc cca tgt gct	1248
Arg Ser Glu Gly Glu Pro Ile Cys Cys Phe Asp Ser Ile Pro Cys Ala	
405 410 415	
gat gga cac gtg tca cgg aaa cca ggt gaa agg gag tgt gaa caa tgt	1296
Asp Gly His Val Ser Arg Lys Pro Gly Glu Arg Glu Cys Glu Gln Cys	
420 425 430	
ggt gaa gac tat tgg tca aat gca caa aag agc gag tgt gtg ctg aaa	1344
Gly Glu Asp Tyr Trp Ser Asn Ala Gln Lys Ser Glu Cys Val Leu Lys	
435 440 445	
gag gtg gaa tac ctt gct tat gat gag gcc ctg gga ttc aca ctt gtc	1392
Glu Val Glu Tyr Leu Ala Tyr Asp Glu Ala Leu Gly Phe Thr Leu Val	
450 455 460	
att ctt tct gtc ttt ggg gca ttt gtg gtc ttg gca gtc aca gct gtg	1440
Ile Leu Ser Val Phe Gly Ala Phe Val Val Leu Ala Val Thr Ala Val	
465 470 475 480	
tat gtg ata cac agg cac act ccc ctg gtg aac gcc agt gac tgg cag	1488
Tyr Val Ile His Arg His Thr Pro Leu Val Asn Ala Ser Asp Trp Gln	
485 490 495	
ctg ggc ttt ctc att cag gtt tct ctg atc atc atg ctg ctg tcg tcc	1536
Leu Gly Phe Leu Ile Gln Val Ser Leu Ile Ile Met Leu Leu Ser Ser	
500 505 510	
atg ctt ttc att gac aag cca cac aac tgg tcc tgc atg gct ggc cag	1584
Met Leu Phe Ile Asp Lys Pro His Asn Trp Ser Cys Met Ala Gly Gln	
515 520 525	
gtc act ctg gca ctg ggc ttt tct ctt tgc ctg tct tgc ctt ctt gga	1632
Val Thr Leu Ala Leu Gly Phe Ser Leu Cys Leu Ser Cys Leu Leu Gly	
530 535 540	
aag act agt tca ctg ttt tta gcc tac aga att tcc aaa tcc aaa act	1680
Lys Thr Ser Ser Leu Phe Leu Ala Tyr Arg Ile Ser Lys Ser Lys Thr	
545 550 555 560	
caa ctt aca tcc atg cac ccc ctt tat cgg aaa atc att gtg cta atc	1728
Gln Leu Thr Ser Met His Pro Leu Tyr Arg Lys Ile Ile Val Leu Ile	
565 570 575	
tct gtt cta gcg gag att ggc ata tgt aca gcc tac ttg ata ttg gaa	1776

115/160

Ser Val Leu Ala Glu Ile Gly Ile Cys Thr Ala Tyr Leu Ile Leu Glu
580 585 590

cct ccc atg gta tac aag aac atg gaa tct caa aat aca aag atc att 1824
Pro Pro Met Val Tyr Lys Asn Met Glu Ser Gln Asn Thr Lys Ile Ile
595 600 605

ctg gga tgc aat gaa att tcc ata gag ttt ttg tac tcg atg ttt gga 1872
Leu Gly Cys Asn Glu Ile Ser Ile Glu Phe Leu Tyr Ser Met Phe Gly
610 615 620

att gat gcc ttc tta gcc ttg cta tgc ttt ctt aca act ttt gtg gct 1920
Ile Asp Ala Phe Leu Ala Leu Leu Cys Phe Leu Thr Thr Phe Val Ala
625 630 635 640

cgc cag tta cca gat aat tac tat gaa gga aaa tgc atc acc ttt ggg 1968
Arg Gln Leu Pro Asp Asn Tyr Tyr Glu Gly Lys Cys Ile Thr Phe Gly
645 650 655

atg ctt gtc ttt ttc atc att tgg atg tct ttt gtc cct gtt tat ttg 2016
Met Leu Val Phe Phe Ile Ile Trp Met Ser Phe Val Pro Val Tyr Leu
660 665 670

agc acc aaa ggc aag ttc aaa atg gct gtg gaa ata ttt gca atc ttg 2064
Ser Thr Lys Gly Lys Phe Lys Met Ala Val Glu Ile Phe Ala Ile Leu
675 680 685

gca tcc agc cat ggc ttg ttg ggt tgt ata ttt gct cct aag tgc ctc 2112
Ala Ser Ser His Gly Leu Leu Gly Cys Ile Phe Ala Pro Lys Cys Leu
690 695 700

att att ttg ctg agg cca gag agg aac acc agt gaa att gtt tgt gga 2160
Ile Ile Leu Leu Arg Pro Glu Arg Asn Thr Ser Glu Ile Val Cys Gly
705 710 715 720

<210> 86

<211> 720

<212> PRT

<213> Homo sapiens

<400> 86

Gly Gly Gly Ile Leu Phe Met Leu Leu Phe Pro Ser Lys Ile His Leu
1 5 10 15
Ile Thr Tyr Lys Val Tyr Phe Phe Phe Arg Phe Asn Phe Gln Arg Phe
20 25 30
Arg Trp Met Lys Ala Met Ile His Met Ile Lys Glu Ile Asn Lys Arg
35 40 45
Lys Asp Ile Leu Pro Asn Ile Thr Leu Gly Tyr Gln Ile Phe Asp Thr
50 55 60
Cys Phe Thr Ile Ser Lys Ser Val Glu Ala Val Leu Val Phe Leu Thr
65 70 75 80
Gly Gln Glu Glu Asn Arg Pro Asn Phe Arg Asn Ser Thr Gly Ala Phe
85 90 95
Pro Ala Gly Ile Val Gly Ala Gly Gly Ser Phe Leu Ser Val Pro Ala
100 105 110
Ser Arg Ile Leu Gly Leu Tyr Tyr Leu Pro Gln Val Gly Tyr Thr Ser
115 120 125
Thr Cys Val Ile Leu Ser Asp Lys Tyr Gln Phe Pro Ser Tyr Leu Arg
130 135 140

116/160

Val Ile Ala Ser Asp Lys Ile Gln Ser Lys Ala Val Val Lys Arg Ile
 145 150 155 160
 Gln His Phe His Phe Leu Thr Leu Ser Pro Arg Leu Glu Cys Ser Gly
 165 170 175
 Ala Ile Leu Ala His Gly Asn Leu Cys Leu Pro Val Ala Gly Ile Thr
 180 185 190
 Gly Val Cys His His Ala Arg Leu Ile Phe Val Phe Leu Val Glu Thr
 195 200 205
 Gly Phe Cys His Val Ala Gln Ala Asp Gly Val Ser Leu Cys Cys His
 210 215 220
 Ala Gly Val Tyr Asn Ser Pro Ala Ser Ala Pro Leu Val Ala Gly Thr
 225 230 235 240
 Thr Gly Ala His His His Ala Gln Leu Ile Phe Val Phe Leu Arg Tyr
 245 250 255
 Val Thr Leu Leu Ser Leu Gln Lys Gly Gln Ser Cys Pro Asn Val Phe
 260 265 270
 Met His Tyr Leu Gly Glu Glu Tyr Phe Gln His Arg Glu Gln His Leu
 275 280 285
 Leu Asn Pro Glu Ala Arg Val Ala Gly Thr Leu Glu Glu Gln Lys Arg
 290 295 300
 Ser Gln Cys Gly Trp Lys Asp Leu Ser Ile Val Tyr Thr Tyr Phe Cys
 305 310 315 320
 Asn Val Met Tyr His Asn Leu Ala Gln Arg Leu Val Ile Phe Ser Met
 325 330 335
 Leu Phe Asn Ser Asp Leu Leu Trp Lys Thr Gln His Met Lys Ile Leu
 340 345 350
 Ile Ser Lys Ile Asn Ile Lys Gly Lys Tyr Phe Leu Gly Phe Gln Asp
 355 360 365
 Asp Ser Trp Asn His Arg Ser Phe Thr Ser Arg Asn Arg Pro Leu Pro
 370 375 380
 His Ser Val Cys Thr Asp Val Cys Pro Pro Gly Thr Arg Lys Gly Ile
 385 390 395 400
 Arg Ser Glu Gly Glu Pro Ile Cys Cys Phe Asp Ser Ile Pro Cys Ala
 405 410 415
 Asp Gly His Val Ser Arg Lys Pro Gly Glu Arg Glu Cys Glu Gln Cys
 420 425 430
 Gly Glu Asp Tyr Trp Ser Asn Ala Gln Lys Ser Glu Cys Val Leu Lys
 435 440 445
 Glu Val Glu Tyr Leu Ala Tyr Asp Glu Ala Leu Gly Phe Thr Leu Val
 450 455 460
 Ile Leu Ser Val Phe Gly Ala Phe Val Val Leu Ala Val Thr Ala Val
 465 470 475 480
 Tyr Val Ile His Arg His Thr Pro Leu Val Asn Ala Ser Asp Trp Gln
 485 490 495
 Leu Gly Phe Leu Ile Gln Val Ser Leu Ile Ile Met Leu Leu Ser Ser
 500 505 510
 Met Leu Phe Ile Asp Lys Pro His Asn Trp Ser Cys Met Ala Gly Gln
 515 520 525
 Val Thr Leu Ala Leu Gly Phe Ser Leu Cys Leu Ser Cys Leu Leu Gly
 530 535 540
 Lys Thr Ser Ser Leu Phe Leu Ala Tyr Arg Ile Ser Lys Ser Lys Thr
 545 550 555 560
 Gln Leu Thr Ser Met His Pro Leu Tyr Arg Lys Ile Ile Val Leu Ile
 565 570 575
 Ser Val Leu Ala Glu Ile Gly Ile Cys Thr Ala Tyr Leu Ile Leu Glu
 580 585 590
 Pro Pro Met Val Tyr Lys Asn Met Glu Ser Gln Asn Thr Lys Ile Ile
 595 600 605
 Leu Gly Cys Asn Glu Ile Ser Ile Glu Phe Leu Tyr Ser Met Phe Gly
 610 615 620
 Ile Asp Ala Phe Leu Ala Leu Leu Cys Phe Leu Thr Thr Phe Val Ala
 625 630 635 640
 Arg Gln Leu Pro Asp Asn Tyr Tyr Glu Gly Lys Cys Ile Thr Phe Gly

117/160

				645					650					655			
Met	Leu	Val	Phe	Phe	Ile	Ile	Trp	Met	Ser	Phe	Val	Pro	Val	Tyr	Leu		
			660					665						670			
Ser	Thr	Lys	Gly	Lys	Phe	Lys	Met	Ala	Val	Glu	Ile	Phe	Ala	Ile	Leu		
		675					680					685					
Ala	Ser	Ser	His	Gly	Leu	Leu	Gly	Cys	Ile	Phe	Ala	Pro	Lys	Cys	Leu		
	690					695					700						
Ile	Ile	Leu	Leu	Arg	Pro	Glu	Arg	Asn	Thr	Ser	Glu	Ile	Val	Cys	Gly		
705					710					715					720		

<210> 87
 <211> 933
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(933)

<400> 87
 cgg ctg gtg ctg gcc gcg gtg gag aca acc gtg ctg gtg ctc atc ttt 48
 Arg Leu Val Leu Ala Ala Val Glu Thr Thr Val Leu Val Leu Ile Phe
 1 5 10 15

gca gtg tcg ctg ctg gcc aac gtg tgc gcc ctg gtg ctg gtg gcg cgc 96
 Ala Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu Val Ala Arg
 20 25 30

cga cga cgc cgc gcc gcg act gcc tgc ctg gta ctc aac ctc ttc tgc 144
 Arg Arg Arg Arg Gly Ala Thr Ala Cys Leu Val Leu Asn Leu Phe Cys
 35 40 45

gcg gac ctg ctc ttc atc agc gct atc cct ctg gtg ctg gcc gtg cgc 192
 Ala Asp Leu Leu Phe Ile Ser Ala Ile Pro Leu Val Leu Ala Val Arg
 50 55 60

tgg act gag gcc tgg ctg ctg gcc ccc gtt gcc tgc cac ctg ctc ttc 240
 Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Ala Cys His Leu Leu Phe
 65 70 75 80

tac gtg atg acc ctg agc gcc agc gtc acc atc ctc acg ctg gcc gcg 288
 Tyr Val Met Thr Leu Ser Gly Ser Val Thr Ile Leu Thr Leu Ala Ala
 85 90 95

gtc agc ctg gag cgc atg gtg tgc atc gtg cac ctg cag cgc gcc gtg 336
 Val Ser Leu Glu Arg Met Val Cys Ile Val His Leu Gln Arg Gly Val
 100 105 110

cgg ggt cct ggg cgg cgg gcg cgg gca gtg ctg ctg gcg ctc atc tgg 384
 Arg Gly Pro Gly Arg Arg Ala Arg Ala Val Leu Leu Ala Leu Ile Trp
 115 120 125

ggc tat tcg gcg gtc gcc gct ctg cct ctc tgc gtc ttc ttc cga gtc 432
 Gly Tyr Ser Ala Val Ala Leu Pro Leu Cys Val Phe Phe Arg Val
 130 135 140

gtc ccg caa cgg ctc ccc gcc gcc gac cag gtg agc gcc cct ctg tgt 480
 Val Pro Gln Arg Leu Pro Gly Ala Asp Gln Val Ser Ala Pro Leu Cys
 145 150 155 160

atc tcg tgg gat gtc tct ttt gtt act ttg aac ttc ttg gtg cca gga 528
 Ile Ser Trp Asp Val Ser Phe Val Thr Leu Asn Phe Leu Val Pro Gly

118/160

165										170					175					
ctg gtc att gtg atc agt tac tcc aaa att tta cag atc cgc gtg tcc	576																			
Leu Val Ile Val Ile Ser Tyr Ser Lys Ile Leu Gln Ile Arg Val Ser																				
180 185 190																				
cag cag gac ttc cgg ctc ttc cgc acc ctc ttc ctc ctc atg gtc tcc	624																			
Gln Gln Asp Phe Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser																				
195 200 205																				
ttc ttc atc atg tgg agc ccc atc atc atc acc atc ctc ctc atc ctg	672																			
Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile Leu Leu Ile Leu																				
210 215 220																				
atc cag aac ttc aag caa gac ctg gtc atc tgg ccg tcc ctc ttc ttc	720																			
Ile Gln Asn Phe Lys Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe																				
225 230 235 240																				
tgg gtg gtg gcc ttc aca ttt gct aat tca gcc cta aac ccc atc ctc	768																			
Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu																				
245 250 255																				
tac aac atg aca ctc aga gtc ttc agg cac agg gtc ctg gag att agg	816																			
Tyr Asn Met Thr Leu Arg Val Phe Arg His Arg Val Leu Glu Ile Arg																				
260 265 270																				
gac aaa ctt tgg ccc ctg aca att ttg cat aag ttc agc tct ggc aca	864																			
Asp Lys Leu Trp Pro Leu Thr Ile Leu His Lys Phe Ser Ser Gly Thr																				
275 280 285																				
agt cta cca ttg gga cat aca cac aca cag gca cac aca cac aca cat	912																			
Ser Leu Pro Leu Gly His Thr His Thr Gln Ala His Thr His Thr His																				
290 295 300																				
gca cac aca cac ttg cac aca	933																			
Ala His Thr His Leu His Thr																				
305 310																				

<210> 88

<211> 311

<212> PRT

<213> Homo sapiens

<400> 88

Arg Leu Val Leu Ala Ala Val Glu Thr Thr Val Leu Val Leu Ile Phe	
1 5 10 15	
Ala Val Ser Leu Leu Gly Asn Val Cys Ala Leu Val Leu Val Ala Arg	
20 25 30	
Arg Arg Arg Arg Gly Ala Thr Ala Cys Leu Val Leu Asn Leu Phe Cys	
35 40 45	
Ala Asp Leu Leu Phe Ile Ser Ala Ile Pro Leu Val Leu Ala Val Arg	
50 55 60	
Trp Thr Glu Ala Trp Leu Leu Gly Pro Val Ala Cys His Leu Leu Phe	
65 70 75 80	
Tyr Val Met Thr Leu Ser Gly Ser Val Thr Ile Leu Thr Leu Ala Ala	
85 90 95	
Val Ser Leu Glu Arg Met Val Cys Ile Val His Leu Gln Arg Gly Val	
100 105 110	
Arg Gly Pro Gly Arg Arg Ala Arg Ala Val Leu Leu Ala Leu Ile Trp	
115 120 125	
Gly Tyr Ser Ala Val Ala Ala Leu Pro Leu Cys Val Phe Phe Arg Val	

119/160

130	135	140
Val Pro Gln Arg Leu Pro Gly Ala Asp Gln Val Ser Ala Pro Leu Cys		
145	150	155
Ile Ser Trp Asp Val Ser Phe Val Thr Leu Asn Phe Leu Val Pro Gly		160
	165	170
Leu Val Ile Val Ile Ser Tyr Ser Lys Ile Leu Gln Ile Arg Val Ser		175
	180	185
Gln Gln Asp Phe Arg Leu Phe Arg Thr Leu Phe Leu Leu Met Val Ser		190
	195	200
Phe Phe Ile Met Trp Ser Pro Ile Ile Ile Thr Ile Leu Leu Ile Leu		205
	210	215
Ile Gln Asn Phe Lys Gln Asp Leu Val Ile Trp Pro Ser Leu Phe Phe		220
225	230	235
Trp Val Val Ala Phe Thr Phe Ala Asn Ser Ala Leu Asn Pro Ile Leu		240
	245	250
Tyr Asn Met Thr Leu Arg Val Phe Arg His Arg Val Leu Glu Ile Arg		255
	260	265
		270
Asp Lys Leu Trp Pro Leu Thr Ile Leu His Lys Phe Ser Ser Gly Thr		
	275	280
Ser Leu Pro Leu Gly His Thr His Thr Gln Ala His Thr His Thr His		285
	290	295
Ala His Thr His Leu His Thr		300
305	310	

<210> 89

<211> 1059

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (1059)

<400> 89

atg gga agt gga att agt tca gag agc aag gag tca gcc aaa aga tca	48
Met Gly Ser Gly Ile Ser Ser Glu Ser Lys Glu Ser Ala Lys Arg Ser	
1 5 10 15	

aaa gaa ctg gag aaa aag ctt cag gag gat gct gag cga gat gca aga	96
Lys Glu Leu Glu Lys Lys Leu Gln Glu Asp Ala Glu Arg Asp Ala Arg	
20 25 30	

acc gta aag ctg cta cta tta gga gca gga gaa tct ggg aaa agt act	144
Thr Val Lys Leu Leu Leu Leu Gly Ala Gly Glu Ser Gly Lys Ser Thr	
35 40 45	

att gtt aaa caa atg aag aga ata ata cag gga aaa cat tat aca tcg	192
Ile Val Lys Gln Met Lys Arg Ile Ile Gln Gly Lys His Tyr Thr Ser	
50 55 60	

gag gaa tct gct gca tgg agc ttg agt gcc tgg tcg aac ata cac aaa	240
Glu Glu Ser Ala Ala Trp Ser Leu Ser Ala Trp Ser Asn Ile His Lys	
65 70 75 80	

tca ata aac tta atc cat cac ata aac aga acc aag aac aaa aac cac	288
Ser Ile Asn Leu Ile His His Ile Asn Arg Thr Lys Asn Lys Asn His	
85 90 95	

atg att agc tca ata gaa gca gaa aag gcc ttc cac aaa att caa cag	336
Met Ile Ser Ser Ile Glu Ala Glu Lys Ala Phe His Lys Ile Gln Gln	
100 105 110	

120/160

cct ttg atg cta aaa act ctc aat aaa caa gag aga gag acg ata agt	384
Pro Leu Met Leu Lys Thr Leu Asn Lys Gln Glu Arg Glu Thr Ile Ser	
115 120 125	
aat cta tgg tca ggg gtt aat atc caa aat tta tat tca tac acc gaa	432
Asn Leu Trp Ser Gly Val Asn Ile Gln Asn Leu Tyr Ser Tyr Thr Glu	
130 135 140	
tat tta ata cca gcc tgc aca aca agc tac ctt aat gat tta gat aga	480
Tyr Leu Ile Pro Ala Cys Thr Thr Ser Tyr Leu Asn Asp Leu Asp Arg	
145 150 155 160	
ata aca gca tct ggg tat gtg cca aat gaa caa gat gtt ctc cat tct	528
Ile Thr Ala Ser Gly Tyr Val Pro Asn Glu Gln Asp Val Leu His Ser	
165 170 175	
cga gtg aaa acg act gga atc att gaa act caa ttc tcc ttt aaa gac	576
Arg Val Lys Thr Thr Gly Ile Ile Glu Thr Gln Phe Ser Phe Lys Asp	
180 185 190	
ttg cac ttc agg atg ttt gat gta ggt gga cag aga tct gag aga aag	624
Leu His Phe Arg Met Phe Asp Val Gly Gly Gln Arg Ser Glu Arg Lys	
195 200 205	
aag tgg att cac tgc ttt gaa gga gtt aca tgc att ata ttt tgt gct	672
Lys Trp Ile His Cys Phe Glu Gly Val Thr Cys Ile Ile Phe Cys Ala	
210 215 220	
gca ctt agt gcc tat gac atg gtc ctc gtg gaa gac gaa gaa gtg aat	720
Ala Leu Ser Ala Tyr Asp Met Val Leu Val Glu Asp Glu Glu Val Asn	
225 230 235 240	
aga atg cat gaa agc ctt cac ctg ttc aac agt atc tgt aat cac aag	768
Arg Met His Glu Ser Leu His Leu Phe Asn Ser Ile Cys Asn His Lys	
245 250 255	
tat ttt tca aca acc tcc att gtc ctg ttc ctc aac aaa aaa gat atc	816
Tyr Phe Ser Thr Thr Ser Ile Val Leu Phe Leu Asn Lys Lys Asp Ile	
260 265 270	
ttt caa gaa aag gta acc aag gtg cat ctt agt atc tgc ttt cca gaa	864
Phe Gln Glu Lys Val Thr Lys Val His Leu Ser Ile Cys Phe Pro Glu	
275 280 285	
tac act ggg cca aat aca ttt gaa gat gca gga aac tac atc aag aac	912
Tyr Thr Gly Pro Asn Thr Phe Glu Asp Ala Gly Asn Tyr Ile Lys Asn	
290 295 300	
cag ttt cta gac ctg aat tta aaa aaa gaa gat aag gaa att tat tcc	960
Gln Phe Leu Asp Leu Asn Leu Lys Lys Glu Asp Lys Glu Ile Tyr Ser	
305 310 315 320	
cac atg acc tgt gct act gac acc caa aat gtc aag ttt gtg ttt gac	1008
His Met Thr Cys Ala Thr Asp Thr Gln Asn Val Lys Phe Val Phe Asp	
325 330 335	
gca gtt aca gat ata ata atc aaa gag aat cta aaa gac tgt ggg ctt	1056
Ala Val Thr Asp Ile Ile Ile Lys Glu Asn Leu Lys Asp Cys Gly Leu	
340 345 350	
ttc	1059
Phe	

121/160

<210> 90
 <211> 353
 <212> PRT
 <213> Homo sapiens

<400> 90
 Met Gly Ser Gly Ile Ser Ser Glu Ser Lys Glu Ser Ala Lys Arg Ser
 1 5 10 15
 Lys Glu Leu Glu Lys Lys Leu Gln Glu Asp Ala Glu Arg Asp Ala Arg
 20 25 30
 Thr Val Lys Leu Leu Leu Leu Gly Ala Gly Glu Ser Gly Lys Ser Thr
 35 40 45
 Ile Val Lys Gln Met Lys Arg Ile Ile Gln Gly Lys His Tyr Thr Ser
 50 55 60
 Glu Glu Ser Ala Ala Trp Ser Leu Ser Ala Trp Ser Asn Ile His Lys
 65 70 75 80
 Ser Ile Asn Leu Ile His His Ile Asn Arg Thr Lys Asn Lys Asn His
 85 90 95
 Met Ile Ser Ser Ile Glu Ala Glu Lys Ala Phe His Lys Ile Gln Gln
 100 105 110
 Pro Leu Met Leu Lys Thr Leu Asn Lys Gln Glu Arg Glu Thr Ile Ser
 115 120 125
 Asn Leu Trp Ser Gly Val Asn Ile Gln Asn Leu Tyr Ser Tyr Thr Glu
 130 135 140
 Tyr Leu Ile Pro Ala Cys Thr Thr Ser Tyr Leu Asn Asp Leu Asp Arg
 145 150 155 160
 Ile Thr Ala Ser Gly Tyr Val Pro Asn Glu Gln Asp Val Leu His Ser
 165 170 175
 Arg Val Lys Thr Thr Gly Ile Ile Glu Thr Gln Phe Ser Phe Lys Asp
 180 185 190
 Leu His Phe Arg Met Phe Asp Val Gly Gly Gln Arg Ser Glu Arg Lys
 195 200 205
 Lys Trp Ile His Cys Phe Glu Gly Val Thr Cys Ile Ile Phe Cys Ala
 210 215 220
 Ala Leu Ser Ala Tyr Asp Met Val Leu Val Glu Asp Glu Glu Val Asn
 225 230 235 240
 Arg Met His Glu Ser Leu His Leu Phe Asn Ser Ile Cys Asn His Lys
 245 250 255
 Tyr Phe Ser Thr Thr Ser Ile Val Leu Phe Leu Asn Lys Lys Asp Ile
 260 265 270
 Phe Gln Glu Lys Val Thr Lys Val His Leu Ser Ile Cys Phe Pro Glu
 275 280 285
 Tyr Thr Gly Pro Asn Thr Phe Glu Asp Ala Gly Asn Tyr Ile Lys Asn
 290 295 300
 Gln Phe Leu Asp Leu Asn Leu Lys Lys Glu Asp Lys Glu Ile Tyr Ser
 305 310 315 320
 His Met Thr Cys Ala Thr Asp Thr Gln Asn Val Lys Phe Val Phe Asp
 325 330 335
 Ala Val Thr Asp Ile Ile Ile Lys Glu Asn Leu Lys Asp Cys Gly Leu
 340 345 350
 Phe

<210> 91
 <211> 960
 <212> DNA
 <213> Homo sapiens

<220>

122/160

<221> CDS

<222> (1)...(960)

<400> 91

tcg ccg gga tcc cgg gtg att ctg tac ata gtg ttt ggc ttt ggg gct	48
Ser Pro Gly Ser Arg Val Ile Leu Tyr Ile Val Phe Gly Phe Gly Ala	
1 5 10 15	
gtg ctg gct gtg ttt gga aac ctc ctg gtg atg att tca atc ctc cat	96
Val Leu Ala Val Phe Gly Asn Leu Leu Val Met Ile Ser Ile Leu His	
20 25 30	
ttc aag cag ctg cac tct ccg acc aat ttt ctc gtt gcc tct ctg gcc	144
Phe Lys Gln Leu His Ser Pro Thr Asn Phe Leu Val Ala Ser Leu Ala	
35 40 45	
tgc gct gat ttc ttg gtg ggt gtg act gtg atg ccc ttc agc atg gtc	192
Cys Ala Asp Phe Leu Val Gly Val Thr Val Met Pro Phe Ser Met Val	
50 55 60	
agg acg gtg gag agc tgc tgg tat ttt ggg agg agt ttt tgt act ttc	240
Arg Thr Val Glu Ser Cys Trp Tyr Phe Gly Arg Ser Phe Cys Thr Phe	
65 70 75 80	
cac acc tgc tgt gat gtg gca ttt tgt tac tct tct ctc ttt cac ttg	288
His Thr Cys Cys Asp Val Ala Phe Cys Tyr Ser Ser Leu Phe His Leu	
85 90 95	
tgc ttc atc tcc atc gac agg tac att gcg gtt act gac ccc ctg gtc	336
Cys Phe Ile Ser Ile Asp Arg Tyr Ile Ala Val Thr Asp Pro Leu Val	
100 105 110	
tat cct acc aag ttc acc gta tct gtg tca gga att tgc atc agc gtg	384
Tyr Pro Thr Lys Phe Thr Val Ser Val Ser Gly Ile Cys Ile Ser Val	
115 120 125	
tcc tgg atc ctg ccc ctc atg tac agc ggt gct gtg ttc tac aca ggt	432
Ser Trp Ile Leu Pro Leu Met Tyr Ser Gly Ala Val Phe Tyr Thr Gly	
130 135 140	
gtc tat gac gat ggg ctg gag gaa tta tct gat gcc cta aac tgt ata	480
Val Tyr Asp Asp Gly Leu Glu Glu Leu Ser Asp Ala Leu Asn Cys Ile	
145 150 155 160	
gga ggt tgt cag acc gtt gta aat caa aac tgg gtg ttg aca gat ttt	528
Gly Gly Cys Gln Thr Val Val Asn Gln Asn Trp Val Leu Thr Asp Phe	
165 170 175	
cta tcc ttc ttt ata cct acc ttt att atg ata att ctg tat ggt aac	576
Leu Ser Phe Phe Ile Pro Thr Phe Ile Met Ile Ile Leu Tyr Gly Asn	
180 185 190	
ata ttt ctt gtg gct aga cga cag gcg aaa aag ata gaa aat act gag	624
Ile Phe Leu Val Ala Arg Arg Gln Ala Lys Lys Ile Glu Asn Thr Glu	
195 200 205	
aga aaa gca gct aaa acc ctg ggg gtc aca gtg gta gca ttt atg att	672
Arg Lys Ala Ala Lys Thr Leu Gly Val Thr Val Val Ala Phe Met Ile	
210 215 220	
tca tgg tta cca tat agc att gat tca tta att gat gcc ttt atg ggc	720

123/160

Ser Trp Leu Pro Tyr Ser Ile Asp Ser Leu Ile Asp Ala Phe Met Gly
 225 230 235 240

ttt ata acc cct gcc tgt att tat gag att tgc tgt tgg tgt gct tat 768
 Phe Ile Thr Pro Ala Cys Ile Tyr Glu Ile Cys Cys Trp Cys Ala Tyr
 245 250 255

tat aac tca gcc atg aat cct ttg att tat gct tta ttt tac cca tgg 816
 Tyr Asn Ser Ala Met Asn Pro Leu Ile Tyr Ala Leu Phe Tyr Pro Trp
 260 265 270

ttt agg aaa gca ata aaa aaa ctg aga aag tgc aaa gtg ttt agg gaa 864
 Phe Arg Lys Ala Ile Lys Lys Leu Arg Lys Cys Lys Val Phe Arg Glu
 275 280 285

tat gaa aat aaa aca act agg ctg ggc gtg gtg ggt cac gcc tgt aat 912
 Tyr Glu Asn Lys Thr Thr Arg Leu Gly Val Val Gly His Ala Cys Asn
 290 295 300

ccc agc act ttg gga ggc caa ggc ggg tgg atc aca agg tca aaa gat 960
 Pro Ser Thr Leu Gly Gly Gln Gly Gly Trp Ile Thr Arg Ser Lys Asp
 305 310 315 320

<210> 92

<211> 320

<212> PRT

<213> Homo sapiens

<400> 92

Ser Pro Gly Ser Arg Val Ile Leu Tyr Ile Val Phe Gly Phe Gly Ala
 1 5 10 15

Val Leu Ala Val Phe Gly Asn Leu Leu Val Met Ile Ser Ile Leu His
 20 25 30

Phe Lys Gln Leu His Ser Pro Thr Asn Phe Leu Val Ala Ser Leu Ala
 35 40 45

Cys Ala Asp Phe Leu Val Gly Val Thr Val Met Pro Phe Ser Met Val
 50 55 60

Arg Thr Val Glu Ser Cys Trp Tyr Phe Gly Arg Ser Phe Cys Thr Phe
 65 70 75 80

His Thr Cys Cys Asp Val Ala Phe Cys Tyr Ser Ser Leu Phe His Leu
 85 90 95

Cys Phe Ile Ser Ile Asp Arg Tyr Ile Ala Val Thr Asp Pro Leu Val
 100 105 110

Tyr Pro Thr Lys Phe Thr Val Ser Val Ser Gly Ile Cys Ile Ser Val
 115 120 125

Ser Trp Ile Leu Pro Leu Met Tyr Ser Gly Ala Val Phe Tyr Thr Gly
 130 135 140

Val Tyr Asp Asp Gly Leu Glu Glu Leu Ser Asp Ala Leu Asn Cys Ile
 145 150 155 160

Gly Gly Cys Gln Thr Val Val Asn Gln Asn Trp Val Leu Thr Asp Phe
 165 170 175

Leu Ser Phe Phe Ile Pro Thr Phe Ile Met Ile Ile Leu Tyr Gly Asn
 180 185 190

Ile Phe Leu Val Ala Arg Arg Gln Ala Lys Lys Ile Glu Asn Thr Glu
 195 200 205

Arg Lys Ala Ala Lys Thr Leu Gly Val Thr Val Val Ala Phe Met Ile
 210 215 220

Ser Trp Leu Pro Tyr Ser Ile Asp Ser Leu Ile Asp Ala Phe Met Gly
 225 230 235 240

124/160

Phe Ile Thr Pro Ala Cys Ile Tyr Glu Ile Cys Cys Trp Cys Ala Tyr
 245 250 255
 Tyr Asn Ser Ala Met Asn Pro Leu Ile Tyr Ala Leu Phe Tyr Pro Trp
 260 265 270
 Phe Arg Lys Ala Ile Lys Lys Leu Arg Lys Cys Lys Val Phe Arg Glu
 275 280 285
 Tyr Glu Asn Lys Thr Thr Arg Leu Gly Val Val Gly His Ala Cys Asn
 290 295 300
 Pro Ser Thr Leu Gly Gly Gln Gly Gly Trp Ile Thr Arg Ser Lys Asp
 305 310 315 320

<210> 93

<211> 912

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(912)

<400> 93

tgc tac aat cag acc ctg agc ttc acg gtg ctg acg tgc atc att tcc 48
 Cys Tyr Asn Gln Thr Leu Ser Phe Thr Val Leu Thr Cys Ile Ile Ser
 1 5 10 15

ctt gtc gga ctg aca gga aac gcg gtt gtg ctc tgg ctc ctg ggc tac 96
 Leu Val Gly Leu Thr Gly Asn Ala Val Val Leu Trp Leu Leu Gly Tyr
 20 25 30

cgc atg cgc agg aac gct gtc tcc atc tac atc ctc aac ctg gcc gca 144
 Arg Met Arg Arg Asn Ala Val Ser Ile Tyr Ile Leu Asn Leu Ala Ala
 35 40 45

gca gac ttc ctc ttc ctc agc ttc cag att ata cgt ttg cca tta cgc 192
 Ala Asp Phe Leu Phe Leu Ser Phe Gln Ile Ile Arg Leu Pro Leu Arg
 50 55 60

ctc atc aat atc agc cat ctc atc cgc aaa atc ctc gtt tct gtg atg 240
 Leu Ile Asn Ile Ser His Leu Ile Arg Lys Ile Leu Val Ser Val Met
 65 70 75 80

acc ttt ccc tac ttt aca ggc ctg agt atg ctg agc gcc atc agc acc 288
 Thr Phe Pro Tyr Phe Thr Gly Leu Ser Met Leu Ser Ala Ile Ser Thr
 85 90 95

gag cgc tgc ctg tct gtt ctg tgg ccc atc tgg tac cgc tgc cgc cgc 336
 Glu Arg Cys Leu Ser Val Leu Trp Pro Ile Trp Tyr Arg Cys Arg Arg
 100 105 110

ccc aca cac ctg tca gcg gtc gtg tgt gtc ctg ctc tgg ggc ctg tcc 384
 Pro Thr His Leu Ser Ala Val Val Cys Val Leu Leu Trp Gly Leu Ser
 115 120 125

ctg ctg ttt agt atg ctg gag tgg agg ttc tgt gac ttc ctg ttt agt 432
 Leu Leu Phe Ser Met Leu Glu Trp Arg Phe Cys Asp Phe Leu Phe Ser
 130 135 140

ggg gct gat tct agt tgg tgt gaa acg tca gat ttc atc cca gtc gcg 480
 Gly Ala Asp Ser Ser Trp Cys Glu Thr Ser Asp Phe Ile Pro Val Ala
 145 150 155 160

tgg ctg att ttt tta tgt gtg gtt ctc tgt gtt tcc agc ctg gtc ctg 528

125/160

Trp	Leu	Ile	Phe	Leu	Cys	Val	Val	Leu	Cys	Val	Ser	Ser	Leu	Val	Leu		
				165					170					175			
ctg	gtc	agg	atc	ctc	tgt	gga	tcc	cgg	aag	atg	cgc	ctg	acc	agg	ctg	576	
Leu	Val	Arg	Ile	Leu	Cys	Gly	Ser	Arg	Lys	Met	Pro	Leu	Thr	Arg	Leu		
			180					185					190				
tac	gtg	acc	atc	ctg	ctc	aca	gtg	ctg	gtc	ttc	ctc	ctc	tgc	ggc	ctg	624	
Tyr	Val	Thr	Ile	Leu	Leu	Thr	Val	Leu	Val	Phe	Leu	Leu	Cys	Gly	Leu		
			195				200					205					
ccc	ttc	ggc	att	ctg	ggg	gcc	cta	att	tac	agg	atg	cac	ctg	aat	ttg	672	
Pro	Phe	Gly	Ile	Leu	Gly	Ala	Leu	Ile	Tyr	Arg	Met	His	Leu	Asn	Leu		
			210			215					220						
gaa	gtc	tta	tat	tgt	cat	gtt	tat	ctg	gtt	tgc	atg	tcc	ctg	tcc	tct	720	
Glu	Val	Leu	Tyr	Cys	His	Val	Tyr	Leu	Val	Cys	Met	Ser	Leu	Ser	Ser		
				230						235					240		
cta	aac	agt	agt	gcc	aac	ccc	atc	att	tac	ttc	ttc	gtg	ggc	tcc	ttt	768	
Leu	Asn	Ser	Ser	Ala	Asn	Pro	Ile	Ile	Tyr	Phe	Phe	Val	Gly	Ser	Phe		
				245					250					255			
agg	cag	cgt	caa	aat	agg	cag	aac	ctg	aag	ctg	gtt	ctc	cag	agg	gct	816	
Arg	Gln	Arg	Gln	Asn	Arg	Gln	Asn	Leu	Lys	Leu	Val	Leu	Gln	Arg	Ala		
				260				265					270				
ctg	cag	gac	aag	cct	gag	gtg	gat	aaa	gca	tct	gca	acg	agg	agc	cgg	864	
Leu	Gln	Asp	Lys	Pro	Glu	Val	Asp	Lys	Ala	Ser	Ala	Thr	Arg	Ser	Arg		
			275				280					285					
acg	aga	acc	acc	tca	acc	tca	tcc	gcg	tca	acg	cca	cca	agg	cct	acg	912	
Thr	Arg	Thr	Thr	Ser	Thr	Ser	Ser	Ala	Ser	Thr	Pro	Pro	Arg	Pro	Thr		
			290				295				300						

<210> 94

<211> 304

<212> PRT

<213> Homo sapiens

<400> 94

Cys	Tyr	Asn	Gln	Thr	Leu	Ser	Phe	Thr	Val	Leu	Thr	Cys	Ile	Ile	Ser		
1				5					10					15			
Leu	Val	Gly	Leu	Thr	Gly	Asn	Ala	Val	Val	Leu	Trp	Leu	Leu	Gly	Tyr		
			20					25				30					
Arg	Met	Arg	Arg	Asn	Ala	Val	Ser	Ile	Tyr	Ile	Leu	Asn	Leu	Ala	Ala		
			35				40					45					
Ala	Asp	Phe	Leu	Phe	Leu	Ser	Phe	Gln	Ile	Ile	Arg	Leu	Pro	Leu	Arg		
			50			55					60						
Leu	Ile	Asn	Ile	Ser	His	Leu	Ile	Arg	Lys	Ile	Leu	Val	Ser	Val	Met		
					70					75					80		
Thr	Phe	Pro	Tyr	Phe	Thr	Gly	Leu	Ser	Met	Leu	Ser	Ala	Ile	Ser	Thr		
				85					90					95			
Glu	Arg	Cys	Leu	Ser	Val	Leu	Trp	Pro	Ile	Trp	Tyr	Arg	Cys	Arg	Arg		
			100					105					110				
Pro	Thr	His	Leu	Ser	Ala	Val	Val	Cys	Val	Leu	Leu	Trp	Gly	Leu	Ser		
			115				120					125					
Leu	Leu	Phe	Ser	Met	Leu	Glu	Trp	Arg	Phe	Cys	Asp	Phe	Leu	Phe	Ser		
			130			135					140						
Gly	Ala	Asp	Ser	Ser	Trp	Cys	Glu	Thr	Ser	Asp	Phe	Ile	Pro	Val	Ala		
					150					155							

126/160

Trp Leu Ile Phe Leu Cys Val Val Leu Cys Val Ser Ser Leu Val Leu
 165 170 175
 Leu Val Arg Ile Leu Cys Gly Ser Arg Lys Met Pro Leu Thr Arg Leu
 180 185 190
 Tyr Val Thr Ile Leu Leu Thr Val Leu Val Phe Leu Leu Cys Gly Leu
 195 200 205
 Pro Phe Gly Ile Leu Gly Ala Leu Ile Tyr Arg Met His Leu Asn Leu
 210 215 220
 Glu Val Leu Tyr Cys His Val Tyr Leu Val Cys Met Ser Leu Ser Ser
 225 230 235 240
 Leu Asn Ser Ser Ala Asn Pro Ile Ile Tyr Phe Phe Val Gly Ser Phe
 245 250 255
 Arg Gln Arg Gln Asn Arg Gln Asn Leu Lys Leu Val Leu Gln Arg Ala
 260 265 270
 Leu Gln Asp Lys Pro Glu Val Asp Lys Ala Ser Ala Thr Arg Ser Arg
 275 280 285
 Thr Arg Thr Thr Ser Thr Ser Ser Ala Ser Thr Pro Pro Arg Pro Thr
 290 295 300

<210> 95
 <211> 921
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(921)

<400> 95
 tgt ggc aag gag acc ctg atc ccg gtc ttc ctg atc ctt ttc att gcc 48
 Cys Gly Lys Glu Thr Leu Ile Pro Val Phe Leu Ile Leu Phe Ile Ala
 1 5 10 15
 ctg gtc ggg ctg gta gga aac ggg ttt gtg ctc tgg ctc ctg ggc ttc 96
 Leu Val Gly Leu Val Gly Asn Gly Phe Val Leu Trp Leu Leu Gly Phe
 20 25 30
 cgc atg cgc agg aac gcc ttc tct gtc tac gtc ctc agc ctg gcc ggg 144
 Arg Met Arg Arg Asn Ala Phe Ser Val Tyr Val Leu Ser Leu Ala Gly
 35 40 45
 gcc gac ttc ctc ttc ctc tgc ttc cag att ata aat tgc ctg gtg tac 192
 Ala Asp Phe Leu Phe Leu Cys Phe Gln Ile Ile Asn Cys Leu Val Tyr
 50 55 60
 ctc agt aac ttc ttc tgt tcc atc tcc atc aat ttc cct agc ttc ttc 240
 Leu Ser Asn Phe Phe Cys Ser Ile Ser Ile Asn Phe Pro Ser Phe Phe
 65 70 75 80
 acc act gtg atg acc tgt gcc tac ctt gca ggc ctg agc atg ctg agc 288
 Thr Thr Val Met Thr Cys Ala Tyr Leu Ala Gly Leu Ser Met Leu Ser
 85 90 95
 acc gtc agc acc gag cgc tgc ctg tcc gtc ctg tgg ccc atc tgg tat 336
 Thr Val Ser Thr Glu Arg Cys Leu Ser Val Leu Trp Pro Ile Trp Tyr
 100 105 110
 cgc tgc cgc cgc ccc aga cac ctg tca gcg gtc gtg tgt gtc ctg ctc 384
 Arg Cys Arg Arg Pro Arg His Leu Ser Ala Val Val Cys Val Leu Leu
 115 120 125
 tgg gcc ctg tcc cta ctg ctg agc atc ttg gaa ggg aag ttc tgt ggc 432

127/160

Trp Ala Leu Ser Leu Leu Leu Ser Ile Leu Glu Gly Lys Phe Cys Gly
 130 135 140
 ttc tta ttt agt gat ggt gac tct ggt tgg tgt cag aca ttt gat ttc 480
 Phe Leu Phe Ser Asp Gly Asp Ser Gly Trp Cys Gln Thr Phe Asp Phe
 145 150 155 160

 atc act gca gcg tgg ctg att ttt tta ttc atg gtt ctc tgt ggg tcc 528
 Ile Thr Ala Ala Trp Leu Ile Phe Leu Phe Met Val Leu Cys Gly Ser
 165 170 175

 agt ctg gcc ctg ctg gtc agg atc ctc tgt gcc tcc agg ggt ctg cca 576
 Ser Leu Ala Leu Leu Val Arg Ile Leu Cys Gly Ser Arg Gly Leu Pro
 180 185 190

 ctg acc agg ctg tac ctg acc atc ctg ctc aca gtg ctg gtg ttc ctc 624
 Leu Thr Arg Leu Tyr Leu Thr Ile Leu Leu Thr Val Leu Val Phe Leu
 195 200 205

 ctc tgc ggc ctg ccc ttt ggc att cag tgg ttc cta ata tta tgg atc 672
 Leu Cys Gly Leu Pro Phe Gly Ile Gln Trp Phe Leu Ile Leu Trp Ile
 210 215 220

 tgg aag gat tct gat gtc tta ttt tgt cat att cat cca gtt tca gtt 720
 Trp Lys Asp Ser Asp Val Leu Phe Cys His Ile His Pro Val Ser Val
 225 230 235 240

 gtc ctg tca tct ctt aac agc agt gcc aac ccc atc att tac ttc ttc 768
 Val Leu Ser Ser Leu Asn Ser Ser Ala Asn Pro Ile Ile Tyr Phe Phe
 245 250 255

 gtg ggc tct ttt agg aag cag gag tgc tca ctc tcc tgt tta agc aag 816
 Val Gly Ser Phe Arg Lys Gln Glu Cys Ser Leu Ser Cys Leu Ser Lys
 260 265 270

 cag aag tct ccc acc ctc ctt tca gag aga gac ttc tgg att gca gtt 864
 Gln Lys Ser Pro Thr Leu Leu Ser Glu Arg Asp Phe Trp Ile Ala Val
 275 280 285

 att gct gaa gta agc cga gga aga aga cac gag ggg ttc aca ctt tcc 912
 Ile Ala Glu Val Ser Arg Gly Arg Arg His Glu Gly Phe Thr Leu Ser
 290 295 300

 ttt tta ggc 921
 Phe Leu Gly
 305

<210> 96

<211> 307

<212> PRT

<213> Homo sapiens

<400> 96

Cys Gly Lys Glu Thr Leu Ile Pro Val Phe Leu Ile Leu Phe Ile Ala
 1 5 10 15
 Leu Val Gly Leu Val Gly Asn Gly Phe Val Leu Trp Leu Leu Gly Phe
 20 25 30
 Arg Met Arg Arg Asn Ala Phe Ser Val Tyr Val Leu Ser Leu Ala Gly
 35 40 45
 Ala Asp Phe Leu Phe Leu Cys Phe Gln Ile Ile Asn Cys Leu Val Tyr

128/160

```

      50              55              60
Leu Ser Asn Phe Phe Cys Ser Ile Ser Ile Asn Phe Pro Ser Phe Phe
65      70      75      80
Thr Thr Val Met Thr Cys Ala Tyr Leu Ala Gly Leu Ser Met Leu Ser
      85      90      95
Thr Val Ser Thr Glu Arg Cys Leu Ser Val Leu Trp Pro Ile Trp Tyr
      100      105      110

Arg Cys Arg Arg Pro Arg His Leu Ser Ala Val Val Cys Val Leu Leu
      115      120      125
Trp Ala Leu Ser Leu Leu Leu Ser Ile Leu Glu Gly Lys Phe Cys Gly
      130      135      140
Phe Leu Phe Ser Asp Gly Asp Ser Gly Trp Cys Gln Thr Phe Asp Phe
145      150      155      160
Ile Thr Ala Ala Trp Leu Ile Phe Leu Phe Met Val Leu Cys Gly Ser
      165      170      175
Ser Leu Ala Leu Leu Val Arg Ile Leu Cys Gly Ser Arg Gly Leu Pro
      180      185      190
Leu Thr Arg Leu Tyr Leu Thr Ile Leu Leu Thr Val Leu Val Phe Leu
      195      200      205
Leu Cys Gly Leu Pro Phe Gly Ile Gln Trp Phe Leu Ile Leu Trp Ile
      210      215      220
Trp Lys Asp Ser Asp Val Leu Phe Cys His Ile His Pro Val Ser Val
225      230      235      240
Val Leu Ser Ser Leu Asn Ser Ser Ala Asn Pro Ile Ile Tyr Phe Phe
      245      250      255
Val Gly Ser Phe Arg Lys Gln Glu Cys Ser Leu Ser Cys Leu Ser Lys
      260      265      270
Gln Lys Ser Pro Thr Leu Leu Ser Glu Arg Asp Phe Trp Ile Ala Val
      275      280      285
Ile Ala Glu Val Ser Arg Gly Arg Arg His Glu Gly Phe Thr Leu Ser
      290      295      300
Phe Leu Gly
305

```

<210> 97
 <211> 912
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(912)

```

<400> 97
tgc tac aag cag acc ctg agc ttc acg ggg ctg acg tgc atc gtt tcc 48
Cys Tyr Lys Gln Thr Leu Ser Phe Thr Gly Leu Thr Cys Ile Val Ser
  1              5              10              15

ctt gtc gcg ctg aca gga aac gcg gtt gtg ctc tgg ctc ctg ggc tgc 96
Leu Val Ala Leu Thr Gly Asn Ala Val Val Leu Trp Leu Leu Gly Cys
      20              25              30

cgc atg cgc agg aac gct gtc tcc atc tac atc ctc aac ctg gtc gcg 144
Arg Met Arg Arg Asn Ala Val Ser Ile Tyr Ile Leu Asn Leu Val Ala
      35              40              45

gcc gac ttc ctc ttc ctt agc ggc cac att ata tgt tgc ccg tta cgc 192
Ala Asp Phe Leu Phe Leu Ser Gly His Ile Ile Cys Ser Pro Leu Arg
  50              55              60

ctc atc aat atc cgc cat ccc atc tcc aaa atc ctc agt cct gtg atg 240

```

129/160

Leu	Ile	Asn	Ile	Arg	His	Pro	Ile	Ser	Lys	Ile	Leu	Ser	Pro	Val	Met		
65					70					75					80		
acc	ttt	ccc	tac	ttt	ata	ggc	cta	agc	atg	ctg	agc	gcc	atc	agc	acc	288	
Thr	Phe	Pro	Tyr	Phe	Ile	Gly	Leu	Ser	Met	Leu	Ser	Ala	Ile	Ser	Thr		
				85					90					95			
gag	cgc	tgc	ctg	tcc	atc	ctg	tgg	ccc	atc	tgg	tac	cac	tgc	cgc	cgc	336	
Glu	Arg	Cys	Leu	Ser	Ile	Leu	Trp	Pro	Ile	Trp	Tyr	His	Cys	Arg	Arg		
			100					105					110				
ccc	aga	tac	ctg	tca	tca	gtc	atg	tgt	gtc	ctg	ctc	tgg	gcc	ctg	tcc	384	
Pro	Arg	Tyr	Leu	Ser	Ser	Val	Met	Cys	Val	Leu	Leu	Trp	Ala	Leu	Ser		
		115					120					125					
ctg	ctg	cgg	agt	atc	ctg	gag	tgg	atg	ttc	tgt	gac	ttc	ctg	ttt	agt	432	
Leu	Leu	Arg	Ser	Ile	Leu	Glu	Trp	Met	Phe	Cys	Asp	Phe	Leu	Phe	Ser		
	130					135					140						
ggg	gct	aat	tct	gtt	tgg	tgt	gaa	acg	tca	gat	ttc	att	aca	atc	gcg	480	
Gly	Ala	Asn	Ser	Val	Trp	Cys	Glu	Thr	Ser	Asp	Phe	Ile	Thr	Ile	Ala		
145					150					155					160		
tgg	ctg	gtt	ttt	tta	tgt	gtg	gtt	ctc	tgt	ggg	tcc	agc	ctg	gtc	ctg	528	
Trp	Leu	Val	Phe	Leu	Cys	Val	Val	Leu	Cys	Gly	Ser	Ser	Leu	Val	Leu		
			165						170					175			
ctg	gtc	agg	att	ctc	tgt	gga	tcc	cgg	aag	atg	ccg	ctg	acc	agg	ctg	576	
Leu	Val	Arg	Ile	Leu	Cys	Gly	Ser	Arg	Lys	Met	Pro	Leu	Thr	Arg	Leu		
		180			-			185					190				
tac	gtg	acc	atc	ctc	ctc	aca	gtg	ctg	gtc	ttc	ctc	ctc	tgt	ggc	ctg	624	
Tyr	Val	Thr	Ile	Leu	Leu	Thr	Val	Leu	Val	Phe	Leu	Leu	Cys	Gly	Leu		
		195					200					205					
ccc	ttt	ggc	att	cag	tgg	gcc	ctg	ttt	tcc	agg	atc	cac	ctg	gat	tgg	672	
Pro	Phe	Gly	Ile	Gln	Trp	Ala	Leu	Phe	Ser	Arg	Ile	His	Leu	Asp	Trp		
	210					215				220							
aaa	gtc	tta	ttt	tgt	cat	gtg	cat	cta	gtt	tcc	att	ttc	ctg	tcc	gct	720	
Lys	Val	Leu	Phe	Cys	His	Val	His	Leu	Val	Ser	Ile	Phe	Leu	Ser	Ala		
225					230					235					240		
ctt	aac	agc	agt	gcc	aac	ccc	atc	att	tac	ttc	ttc	gtg	ggc	tcc	ttt	768	
Leu	Asn	Ser	Ser	Ala	Asn	Pro	Ile	Ile	Tyr	Phe	Phe	Val	Gly	Ser	Phe		
				245					250					255			
agg	cag	cgt	caa	aat	agg	cag	aac	ctg	aag	ctg	gac	agc	atg	tgc	agg	816	
Arg	Gln	Arg	Gln	Asn	Arg	Gln	Asn	Leu	Lys	Leu	Asp	Ser	Met	Cys	Arg		
			260					265					270				
aga	acg	gcc	ctt	tat	aaa	acc	atc	aga	tct	cgt	gag	agt	tat	tca	cta	864	
Arg	Thr	Ala	Leu	Tyr	Lys	Thr	Ile	Arg	Ser	Arg	Glu	Ser	Tyr	Ser	Leu		
		275					280					285					
tca	cga	gaa	cag	cag	agg	gaa	gac	cca	acc	cat	gat	tca	ata	ctt	tcc	912	
Ser	Arg	Glu	Gln	Gln	Arg	Glu	Asp	Pro	Thr	His	Asp	Ser	Ile	Leu	Ser		
	290					295					300						

<210> 98

<211> 304

130/160

<212> PRT

<213> Homo sapiens

<400> 98

```

Cys Tyr Lys Gln Thr Leu Ser Phe Thr Gly Leu Thr Cys Ile Val Ser
 1           5           10           15
Leu Val Ala Leu Thr Gly Asn Ala Val Val Leu Trp Leu Leu Gly Cys
          20           25           30
Arg Met Arg Arg Asn Ala Val Ser Ile Tyr Ile Leu Asn Leu Val Ala
          35           40           45
Ala Asp Phe Leu Phe Leu Ser Gly His Ile Ile Cys Ser Pro Leu Arg
          50           55           60
Leu Ile Asn Ile Arg His Pro Ile Ser Lys Ile Leu Ser Pro Val Met
          65           70           75           80
Thr Phe Pro Tyr Phe Ile Gly Leu Ser Met Leu Ser Ala Ile Ser Thr
          85           90           95
Glu Arg Cys Leu Ser Ile Leu Trp Pro Ile Trp Tyr His Cys Arg Arg
          100          105          110
Pro Arg Tyr Leu Ser Ser Val Met Cys Val Leu Leu Trp Ala Leu Ser
          115          120          125
Leu Leu Arg Ser Ile Leu Glu Trp Met Phe Cys Asp Phe Leu Phe Ser
          130          135          140
Gly Ala Asn Ser Val Trp Cys Glu Thr Ser Asp Phe Ile Thr Ile Ala
          145          150          155          160
Trp Leu Val Phe Leu Cys Val Val Leu Cys Gly Ser Ser Leu Val Leu
          165          170          175
Leu Val Arg Ile Leu Cys Gly Ser Arg Lys Met Pro Leu Thr Arg Leu
          180          185          190
Tyr Val Thr Ile Leu Leu Thr Val Leu Val Phe Leu Leu Cys Gly Leu
          195          200          205
Pro Phe Gly Ile Gln Trp Ala Leu Phe Ser Arg Ile His Leu Asp Trp
          210          215          220
Lys Val Leu Phe Cys His Val His Leu Val Ser Ile Phe Leu Ser Ala
          225          230          235          240
Leu Asn Ser Ser Ala Asn Pro Ile Ile Tyr Phe Phe Val Gly Ser Phe
          245          250          255
Arg Gln Arg Gln Asn Arg Gln Asn Leu Lys Leu Asp Ser Met Cys Arg
          260          265          270
Arg Thr Ala Leu Tyr Lys Thr Ile Arg Ser Arg Glu Ser Tyr Ser Leu
          275          280          285
Ser Arg Glu Gln Gln Arg Glu Asp Pro Thr His Asp Ser Ile Leu Ser
          290          295          300

```

<210> 99

<211> 975

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(975)

<400> 99

```

cac agc ccc acc cac acc ttc ctc ttc ttt ctg gtc ctg gcc atc ttt 48
His Ser Pro Thr His Thr Phe Leu Phe Phe Leu Val Leu Ala Ile Phe
 1           5           10           15

tca gtg gcc ttc atg gga aac tct gtc atg gtt ctc ctc atc tac ctg 96
Ser Val Ala Phe Met Gly Asn Ser Val Met Val Leu Leu Ile Tyr Leu
          20           25           30

gac acc cag ctc cac acc ccc atg tac ttc ctc ctc agt caa ctg ttc 144

```

131/160

Asp	Thr	Gln	Leu	His	Thr	Pro	Met	Tyr	Phe	Leu	Leu	Ser	Gln	Leu	Phe	
		35					40					45				
ctc	atg	gac	ctc	atg	ctc	atc	tgc	tct	acc	gta	ccc	aag	atg	gcc	ttc	192
Leu	Met	Asp	Leu	Met	Leu	Ile	Cys	Ser	Thr	Val	Pro	Lys	Met	Ala	Phe	
	50					55				60						
aac	tac	ttg	tct	ggc	agc	aag	tcc	att	tct	atg	gct	ggg	tgt	gcc	aca	240
Asn	Tyr	Leu	Ser	Gly	Ser	Lys	Ser	Ile	Ser	Met	Ala	Gly	Cys	Ala	Thr	
	65				70					75					80	
caa	att	ttc	ttc	tat	gta	tca	ctg	ctt	ggc	tcc	gaa	tgc	ttt	ctg	ttg	288
Gln	Ile	Phe	Phe	Tyr	Val	Ser	Leu	Leu	Gly	Ser	Glu	Cys	Phe	Leu	Leu	
				85					90					95		
gct	gtt	atg	tct	tat	gac	cgc	tat	att	gcc	att	tgc	cac	cct	cta	aga	336
Ala	Val	Met	Ser	Tyr	Asp	Arg	Tyr	Ile	Ala	Ile	Cys	His	Pro	Leu	Arg	
			100				105						110			
tac	acc	aat	ctc	atg	aga	ccc	aaa	att	tgt	gga	ctt	atg	act	gcc	ttc	384
Tyr	Thr	Asn	Leu	Met	Arg	Pro	Lys	Ile	Cys	Gly	Leu	Met	Thr	Ala	Phe	
		115					120					125				
tcc	tgg	atc	ctg	ggc	tct	atg	gat	gca	atc	att	gat	gct	gta	gcg	aca	432
Ser	Trp	Ile	Leu	Gly	Ser	Met	Asp	Ala	Ile	Ile	Asp	Ala	Val	Ala	Thr	
	130					135					140					
ttt	tcc	ttc	tcc	tac	tgt	ggg	tct	cgg	gaa	ata	gcc	cac	ttc	ttc	tgt	480
Phe	Ser	Phe	Ser	Tyr	Cys	Gly	Ser	Arg	Glu	Ile	Ala	His	Phe	Phe	Cys	
	145				150				155						160	
gac	ttc	cct	tcc	cta	cta	atc	ctc	tca	tgc	aat	gac	aca	tca	ata	ttt	528
Asp	Phe	Pro	Ser	Leu	Leu	Ile	Leu	Ser	Cys	Asn	Asp	Thr	Ser	Ile	Phe	
				165					170					175		
gaa	aag	gtt	ctt	ttc	atc	tgc	tgt	ata	gta	atg	att	gtt	ttt	cct	gtt	576
Glu	Lys	Val	Leu	Phe	Ile	Cys	Cys	Ile	Val	Met	Ile	Val	Phe	Pro	Val	
			180					185					190			
gca	atc	atc	atc	gct	tcc	tat	gct	cga	gtt	att	ctg	gct	gtc	att	cac	624
Ala	Ile	Ile	Ile	Ala	Ser	Tyr	Ala	Arg	Val	Ile	Leu	Ala	Val	Ile	His	
			195				200					205				
atg	gga	tct	gga	gag	ggg	cgt	cgc	aaa	gct	ttt	act	acc	tgt	tcc	tct	672
Met	Gly	Ser	Gly	Glu	Gly	Arg	Arg	Lys	Ala	Phe	Thr	Thr	Cys	Ser	Ser	
	210					215					220					
cac	ctc	atg	gtg	gtg	gga	atg	tac	tat	gga	gca	ggg	ttg	ttc	atg	tac	720
His	Leu	Met	Val	Val	Gly	Met	Tyr	Tyr	Gly	Ala	Gly	Leu	Phe	Met	Tyr	
	225				230					235					240	
ata	cgg	ccc	aca	tct	gat	cgc	tcc	cct	atg	cag	gac	aag	ctg	gtg	tct	768
Ile	Arg	Pro	Thr	Ser	Asp	Arg	Ser	Pro	Met	Gln	Asp	Lys	Leu	Val	Ser	
				245					250					255		
gta	ttc	tac	acc	atc	ctc	act	ccc	atg	ctg	aat	ccc	ctc	atc	tac	agc	816
Val	Phe	Tyr	Thr	Ile	Leu	Thr	Pro	Met	Leu	Asn	Pro	Leu	Ile	Tyr	Ser	
			260					265					270			
ctc	cgc	aac	aag	gag	gtg	acc	aga	gca	ctc	agg	aaa	gtg	aga	gga	gcc	864
Leu	Arg	Asn	Lys	Glu	Val	Thr	Arg	Ala	Leu	Arg	Lys	Val	Arg	Gly	Ala	

132/160

275

280

285

ccg ctg gaa agg aaa cat tcg gac tcc ggt ttc agc acc tcc tcc aga 912
 Pro Leu Glu Arg Lys His Ser Asp Ser Gly Phe Ser Thr Ser Ser Arg
 290 295 300

agc aca gga tgt gcg acc ttc agc ctt tgt gcc cac ctc cga gcc acc 960
 Ser Thr Gly Cys Ala Thr Phe Ser Leu Cys Ala His Leu Arg Ala Thr
 305 310 315 320

agc tcc gca gaa gta 975
 Ser Ser Ala Glu Val
 325

<210> 100

<211> 325

<212> PRT

<213> Homo sapiens

<400> 100

His Ser Pro Thr His Thr Phe Leu Phe Phe Leu Val Leu Ala Ile Phe
 1 5 10 15
 Ser Val Ala Phe Met Gly Asn Ser Val Met Val Leu Leu Ile Tyr Leu
 20 25 30
 Asp Thr Gln Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln Leu Phe
 35 40 45
 Leu Met Asp Leu Met Leu Ile Cys Ser Thr Val Pro Lys Met Ala Phe
 50 55 60
 Asn Tyr Leu Ser Gly Ser Lys Ser Ile Ser Met Ala Gly Cys Ala Thr
 65 70 75 80
 Gln Ile Phe Phe Tyr Val Ser Leu Leu Gly Ser Glu Cys Phe Leu Leu
 85 90 95
 Ala Val Met Ser Tyr Asp Arg Tyr Ile Ala Ile Cys His Pro Leu Arg
 100 105 110
 Tyr Thr Asn Leu Met Arg Pro Lys Ile Cys Gly Leu Met Thr Ala Phe
 115 120 125
 Ser Trp Ile Leu Gly Ser Met Asp Ala Ile Ile Asp Ala Val Ala Thr
 130 135 140
 Phe Ser Phe Ser Tyr Cys Gly Ser Arg Glu Ile Ala His Phe Phe Cys
 145 150 155 160
 Asp Phe Pro Ser Leu Leu Ile Leu Ser Cys Asn Asp Thr Ser Ile Phe
 165 170 175
 Glu Lys Val Leu Phe Ile Cys Cys Ile Val Met Ile Val Phe Pro Val
 180 185 190
 Ala Ile Ile Ile Ala Ser Tyr Ala Arg Val Ile Leu Ala Val Ile His
 195 200 205
 Met Gly Ser Gly Glu Gly Arg Lys Ala Phe Thr Thr Cys Ser Ser
 210 215 220
 His Leu Met Val Val Gly Met Tyr Tyr Gly Ala Gly Leu Phe Met Tyr
 225 230 235 240
 Ile Arg Pro Thr Ser Asp Arg Ser Pro Met Gln Asp Lys Leu Val Ser
 245 250 255
 Val Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro Leu Ile Tyr Ser
 260 265 270
 Leu Arg Asn Lys Glu Val Thr Arg Ala Leu Arg Lys Val Arg Gly Ala
 275 280 285
 Pro Leu Glu Arg Lys His Ser Asp Ser Gly Phe Ser Thr Ser Ser Arg
 290 295 300
 Ser Thr Gly Cys Ala Thr Phe Ser Leu Cys Ala His Leu Arg Ala Thr
 305 310 315 320

133/160

Ser Ser Ala Glu Val
325

<210> 101
<211> 927
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)...(927)

<400> 101
cga tgg gaa ctt caa att ttc ttc ttt gtg aca ttt tcc ctg atc tac 48
Arg Trp Glu Leu Gln Ile Phe Phe Phe Val Thr Phe Ser Leu Ile Tyr
1 5 10 15
ggg gct act gtg atg gga aac att ctc att atg gtc aca gtg aca tgt 96
Gly Ala Thr Val Met Gly Asn Ile Leu Ile Met Val Thr Val Thr Cys
20 25 30
agg tca acc ctt cat tct ccc ttg tac ttt ctc ctt gga aat ctc tct 144
Arg Ser Thr Leu His Ser Pro Leu Tyr Phe Leu Leu Gly Asn Leu Ser
35 40 45
ttt ttg gac atg tgt ctc tcc act gcc aca aca ccc aag atg atc ata 192
Phe Leu Asp Met Cys Leu Ser Thr Ala Thr Thr Pro Lys Met Ile Ile
50 55 60
gat ttg ctc act gac cac aag acc atc tct gtg tgg ggc tgc gtg acc 240
Asp Leu Leu Thr Asp His Lys Thr Ile Ser Val Trp Gly Cys Val Thr
65 70 75 80
cag atg ttc ttc atg cac ttc ttt ggg ggt gct gag atg act ctt ctg 288
Gln Met Phe Phe Met His Phe Phe Gly Gly Ala Glu Met Thr Leu Leu
85 90 95
ata atc atg gcc ttt gac agg tat gta gcc ata tgt aaa ccc ctg cac 336
Ile Ile Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu His
100 105 110
tat agg aca atc atg agc cac aag ctg cta aag ggg ttt gcg ata ctt 384
Tyr Arg Thr Ile Met Ser His Lys Leu Leu Lys Gly Phe Ala Ile Leu
115 120 125
tca tgg ata att ggt ttt tta cac tcc ata agc cag ata gtt tta aca 432
Ser Trp Ile Ile Gly Phe Leu His Ser Ile Ser Gln Ile Val Leu Thr
130 135 140
atg aac ttg cct ttc tgt ggc cac aat ctt gct tgc att gaa aca tac 480
Met Asn Leu Pro Phe Cys Gly His Asn Leu Ala Cys Ile Glu Thr Tyr
145 150 155 160
acc ctg gaa tta ttt gtc att gct gac agc ggg ctg ctc tct ttc acc 528
Thr Leu Glu Leu Phe Val Ile Ala Asp Ser Gly Leu Leu Ser Phe Thr
165 170 175
tgt ttc atc ctc ttg ctt gtt tct tac att gtc atc ctg gtc agt gta 576
Cys Phe Ile Leu Leu Leu Val Ser Tyr Ile Val Ile Leu Val Ser Val
180 185 190
cca aaa aaa tca tca cat ggg ctc tcc aag gcg ctg tcc aca ttg tct 624

134/160

Pro Lys Lys Ser Ser His Gly Leu Ser Lys Ala Leu Ser Thr Leu Ser
 195 200 205

gcc cac atc att gtg gtc act ctg ttc ttt gga cct tgt att ttt atc 672
 Ala His Ile Ile Val Val Thr Leu Phe Phe Gly Pro Cys Ile Phe Ile
 210 215 220

tat gtt tgg cca ttc agt agt ttg gca agc aat aaa act ctt gcc gta 720
 Tyr Val Trp Pro Phe Ser Ser Leu Ala Ser Asn Lys Thr Leu Ala Val
 225 230 235 240

ttt tat aca gtt atc aca ccc tta ctg aat ccg agt att tat acc ctg 768
 Phe Tyr Thr Val Ile Thr Pro Leu Leu Asn Pro Ser Ile Tyr Thr Leu
 245 250 255

aga aat aag aaa atg caa gag gcc ata aga aaa tta ccg ttc caa tat 816
 Arg Asn Lys Lys Met Gln Glu Ala Ile Arg Lys Leu Arg Phe Gln Tyr
 260 265 270

aat agt tca ccc agc aaa act ttc cct cag aca cga aga aga gat aaa 864
 Asn Ser Ser Pro Ser Lys Thr Phe Pro Gln Thr Arg Arg Arg Asp Lys
 275 280 285

gac tat ccc aga aaa aca aga gct aag gaa ttt cat tac cac caa atc 912
 Asp Tyr Pro Arg Lys Thr Arg Ala Lys Glu Phe His Tyr His Gln Ile
 290 295 300

ttt ttt ata aga aac 927
 Phe Phe Ile Arg Asn
 305

<210> 102
 <211> 309
 <212> PRT
 <213> Homo sapiens

<400> 102
 Arg Trp Glu Leu Gln Ile Phe Phe Phe Val Thr Phe Ser Leu Ile Tyr
 1 5 10 15
 Gly Ala Thr Val Met Gly Asn Ile Leu Ile Met Val Thr Val Thr Cys
 20 25 30
 Arg Ser Thr Leu His Ser Pro Leu Tyr Phe Leu Leu Gly Asn Leu Ser
 35 40 45
 Phe Leu Asp Met Cys Leu Ser Thr Ala Thr Thr Pro Lys Met Ile Ile
 50 55 60
 Asp Leu Leu Thr Asp His Lys Thr Ile Ser Val Trp Gly Cys Val Thr
 65 70 75 80
 Gln Met Phe Phe Met His Phe Phe Gly Gly Ala Glu Met Thr Leu Leu
 85 90 95
 Ile Ile Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Lys Pro Leu His
 100 105 110
 Tyr Arg Thr Ile Met Ser His Lys Leu Leu Lys Gly Phe Ala Ile Leu
 115 120 125
 Ser Trp Ile Ile Gly Phe Leu His Ser Ile Ser Gln Ile Val Leu Thr
 130 135 140
 Met Asn Leu Pro Phe Cys Gly His Asn Leu Ala Cys Ile Glu Thr Tyr
 145 150 155 160
 Thr Leu Glu Leu Phe Val Ile Ala Asp Ser Gly Leu Leu Ser Phe Thr
 165 170 175
 Cys Phe Ile Leu Leu Val Ser Tyr Ile Val Ile Leu Val Ser Val
 180 185 190
 Pro Lys Lys Ser Ser His Gly Leu Ser Lys Ala Leu Ser Thr Leu Ser

135/160

195	200	205
Ala His Ile Ile Val Val Thr	Leu Phe Phe Gly Pro Cys Ile Phe Ile	
210	215	220
Tyr Val Trp Pro Phe Ser Ser	Leu Ala Ser Asn Lys Thr Leu Ala Val	
225	230	235
Phe Tyr Thr Val Ile Thr Pro	Leu Leu Asn Pro Ser Ile Tyr Thr Leu	
245	250	255
Arg Asn Lys Lys Met Gln Glu	Ala Ile Arg Lys Leu Arg Phe Gln Tyr	
260	265	270
Asn Ser Ser Pro Ser Lys Thr	Phe Pro Gln Thr Arg Arg Arg Asp Lys	
275	280	285
Asp Tyr Pro Arg Lys Thr Arg	Ala Lys Glu Phe His Tyr His Gln Ile	
290	295	300
Phe Phe Ile Arg Asn		
305		

<210> 103
 <211> 930
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(930)

<400> 103

tct caa gat att cag ctc ttg gtc ttt gtg ctg atc tta att ttc tac	48
Ser Gln Asp Ile Gln Leu Leu Val Phe Val Leu Ile Leu Ile Phe Tyr	
1 5 10 15	
ctt atc atc ctc cct gga aat ttt ctc att att ttc acc ata agg tca	96
Leu Ile Ile Leu Pro Gly Asn Phe Leu Ile Ile Phe Thr Ile Arg Ser	
20 25 30	
gac cct ggg ctc aca gcc ccc ctc tat tta ttt ctg ggc aac ttg gcc	144
Asp Pro Gly Leu Thr Ala Pro Leu Tyr Leu Phe Leu Gly Asn Leu Ala	
35 40 45	
ttc ctg gat gca tcc tac tcc ttc att gtg gct ccc agg atg ttg gtg	192
Phe Leu Asp Ala Ser Tyr Ser Phe Ile Val Ala Pro Arg Met Leu Val	
50 55 60	
gac ttc ctc tct gag aaa aag gta atc tcc tac aga ggc tgc atc act	240
Asp Phe Leu Ser Glu Lys Lys Val Ile Ser Tyr Arg Gly Cys Ile Thr	
65 70 75 80	
cag ctc ttt ttc ttg cac ttc ctt gga gga ggg gag gga tta ctc ctt	288
Gln Leu Phe Phe Leu His Phe Leu Gly Gly Gly Glu Gly Leu Leu Leu	
85 90 95	
gtt gtg atg gcc ttt gac cgc tac atc gcc atc tgc cgg cct ctg cac	336
Val Val Met Ala Phe Asp Arg Tyr Ile Ala Ile Cys Arg Pro Leu His	
100 105 110	
tgt tca act gtc atg aac cct aga gcc tgc tat gca atg atg ttg gct	384
Cys Ser Thr Val Met Asn Pro Arg Ala Cys Tyr Ala Met Met Leu Ala	
115 120 125	
ctg tgg ctt ggg ggt ttt gtc cac tcc att atc cag gtg gtc ctc atc	432
Leu Trp Leu Gly Gly Phe Val His Ser Ile Ile Gln Val Val Leu Ile	
130 135 140	

136/160

```

ctc cgc ttg cct ttt tgt ggc cca aac cag ctg gac aac ttc ttc tgt 480
Leu Arg Leu Pro Phe Cys Gly Pro Asn Gln Leu Asp Asn Phe Phe Cys
145                      150                      155                      160

gat gtc cga cag ctt cta atg gtc ttc aac agt ggc ctg atg aca ctc 528
Asp Val Arg Gln Leu Leu Met Val Phe Asn Ser Gly Leu Met Thr Leu
165                      170                      175

ctg tgc ttt ctg ggg ctt ctg gct tcc tat gca gtc atc ctc tgc cat 576
Leu Cys Phe Leu Gly Leu Leu Ala Ser Tyr Ala Val Ile Leu Cys His
180                      185                      190

gtt cgt agg gca gct tct gaa ggg aag aac aag gcc atg tcc acg tgc 624
Val Arg Arg Ala Ala Ser Glu Gly Lys Asn Lys Ala Met Ser Thr Cys
195                      200                      205

acc act cgt gtc att att ata ctt ctt atg ttt gga cct gct atc ttc 672
Thr Thr Arg Val Ile Ile Ile Leu Leu Met Phe Gly Pro Ala Ile Phe
210                      215                      220

atc tac atg tgc cct ttc agg gcc tta cca gct gac aag atg gtt tct 720
Ile Tyr Met Cys Pro Phe Arg Ala Leu Pro Ala Asp Lys Met Val Ser
225                      230                      235                      240

ctc ttt cac aca gtg atc ttt cca ttg atg aat cct atg att tat acc 768
Leu Phe His Thr Val Ile Phe Pro Leu Met Asn Pro Met Ile Tyr Thr
245                      250                      255

ctt cgc aac cag gaa gtg aaa act tcc atg aag agg tta ttg att cgt 816
Leu Arg Asn Gln Glu Val Lys Thr Ser Met Lys Arg Leu Leu Ile Arg
260                      265                      270

tgt ctt gtg ctg tgc cga tta atg aca cag act cac aca cgg agt ggg 864
Cys Leu Val Leu Cys Arg Leu Met Thr Gln Thr His Thr Arg Ser Gly
275                      280                      285

tta agg aac aga aag ttt att agg caa gaa gga aga gaa gag ctt ccc 912
Leu Arg Asn Arg Lys Phe Ile Arg Gln Glu Gly Arg Glu Glu Leu Pro
290                      295                      300

cat aca gag gga gaa gca 930
His Thr Glu Gly Glu Ala
305                      310

```

<210> 104

<211> 310

<212> PRT

<213> Homo sapiens

<400> 104

```

Ser Gln Asp Ile Gln Leu Leu Val Phe Val Leu Ile Leu Ile Phe Tyr
1      5      10      15
Leu Ile Ile Leu Pro Gly Asn Phe Leu Ile Ile Phe Thr Ile Arg Ser
20     25     30
Asp Pro Gly Leu Thr Ala Pro Leu Tyr Leu Phe Leu Gly Asn Leu Ala
35     40     45
Phe Leu Asp Ala Ser Tyr Ser Phe Ile Val Ala Pro Arg Met Leu Val
50     55     60
Asp Phe Leu Ser Glu Lys Lys Val Ile Ser Tyr Arg Gly Cys Ile Thr
65     70     75     80

```


Leu	Val	Phe	Leu	Ile	His	Ser	Cys	Ser	Thr	Met	Glu	Ser	Gly	Phe	Phe	
				85					90					95		
ctg	gcc	atg	gct	ttt	gac	cga	tat	gtg	gcc	att	tgc	aat	cca	tta	aga	336
Leu	Ala	Met	Ala	Phe	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Asn	Pro	Leu	Arg	
				100					105					110		
cat	tca	gct	att	ctg	aca	cgc	gct	gta	att	ggg	aga	gtg	ggc	cta	gct	384
His	Ser	Ala	Ile	Leu	Thr	Arg	Ala	Val	Ile	Gly	Arg	Val	Gly	Leu	Ala	
				115					120					125		
att	gtt	ctc	agg	ggc	ata	gca	ctt	ctc	agt	cct	cac	tct	ttc	cta	cta	432
Ile	Val	Leu	Arg	Gly	Ile	Ala	Leu	Leu	Ser	Pro	His	Ser	Phe	Leu	Leu	
				130					135					140		
cgc	tgg	ctt	ccc	tac	tgc	aga	acc	cat	atc	att	tct	cac	acc	tac	tgt	480
Arg	Trp	Leu	Pro	Tyr	Cys	Arg	Thr	His	Ile	Ile	Ser	His	Thr	Tyr	Cys	
				145					150					155		
gag	att	gcc	tgt	gct	gag	aca	aaa	ttc	cgc	aga	gcc	tac	agc	ctc	att	528
Glu	Ile	Ala	Cys	Ala	Glu	Thr	Lys	Phe	Arg	Arg	Ala	Tyr	Ser	Leu	Ile	
				165					170					175		
gtt	gcc	ttc	ctt	act	ggg	gtg	gta	gac	ttt	ata	ttg	atc	att	tat	tct	576
Val	Ala	Phe	Leu	Thr	Gly	Val	Val	Asp	Phe	Ile	Leu	Ile	Ile	Tyr	Ser	
				180					185					190		
tat	gtc	ctc	ata	ctc	cac	act	gtc	ttc	cag	ctc	cca	tcc	aaa	gat	gcc	624
Tyr	Val	Leu	Ile	Leu	His	Thr	Val	Phe	Gln	Leu	Pro	Ser	Lys	Asp	Ala	
				195					200					205		
cgg	ctc	aaa	tct	ttg	ggc	acc	tgt	ggc	tcc	cat	gtc	tgt	gtc	atc	tta	672
Arg	Leu	Lys	Ser	Leu	Gly	Thr	Cys	Gly	Ser	His	Val	Cys	Val	Ile	Leu	
				210					215					220		
gta	tcc	tat	act	cca	gcc	ttc	ttc	tcg	ttt	ctc	acc	cac	agg	ttt	ggg	720
Val	Ser	Tyr	Thr	Pro	Ala	Phe	Phe	Ser	Phe	Leu	Thr	His	Arg	Phe	Gly	
				225					230					235		
cac	cat	gtg	gct	ccc	cat	ttt	cac	ata	ttt	gtg	gcc	aac	atc	tat	ctt	768
His	His	Val	Ala	Pro	His	Phe	His	Ile	Phe	Val	Ala	Asn	Ile	Tyr	Leu	
				245					250					255		
ctt	gtc	cca	ccc	atg	gtg	aac	ccc	att	atc	tat	ggg	gta	aga	acc	aaa	816
Leu	Val	Pro	Pro	Met	Val	Asn	Pro	Ile	Ile	Tyr	Gly	Val	Arg	Thr	Lys	
				260					265					270		
agg	att	tgg	gac	agg	ttc	ctt	aaa	gtt	ttc	agg	tta	aat	ttc	cag	tgc	864
Arg	Ile	Trp	Asp	Arg	Phe	Leu	Lys	Val	Phe	Arg	Leu	Asn	Phe	Gln	Cys	
				275					280					285		
cac	ata	ttt	gta	atc	act	gat	cat	aaa	aga	ctc	agt	ata	ata	tct	tct	912
His	Ile	Phe	Val	Ile	Thr	Asp	His	Lys	Arg	Leu	Ser	Ile	Ile	Ser	Ser	
				290					295					300		
ttc	ccc	ata	aaa	gaa	gca	gcc	tgc	tgc	aaa	caa	agg	ttc	tgc	atg	aag	960
Phe	Pro	Ile	Lys	Glu	Ala	Ala	Cys	Cys	Lys	Gln	Arg	Phe	Cys	Met	Lys	
				305					310					315		
tta	tgc	agg	cga													

139/160

<210> 106
 <211> 324
 <212> PRT
 <213> Homo sapiens

<400> 106
 Leu Glu Ala Ala His Ile Trp Ile Ser Ile Pro Phe Cys Val Val Tyr
 1 5 10 15
 Leu Leu Ala Leu Leu Gly Asn Gly Ser Leu Leu Phe Ile Ile Lys Thr
 20 25 30
 Glu Pro Ser Leu His Glu Pro Met Tyr Leu Phe Leu Cys Met Leu Ala
 35 40 45
 Val Val Asp Leu Val Val Cys Ser Thr Ala Val Pro Lys Leu Leu Ser
 50 55 60
 Leu Phe Trp Phe His Asp Gly Glu Ile Arg Phe Glu Thr Cys Leu Ser
 65 70 75 80
 Leu Val Phe Leu Ile His Ser Cys Ser Thr Met Glu Ser Gly Phe Phe
 85 90 95
 Leu Ala Met Ala Phe Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Arg
 100 105 110
 His Ser Ala Ile Leu Thr Arg Ala Val Ile Gly Arg Val Gly Leu Ala
 115 120 125
 Ile Val Leu Arg Gly Ile Ala Leu Leu Ser Pro His Ser Phe Leu Leu
 130 135 140
 Arg Trp Leu Pro Tyr Cys Arg Thr His Ile Ile Ser His Thr Tyr Cys
 145 150 155 160
 Glu Ile Ala Cys Ala Glu Thr Lys Phe Arg Arg Ala Tyr Ser Leu Ile
 165 170 175
 Val Ala Phe Leu Thr Gly Val Val Asp Phe Ile Leu Ile Ile Tyr Ser
 180 185 190
 Tyr Val Leu Ile Leu His Thr Val Phe Gln Leu Pro Ser Lys Asp Ala
 195 200 205
 Arg Leu Lys Ser Leu Gly Thr Cys Gly Ser His Val Cys Val Ile Leu
 210 215 220
 Val Ser Tyr Thr Pro Ala Phe Phe Ser Phe Leu Thr His Arg Phe Gly
 225 230 235 240
 His His Val Ala Pro His Phe His Ile Phe Val Ala Asn Ile Tyr Leu
 245 250 255
 Leu Val Pro Pro Met Val Asn Pro Ile Ile Tyr Gly Val Arg Thr Lys
 260 265 270
 Arg Ile Trp Asp Arg Phe Leu Lys Val Phe Arg Leu Asn Phe Gln Cys
 275 280 285
 His Ile Phe Val Ile Thr Asp His Lys Arg Leu Ser Ile Ile Ser Ser
 290 295 300
 Phe Pro Ile Lys Glu Ala Ala Cys Cys Lys Gln Arg Phe Cys Met Lys
 305 310 315 320
 Leu Cys Arg Arg

<210> 107
 <211> 951
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(951)

<400> 107
 aac cct gaa atg aat gtt gtc ctt tct gtg ctc ttt cta tta atc tat 48
 Asn Pro Glu Met Asn Val Val Leu Ser Val Leu Phe Leu Leu Ile Tyr
 1 5 10 15

140/160

ctc att act gtc ttg ggc aac ttt tgg att atc ata ata att ctg gct	96
Leu Ile Thr Val Leu Gly Asn Phe Trp Ile Ile Ile Ile Ile Leu Ala	
20 25 30	
agt gcc caa ctc cat tca ccc atg tac ttt ttc ctt agc cag ttg gct	144
Ser Ala Gln Leu His Ser Pro Met Tyr Phe Phe Leu Ser Gln Leu Ala	
35 40 45	
ttc tta gat ttc tgc tat tct tca gtc ttg att cct aaa atg ttg gtg	192
Phe Leu Asp Phe Cys Tyr Ser Ser Val Leu Ile Pro Lys Met Leu Val	
50 55 60	
aat tac ata gca gga cag aaa gtc atc tct tat cac ggt tgc ctc ctt	240
Asn Tyr Ile Ala Gly Gln Lys Val Ile Ser Tyr His Gly Cys Leu Leu	
65 70 75 80	
cag tat tcc ttt gtc agc ttg ttc ctg act act gaa tgc ttc ctc ctg	288
Gln Tyr Ser Phe Val Ser Leu Phe Leu Thr Thr Glu Cys Phe Leu Leu	
85 90 95	
gct gcc atg gca tgt gat cgg tat ctc gct gtt tgc cac cca ctt cac	336
Ala Ala Met Ala Cys Asp Arg Tyr Leu Ala Val Cys His Pro Leu His	
100 105 110	
tac aaa gaa cat aga gtc cag gag cca att aga tgc tgc ctg ata tct	384
Tyr Lys Glu His Arg Val Gln Glu Pro Ile Arg Cys Ser Leu Ile Ser	
115 120 125	
gtc tgg gtg ata agc agt ttg gcg ttc tgt gat tcc agc atc aat cat	432
Val Trp Val Ile Ser Ser Leu Ala Phe Cys Asp Ser Ser Ile Asn His	
130 135 140	
ttt ttt tgt gac acc aca gct ctt tta gca ctc tcc tgt gta gat aca	480
Phe Phe Cys Asp Thr Thr Ala Leu Leu Ala Leu Ser Cys Val Asp Thr	
145 150 155 160	
ttc ggc aca gaa atg gtg agc ttt gtc tta gct gga ttc act ctt ctt	528
Phe Gly Thr Glu Met Val Ser Phe Val Leu Ala Gly Phe Thr Leu Leu	
165 170 175	
agc tct ctc ctt atc atc aca gtc act tat atc atc atc atc tca gcc	576
Ser Ser Leu Leu Ile Ile Thr Val Thr Tyr Ile Ile Ile Ile Ser Ala	
180 185 190	
atc ctg agg atc cag tca gca gca ggc agg cag aag gcc ttc tcc acc	624
Ile Leu Arg Ile Gln Ser Ala Ala Gly Arg Gln Lys Ala Phe Ser Thr	
195 200 205	
tgc gca tcc cac ctc atg gct gta act atc ttt tat ggg tct ctg att	672
Cys Ala Ser His Leu Met Ala Val Thr Ile Phe Tyr Gly Ser Leu Ile	
210 215 220	
ttc acc tat ttg caa cct gat aac aca tca tcg ctg acc cag gcg cag	720
Phe Thr Tyr Leu Gln Pro Asp Asn Thr Ser Ser Leu Thr Gln Ala Gln	
225 230 235 240	
gtg gca tct gta ttc tat acg att gtc att ccc atg ctg aat cca ctc	768
Val Ala Ser Val Phe Tyr Thr Ile Val Ile Pro Met Leu Asn Pro Leu	
245 250 255	

141/160

atc tac agt ctg agg aac aaa gat gtg aaa aat gct ctt ctg aga tgc 816
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asn Ala Leu Leu Arg Cys
 260 265 270

agt ggt gcc gtc tcg gct cac tgc aag ctc tgc ctc ctg aat tca cgc 864
 Ser Gly Ala Val Ser Ala His Cys Lys Leu Cys Leu Leu Asn Ser Arg
 275 280 285

cat tct cct gcc tca gcc tcc caa gtc gct ggg act aca ggc gcc cgc 912
 His Ser Pro Ala Ser Ala Ser Gln Val Ala Gly Thr Thr Gly Ala Arg
 290 295 300

cac cac gca agg cta ttt ttt tta ttt tta gta gag acg 951
 His His Ala Arg Leu Phe Phe Leu Phe Leu Val Glu Thr
 305 310 315

<210> 108

<211> 317

<212> PRT

<213> Homo sapiens

<400> 108

Asn Pro Glu Met Asn Val Val Leu Ser Val Leu Phe Leu Leu Ile Tyr
 1 5 10 15
 Leu Ile Thr Val Leu Gly Asn Phe Trp Ile Ile Ile Ile Ile Leu Ala
 20 25 30
 Ser Ala Gln Leu His Ser Pro Met Tyr Phe Phe Leu Ser Gln Leu Ala
 35 40 45
 Phe Leu Asp Phe Cys Tyr Ser Ser Val Leu Ile Pro Lys Met Leu Val
 50 55 60
 Asn Tyr Ile Ala Gly Gln Lys Val Ile Ser Tyr His Gly Cys Leu Leu
 65 70 75 80
 Gln Tyr Ser Phe Val Ser Leu Phe Leu Thr Thr Glu Cys Phe Leu Leu
 85 90 95
 Ala Ala Met Ala Cys Asp Arg Tyr Leu Ala Val Cys His Pro Leu His
 100 105 110
 Tyr Lys Glu His Arg Val Gln Glu Pro Ile Arg Cys Ser Leu Ile Ser
 115 120 125
 Val Trp Val Ile Ser Ser Leu Ala Phe Cys Asp Ser Ser Ile Asn His
 130 135 140
 Phe Phe Cys Asp Thr Thr Ala Leu Leu Ala Leu Ser Cys Val Asp Thr
 145 150 155 160
 Phe Gly Thr Glu Met Val Ser Phe Val Leu Ala Gly Phe Thr Leu Leu
 165 170 175
 Ser Ser Leu Leu Ile Ile Thr Val Thr Tyr Ile Ile Ile Ile Ser Ala
 180 185 190
 Ile Leu Arg Ile Gln Ser Ala Ala Gly Arg Gln Lys Ala Phe Ser Thr
 195 200 205
 Cys Ala Ser His Leu Met Ala Val Thr Ile Phe Tyr Gly Ser Leu Ile
 210 215 220
 Phe Thr Tyr Leu Gln Pro Asp Asn Thr Ser Ser Leu Thr Gln Ala Gln
 225 230 235 240
 Val Ala Ser Val Phe Tyr Thr Ile Val Ile Pro Met Leu Asn Pro Leu
 245 250 255
 Ile Tyr Ser Leu Arg Asn Lys Asp Val Lys Asn Ala Leu Leu Arg Cys
 260 265 270
 Ser Gly Ala Val Ser Ala His Cys Lys Leu Cys Leu Leu Asn Ser Arg
 275 280 285
 His Ser Pro Ala Ser Ala Ser Gln Val Ala Gly Thr Thr Gly Ala Arg
 290 295 300
 His His Ala Arg Leu Phe Phe Leu Phe Leu Val Glu Thr

142/160

305

310

315

<210> 109
 <211> 948
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(948)

<400> 109
 caa tca aga att ggc ctt ttc gta ttc acc ctc att ttt ctc att ttc 48
 Gln Ser Arg Ile Gly Leu Phe Val Phe Thr Leu Ile Phe Leu Ile Phe
 1 5 10 15
 cta atg gct cta att gga aat cta tcc atg att ctt ctc atc ttt ttg 96
 Leu Met Ala Leu Ile Gly Asn Leu Ser Met Ile Leu Leu Ile Phe Leu
 20 25 30
 gac atc cat ctc cac aca cct atg tat ttc cta ctt agt cag ctc tcc 144
 Asp Ile His Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln Leu Ser
 35 40 45
 ctc att gac cta aat tac atc tcc acc att gtt cca aag atg gtt tat 192
 Leu Ile Asp Leu Asn Tyr Ile Ser Thr Ile Val Pro Lys Met Val Tyr
 50 55 60
 gat ttt ctg tat gga aac aag tct atc tcc ttc act gga tgt ggg att 240
 Asp Phe Leu Tyr Gly Asn Lys Ser Ile Ser Phe Thr Gly Cys Gly Ile
 65 70 75 80
 cag agt ttc ttc ttc ttg act tta gca gtt gca gaa ggg ctg ctc ctg 288
 Gln Ser Phe Phe Phe Leu Thr Leu Ala Val Ala Glu Gly Leu Leu Leu
 85 90 95
 aca tca atg gcc tat gat cgt tat gtg gcc att tgc ttt cct ctc cac 336
 Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
 100 105 110
 tat ccc atc cgt ata agc aaa aga gtg tgt gtg atg atg ata aca gga 384
 Tyr Pro Ile Arg Ile Ser Lys Arg Val Cys Val Met Met Ile Thr Gly
 115 120 125
 tct tgg atg ata agc tct atc aac tct tgt gct cac aca gta tat gca 432
 Ser Trp Met Ile Ser Ser Ile Asn Ser Cys Ala His Thr Val Tyr Ala
 130 135 140
 ctc tgt atc cca tat tgc aag tcc aga gcc atc aat cat ttt ttc tcc 480
 Leu Cys Ile Pro Tyr Cys Lys Ser Arg Ala Ile Asn His Phe Phe Ser
 145 150 155 160
 tgc aca gac act tgg gtc tat gag agc aca gtg ttt ttg agc agc acc 528
 Cys Thr Asp Thr Trp Val Tyr Glu Ser Thr Val Phe Leu Ser Ser Thr
 165 170 175
 atc ttt ctt gtg ctt cct ttc act ggt att gca tgt tcc tat ggc cgg 576
 Ile Phe Leu Val Leu Pro Phe Thr Gly Ile Ala Cys Ser Tyr Gly Arg
 180 185 190
 gtt ctc ctt gct gtc tac cgc atg cac tct gca aaa ggg agg aat aag 624
 Val Leu Leu Ala Val Tyr Arg Met His Ser Ala Lys Gly Arg Asn Lys

143/160

195	200	205	
gtc tat tca acc tgt agc acc cac ctc act gtg gtg tac ttc tac tat			672
Val Tyr Ser Thr Cys Ser Thr His Leu Thr Val Val Tyr Phe Tyr Tyr			
210	215	220	
gca ccc ttt gct tat acc tat gta cgt gca aga tcc ctg cga tct cca			720
Ala Pro Phe Ala Tyr Thr Tyr Val Arg Ala Arg Ser Leu Arg Ser Pro			
225	230	235	240
acc gag gac aag att ctg gct gtt ttc tac acc atc ctc acc cca atg			768
Thr Glu Asp Lys Ile Leu Ala Val Phe Tyr Thr Ile Leu Thr Pro Met			
	245	250	255
ctc aac ccc atc atc tac agc ctg aga aac aag gag agc ttc tgc aca			816
Leu Asn Pro Ile Ile Tyr Ser Leu Arg Asn Lys Glu Ser Phe Cys Thr			
	260	265	270
gca aaa gaa act acc atc aga gtg aac agg caa cct aca gaa tgg gag			864
Ala Lys Glu Thr Thr Ile Arg Val Asn Arg Gln Pro Thr Glu Trp Glu			
	275	280	285
aaa att ttt gca acc tac tca tct gac aaa ggg cta ata tcc aga atc			912
Lys Ile Phe Ala Thr Tyr Ser Ser Asp Lys Gly Leu Ile Ser Arg Ile			
	290	295	300
tac aat gaa ctc aaa caa act tac aag aaa aaa aca			948
Tyr Asn Glu Leu Lys Gln Thr Tyr Lys Lys Lys Thr			
305	310	315	

<210> 110
 <211> 316
 <212> PRT
 <213> Homo sapiens

<400> 110
 Gln Ser Arg Ile Gly Leu Phe Val Phe Thr Leu Ile Phe Leu Ile Phe
 1 5 10 15
 Leu Met Ala Leu Ile Gly Asn Leu Ser Met Ile Leu Leu Ile Phe Leu
 20 25 30
 Asp Ile His Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln Leu Ser
 35 40 45
 Leu Ile Asp Leu Asn Tyr Ile Ser Thr Ile Val Pro Lys Met Val Tyr
 50 55 60
 Asp Phe Leu Tyr Gly Asn Lys Ser Ile Ser Phe Thr Gly Cys Gly Ile
 65 70 75 80
 Gln Ser Phe Phe Phe Leu Thr Leu Ala Val Ala Glu Gly Leu Leu Leu
 85 90 95
 Thr Ser Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
 100 105 110
 Tyr Pro Ile Arg Ile Ser Lys Arg Val Cys Val Met Met Ile Thr Gly
 115 120 125
 Ser Trp Met Ile Ser Ser Ile Asn Ser Cys Ala His Thr Val Tyr Ala
 130 135 140
 Leu Cys Ile Pro Tyr Cys Lys Ser Arg Ala Ile Asn His Phe Phe Ser
 145 150 155 160
 Cys Thr Asp Thr Trp Val Tyr Glu Ser Thr Val Phe Leu Ser Ser Thr
 165 170 175
 Ile Phe Leu Val Leu Pro Phe Thr Gly Ile Ala Cys Ser Tyr Gly Arg
 180 185 190
 Val Leu Leu Ala Val Tyr Arg Met His Ser Ala Lys Gly Arg Asn Lys

144/160

195					200					205					
Val	Tyr	Ser	Thr	Cys	Ser	Thr	His	Leu	Thr	Val	Val	Tyr	Phe	Tyr	Tyr
210					215					220					
Ala	Pro	Phe	Ala	Tyr	Thr	Tyr	Val	Arg	Ala	Arg	Ser	Leu	Arg	Ser	Pro
225					230					235					
Thr	Glu	Asp	Lys	Ile	Leu	Ala	Val	Phe	Tyr	Thr	Ile	Leu	Thr	Pro	Met
245					250					255					
Leu	Asn	Pro	Ile	Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Glu	Ser	Phe	Cys	Thr
260					265					270					
Ala	Lys	Glu	Thr	Thr	Ile	Arg	Val	Asn	Arg	Gln	Pro	Thr	Glu	Trp	Glu
275					280					285					
Lys	Ile	Phe	Ala	Thr	Tyr	Ser	Ser	Asp	Lys	Gly	Leu	Ile	Ser	Arg	Ile
290					295					300					
Tyr	Asn	Glu	Leu	Lys	Gln	Thr	Tyr	Lys	Lys	Lys	Thr				
305					310					315					

```
<210> 111
<211> 939
<212> DNA
<213> Homo sapiens
```

```
<220>  
<221> CDS  
<222> (1) ... (939)
```

<400>	111																
cca	tca	aga	att	gac	ctt	ttc	ttc	ttc	att	ctc	att	gtt	ttc	att	ttc		48
Pro	Ser	Arg	Ile	Asp	Leu	Phe	Phe	Phe	Ile	Leu	Ile	Val	Phe	Ile	Phe		
1				5					10					15			
ctg	atg	gct	cta	att	gga	aac	ctg	tcc	atg	att	ctt	ctc	atc	ttc	ttg		96
Leu	Met	Ala	Leu	Ile	Gly	Asn	Leu	Ser	Met	Ile	Leu	Leu	Ile	Phe	Leu		
			20					25					30				
gac	acc	cat	ctc	cac	aca	ccc	atg	tat	ttc	cta	ctg	agt	cag	ctc	tcc		144
Asp	Thr	His	Leu	His	Thr	Pro	Met	Tyr	Phe	Leu	Leu	Ser	Gln	Leu	Ser		
		35					40					45					
ctc	att	gac	cta	aat	tac	atc	tcc	acc	att	gtt	cct	aag	atg	gca	tct		192
Leu	Ile	Asp	Leu	Asn	Tyr	Ile	Ser	Thr	Ile	Val	Pro	Lys	Met	Ala	Ser		
	50					55					60						
gat	ttt	ctg	cat	gga	aac	aag	tct	atc	tcc	ttc	act	ggg	tgt	ggg	att		240
Asp	Phe	Leu	His	Gly	Asn	Lys	Ser	Ile	Ser	Phe	Thr	Gly	Cys	Gly	Ile		
65				70						75				80			
cag	agt	ttc	ttc	ttc	ttg	gca	tta	gga	ggt	gca	gaa	gca	cta	ctt	ttg		288
Gln	Ser	Phe	Phe	Phe	Leu	Ala	Leu	Gly	Gly	Ala	Glu	Ala	Leu	Leu	Leu		
				85					90					95			
gca	tct	atg	gcc	tat	gat	cgt	tac	att	gct	att	tgc	ttt	cct	ctc	cac		336
Ala	Ser	Met	Ala	Tyr	Asp	Arg	Tyr	Ile	Ala	Ile	Cys	Phe	Pro	Leu	His		
			100					105					110				
tat	ctc	atc	cgc	atg	agc	aaa	aga	gtg	tgt	gtg	ctg	atg	ata	aca	ggg		384
Tyr	Leu	Ile	Arg	Met	Ser	Lys	Arg	Val	Cys	Val	Leu	Met	Ile	Thr	Gly		
		115					120					125					
tct	tgg	atc	ata	ggc	tcg	atc	aat	gct	tgt	gct	cac	act	gta	tat	gta		432
Ser	Trp	Ile	Ile	Gly	Ser	Ile	Asn	Ala	Cys	Ala	His	Thr	Val	Tyr	Val		
	130					135					140						

145/160

```

ctc cat att cct tat tgc cga tcc agg gcc atc aat cat ttc ttc tgt 480
Leu His Ile Pro Tyr Cys Arg Ser Arg Ala Ile Asn His Phe Phe Cys
145                      150                      155                      160

gat gtc cca gca atg ggc aca gtg ttt ttg agt gcc acc atc ttt ctc 528
Asp Val Pro Ala Met Gly Thr Val Phe Leu Ser Ala Thr Ile Phe Leu
                      165                      170                      175

gtg ttt ccc ttc att ggt att tca tgt tcc tat ggc cag gtt ctc ttt 576
Val Phe Pro Phe Ile Gly Ile Ser Cys Ser Tyr Gly Gln Val Leu Phe
                      180                      185                      190

gct gtc tac cac atg aaa tct gca gaa ggg agg aag aaa gcc tat ttg 624
Ala Val Tyr His Met Lys Ser Ala Glu Gly Arg Lys Lys Ala Tyr Leu
                      195                      200                      205

acc tgc agc acc cac ctc act gta gta act ttc tac tat gca cct ttt 672
Thr Cys Ser Thr His Leu Val Val Thr Phe Tyr Tyr Ala Pro Phe
210                      215                      220

gtc tac act tat cta cgt cca aga tcc ctg cga tct cca aca gag gac 720
Val Tyr Thr Tyr Leu Arg Pro Arg Ser Leu Arg Ser Pro Thr Glu Asp
225                      230                      235                      240

aag gtt ctg gct gtc ttc tac acc atc ctc acc cca atg ctc aac ccc 768
Lys Val Leu Ala Val Phe Tyr Thr Ile Leu Thr Pro Met Leu Asn Pro
                      245                      250                      255

atc atc tat agc ctg agg aac aag gag agc aag aga aag aaa aga aag 816
Ile Ile Tyr Ser Leu Arg Asn Lys Glu Ser Lys Arg Lys Lys Arg Lys
260                      265                      270

gaa aga aag aga aaa aga aag aaa aga aag aaa gaa aga gaa aga aag 864
Glu Arg Lys Arg Lys Arg Lys Lys Arg Lys Lys Glu Arg Glu Arg Lys
275                      280                      285

aga gaa aga gag aaa gag aaa gaa aga aaa gaa agg aaa gaa aga gaa 912
Arg Glu Arg Glu Lys Glu Lys Glu Arg Lys Glu Arg Lys Glu Arg Glu
290                      295                      300

aaa gaa aga aaa gaa aga aag aaa gag
Lys Glu Arg Lys Glu Arg Lys Lys Glu
305                      310

```

<210> 112

<211> 313

<212> PRT

<213> Homo sapiens

<400> 112

```

Pro Ser Arg Ile Asp Leu Phe Phe Phe Ile Leu Ile Val Phe Ile Phe
1                      5                      10                      15

Leu Met Ala Leu Ile Gly Asn Leu Ser Met Ile Leu Leu Ile Phe Leu
20                      25                      30
Asp Thr His Leu His Thr Pro Met Tyr Phe Leu Leu Ser Gln Leu Ser
35                      40                      45
Leu Ile Asp Leu Asn Tyr Ile Ser Thr Ile Val Pro Lys Met Ala Ser
50                      55                      60
Asp Phe Leu His Gly Asn Lys Ser Ile Ser Phe Thr Gly Cys Gly Ile
65                      70                      75                      80
Gln Ser Phe Phe Phe Leu Ala Leu Gly Gly Ala Glu Ala Leu Leu Leu

```


147/160

85									90				95							
tct	gtg	atg	gcg	ttt	gac	cgc	tat	ata	gcc	atc	tcc	aag	ccc	ctg	cac	336				
Ser	Val	Met	Ala	Phe	Asp	Arg	Tyr	Ile	Ala	Ile	Ser	Lys	Pro	Leu	His					
			100						105						110					
tat	atg	acc	atc	atg	agt	agg	ggg	cga	tgc	aca	ggc	ctc	atc	gtg	ggc	384				
Tyr	Met	Thr	Ile	Met	Ser	Arg	Gly	Arg	Cys	Thr	Gly	Leu	Ile	Val	Gly					
			115						120						125					
ttc	ctg	ggg	ggg	ggg	ctt	gtc	cac	tcc	ata	gcg	cag	att	tct	cta	ttg	432				
Phe	Leu	Gly	Gly	Gly	Leu	Val	His	Ser	Ile	Ala	Gln	Ile	Ser	Leu	Leu					
			130						135						140					
ctc	cca	ctc	cct	gtc	tgt	gga	ccc	aat	gtt	ctt	gac	act	ttc	tac	tgc	480				
Leu	Pro	Leu	Pro	Val	Cys	Gly	Pro	Asn	Val	Leu	Asp	Thr	Phe	Tyr	Cys					
									150						155					
gat	gtc	ccc	cag	gtc	ctc	aaa	ctt	gcc	tgc	act	gac	acc	ttc	act	ctg	528				
Asp	Val	Pro	Gln	Val	Leu	Lys	Leu	Ala	Cys	Thr	Asp	Thr	Phe	Thr	Leu					
									165						170					
gag	ctc	ctg	atg	att	tca	aat	aat	ggg	tta	gtc	agt	tgg	ttt	gta	ttc	576				
Glu	Leu	Leu	Met	Ile	Ser	Asn	Asn	Gly	Leu	Val	Ser	Trp	Phe	Val	Phe					
			180						185						190					
ttc	ttt	ctc	ctc	ata	tct	tac	acg	gtc	atc	ttg	atg	atg	ctg	agg	tct	624				
Phe	Phe	Leu	Leu	Ile	Ser	Tyr	Thr	Val	Ile	Leu	Met	Met	Leu	Arg	Ser					
			195						200						205					
cac	act	ggg	gaa	ggc	agg	agg	aaa	gcc	atc	tcc	acc	tgc	acc	tcc	cac	672				
His	Thr	Gly	Glu	Gly	Arg	Arg	Lys	Ala	Ile	Ser	Thr	Cys	Thr	Ser	His					
			210						215						220					
atc	acc	gtg	gtg	acc	ctg	cat	ttc	gtg	ccc	tgc	atc	tat	gtc	tat	gcc	720				
Ile	Thr	Val	Val	Thr	Leu	His	Phe	Val	Pro	Cys	Ile	Tyr	Val	Tyr	Ala					
									230						235					
cgg	ccc	ttc	act	gcc	ctc	ccc	aca	gac	act	gcc	atc	tct	gtc	acc	ttc	768				
Arg	Pro	Phe	Thr	Ala	Leu	Pro	Thr	Asp	Thr	Ala	Ile	Ser	Val	Thr	Phe					
									245						250					
act	gtc	atc	tcc	cct	ttg	ctc	aat	cct	ata	att	tac	acg	ctg	agg	aat	816				
Thr	Val	Ile	Ser	Pro	Leu	Leu	Asn	Pro	Ile	Ile	Tyr	Thr	Leu	Arg	Asn					
			260						265						270					
cag	gaa	atg	aac	aac	aga	tca	aga	cac	ttg	tca	aaa	aaa	aaa	aag	aaa	864				
Gln	Glu	Met	Asn	Asn	Arg	Ser	Arg	His	Leu	Ser	Lys	Lys	Lys	Lys	Lys					
			275						280						285					
aga	aaa	gac	aaa	aag	aaa	cca	gca	tgc	gca	aag	aaa	gaa	aat	gag	gtg	912				
Arg	Lys	Asp	Lys	Lys	Lys	Pro	Ala	Cys	Ala	Lys	Lys	Glu	Asn	Glu	Val					
			290						295						300					
aga	ttg	tgc	cac	att	tgt	gta	aca	gtg	aac	tca	gtg	cag	cca	tgg	cgt	960				
Arg	Leu	Cys	His	Ile	Cys	Val	Thr	Val	Asn	Ser	Val	Gln	Pro	Trp	Arg					
			30																	

148/160

<210> 114
 <211> 322
 <212> PRT
 <213> Homo sapiens

<400> 114
 Ser Arg Glu Leu Ser Gln Val Leu Phe Thr Phe Leu Phe Leu Val Tyr
 1 5 10 15
 Met Thr Thr Leu Met Gly Asn Phe Leu Ile Met Val Thr Val Thr Cys
 20 25 30
 Glu Ser His Leu His Thr Pro Met Tyr Phe Leu Leu Arg Asn Leu Ser
 35 40 45
 Ile Leu Asp Ile Cys Phe Ser Ser Ile Thr Ala Pro Lys Val Leu Ile
 50 55 60
 Asp Leu Leu Ser Glu Thr Lys Thr Ile Ser Phe Ser Gly Cys Val Thr
 65 70 75 80
 Gln Met Phe Phe Phe His Leu Leu Gly Gly Ala Asp Val Phe Ser Leu
 85 90 95
 Ser Val Met Ala Phe Asp Arg Tyr Ile Ala Ile Ser Lys Pro Leu His
 100 105 110
 Tyr Met Thr Ile Met Ser Arg Gly Arg Cys Thr Gly Leu Ile Val Gly
 115 120 125
 Phe Leu Gly Gly Gly Leu Val His Ser Ile Ala Gln Ile Ser Leu Leu
 130 135 140
 Leu Pro Leu Pro Val Cys Gly Pro Asn Val Leu Asp Thr Phe Tyr Cys
 145 150 155 160
 Asp Val Pro Gln Val Leu Lys Leu Ala Cys Thr Asp Thr Phe Thr Leu
 165 170 175
 Glu Leu Leu Met Ile Ser Asn Asn Gly Leu Val Ser Trp Phe Val Phe
 180 185 190
 Phe Phe Leu Leu Ile Ser Tyr Thr Val Ile Leu Met Met Leu Arg Ser
 195 200 205
 His Thr Gly Glu Gly Arg Arg Lys Ala Ile Ser Thr Cys Thr Ser His
 210 215 220
 Ile Thr Val Val Thr Leu His Phe Val Pro Cys Ile Tyr Val Tyr Ala
 225 230 235 240
 Arg Pro Phe Thr Ala Leu Pro Thr Asp Thr Ala Ile Ser Val Thr Phe
 245 250 255
 Thr Val Ile Ser Pro Leu Leu Asn Pro Ile Ile Tyr Thr Leu Arg Asn
 260 265 270
 Gln Glu Met Asn Asn Arg Ser Arg His Leu Ser Lys Lys Lys Lys
 275 280 285
 Arg Lys Asp Lys Lys Lys Pro Ala Cys Ala Lys Lys Glu Asn Glu Val
 290 295 300
 Arg Leu Cys His Ile Cys Val Thr Val Asn Ser Val Gln Pro Trp Arg
 305 310 315 320
 Asn Thr

<210> 115
 <211> 975
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(975)

<400> 115
 tgg caa caa cag cag gtg cta ctc ttt gca ctt ttc ctg tgt ctc tat 48

149/160

Trp	Gln	Gln	Gln	Gln	Val	Leu	Leu	Phe	Ala	Leu	Phe	Leu	Cys	Leu	Tyr		
1				5					10					15			
tta	aca	ggg	ctg	ttt	gga	aac	tta	ctc	atc	ttg	ctg	gcc	att	ggc	tcg	96	
Leu	Thr	Gly	Leu	Phe	Gly	Asn	Leu	Leu	Ile	Leu	Leu	Ala	Ile	Gly	Ser		
			20					25					30				
gat	cac	tgc	ctt	cac	aca	ccc	atg	tat	ttc	ttc	ctt	gcc	aat	ctg	tcc	144	
Asp	His	Cys	Leu	His	Thr	Pro	Met	Tyr	Phe	Phe	Leu	Ala	Asn	Leu	Ser		
		35					40					45					
ttg	gta	gac	ctc	tgc	ctt	ccc	tca	gcc	aca	gtc	ccc	aag	atg	cta	ctg	192	
Leu	Val	Asp	Leu	Cys	Leu	Pro	Ser	Ala	Thr	Val	Pro	Lys	Met	Leu	Leu		
	50					55					60						
aac	atc	caa	acc	caa	acc	caa	acc	atc	tcc	tat	ccc	ggc	tgc	ctg	gct	240	
Asn	Ile	Gln	Thr	Gln	Thr	Gln	Thr	Ile	Ser	Tyr	Pro	Gly	Cys	Leu	Ala		
65					70				75						80		
cag	atg	tat	ttc	tgt	atg	atg	ttt	gcc	aat	atg	gac	aat	ttt	ctt	ctc	288	
Gln	Met	Tyr	Phe	Cys	Met	Met	Phe	Ala	Asn	Met	Asp	Asn	Phe	Leu	Leu		
				85				90						95			
aca	gtg	atg	gca	tat	gac	cgt	tac	gtg	gcc	atc	tgt	cac	cct	tta	cat	336	
Thr	Val	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	His	Pro	Leu	His		
			100					105					110				
tac	tcc	acc	att	atg	gcc	ctg	cgc	ctc	tgt	gcc	tct	ctg	gta	gct	gca	384	
Tyr	Ser	Thr	Ile	Met	Ala	Leu	Arg	Leu	Cys	Ala	Ser	Leu	Val	Ala	Ala		
		115					120					125					
cct	tgg	gtc	att	gcc	att	ttg	aac	cct	ctc	ttg	cac	act	ctt	atg	atg	432	
Pro	Trp	Val	Ile	Ala	Ile	Leu	Asn	Pro	Leu	Leu	His	Thr	Leu	Met	Met		
	130					135					140						
gcc	cat	ctg	cac	ttc	tgc	tct	gat	aat	gtt	atc	cac	cat	ttc	ttc	tgt	480	
Ala	His	Leu	His	Phe	Cys	Ser	Asp	Asn	Val	Ile	His	His	Phe	Phe	Cys		
145					150				155						160		
gat	atc	aac	tct	ctc	ctc	cct	ctg	tcc	tgt	tcc	gac	acc	agt	ctt	aat	528	
Asp	Ile	Asn	Ser	Leu	Leu	Pro	Leu	Ser	Cys	Ser	Asp	Thr	Ser	Leu	Asn		
				165				170						175			
cag	ttg	agt	gtt	ctg	gct	acg	gtg	ggg	ctg	atc	ttt	gtg	gta	cct	tca	576	
Gln	Leu	Ser	Val	Leu	Ala	Thr	Val	Gly	Leu	Ile	Phe	Val	Val	Pro	Ser		
			180					185					190				
gtg	tgt	atc	ctg	gta	tcc	tat	atc	ctc	att	gtt	tct	gct	gtg	atg	aaa	624	
Val	Cys	Ile	Leu	Val	Ser	Tyr	Ile	Leu	Ile	Val	Ser	Ala	Val	Met	Lys		
		195					200					205					
gtc	cct	tct	gcc	caa	gga	aaa	ctc	aag	gct	ttc	tct	acc	tgt	gga	tct	672	
Val	Pro	Ser	Ala	Gln	Gly	Lys	Leu	Lys	Ala	Phe	Ser	Thr	Cys	Gly	Ser		
	210					215					220						
cac	ctt	gcc	ttg	gtc	att	ctt	ttc	tat	gga	gca	atc	aca	ggg	gtc	tat	720	
His	Leu	Ala	Leu	Val	Ile	Leu	Phe	Tyr	Gly	Ala	Ile	Thr	Gly	Val	Tyr		
225					230				235						240		
atg	agc	ccc	tta	tcc	aat	cac	tct	act	gaa	aaa	gac	tca	gcc	gca	tca	768	
Met	Ser	Pro	Leu	Ser	Asn	His	Ser	Thr	Glu	Lys	Asp	Ser	Ala	Ala	Ser		
				245					250					255			

150/160

```

gtc att ttt atg gtt gta gca cct gtg ttg aat cca ttc att tac agt 816
Val Ile Phe Met Val Val Ala Pro Val Leu Asn Pro Phe Ile Tyr Ser
      260                      265                      270

tta aga aac aat gaa ctg aag ggg act tta aaa aag acc cta agc cga 864
Leu Arg Asn Asn Glu Leu Lys Gly Thr Leu Lys Lys Thr Leu Ser Arg
      275                      280                      285

ccg ggc gcg gtg gct cac gcc tgt aat ccc agc act ttg gga ggc cga 912
Pro Gly Ala Val Ala His Ala Cys Asn Pro Ser Thr Leu Gly Gly Arg
      290                      295                      300

ggc gga aat aca tgg aca gaa gca aaa tat gtt cat aga gaa gta cat 960
Gly Gly Asn Thr Trp Thr Glu Ala Lys Tyr Val His Arg Glu Val His
305                      310                      315                      320

ata atg atc aag aga 975
Ile Met Ile Lys Arg
      325

```

<210> 116
 <211> 325
 <212> PRT
 <213> Homo sapiens

```

<400> 116
Trp Gln Gln Gln Gln Val Leu Leu Phe Ala Leu Phe Leu Cys Leu Tyr
 1      5      10      15
Leu Thr Gly Leu Phe Gly Asn Leu Leu Ile Leu Leu Ala Ile Gly Ser
      20      25      30
Asp His Cys Leu His Thr Pro Met Tyr Phe Phe Leu Ala Asn Leu Ser
      35      40      45
Leu Val Asp Leu Cys Leu Pro Ser Ala Thr Val Pro Lys Met Leu Leu
      50      55      60
Asn Ile Gln Thr Gln Thr Gln Thr Ile Ser Tyr Pro Gly Cys Leu Ala
65      70      75      80
Gln Met Tyr Phe Cys Met Met Phe Ala Asn Met Asp Asn Phe Leu Leu
      85      90      95
Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
      100      105      110
Tyr Ser Thr Ile Met Ala Leu Arg Leu Cys Ala Ser Leu Val Ala Ala
      115      120      125
Pro Trp Val Ile Ala Ile Leu Asn Pro Leu Leu His Thr Leu Met Met
      130      135      140
Ala His Leu His Phe Cys Ser Asp Asn Val Ile His His Phe Phe Cys
145      150      155      160
Asp Ile Asn Ser Leu Leu Pro Leu Ser Cys Ser Asp Thr Ser Leu Asn
      165      170      175

Gln Leu Ser Val Leu Ala Thr Val Gly Leu Ile Phe Val Val Pro Ser
      180      185      190
Val Cys Ile Leu Val Ser Tyr Ile Leu Ile Val Ser Ala Val Met Lys
      195      200      205
Val Pro Ser Ala Gln Gly Lys Leu Lys Ala Phe Ser Thr Cys Gly Ser
      210      215      220
His Leu Ala Leu Val Ile Leu Phe Tyr Gly Ala Ile Thr Gly Val Tyr
225      230      235      240
Met Ser Pro Leu Ser Asn His Ser Thr Glu Lys Asp Ser Ala Ala Ser
      245      250      255
Val Ile Phe Met Val Val Ala Pro Val Leu Asn Pro Phe Ile Tyr Ser
      260      265      270
Leu Arg Asn Asn Glu Leu Lys Gly Thr Leu Lys Lys Thr Leu Ser Arg

```

[illegible]

```
<220>
<221> CDS
<222> (1)...(963)
```

<400> 117																	
tac	cca	gaa	atc	cag	gtt	cca	ctc	ttt	ctg	gtt	ttc	ttg	ttc	gtc	tac	48	
Tyr	Pro	Glu	Ile	Gln	Val	Pro	Leu	Phe	Leu	Val	Phe	Leu	Phe	Val	Tyr		
1				5					10					15			
aca gtc act gta gtg ggg aac ttg ggc atg ata ata atc atc aga ctc 96																	
Thr	Val	Thr	Val	Val	Gly	Asn	Leu	Gly	Met	Ile	Ile	Ile	Ile	Arg	Leu		
			20					25					30				
aat tca aaa ctc cat aca atc atg tgc ttt ttc ctt agt cac ttg tcc 144																	
Asn	Ser	Lys	Leu	His	Thr	Ile	Met	Cys	Phe	Phe	Leu	Ser	His	Leu	Ser		
		35					40					45					
ttg aca gac ttc tgt ttt tcc act gta gtt aca cct aaa ctg ttg gag 192																	
Leu	Thr	Asp	Phe	Cys	Phe	Ser	Thr	Val	Val	Thr	Pro	Lys	Leu	Leu	Glu		
	50					55					60						
aac ttg gtt gtg gaa tac aga acc atc tct ttc tct ggt tgc atc atg 240																	
Asn	Leu	Val	Val	Glu	Tyr	Arg	Thr	Ile	Ser	Phe	Ser	Gly	Cys	Ile	Met		
65					70					75					80		
caa ttt tgt ttt gct tgc att ttt gga gtg aca gaa act ttc atg tta 288																	
Gln	Phe	Cys	Phe	Ala	Cys	Ile	Phe	Gly	Val	Thr	Glu	Thr	Phe	Met	Leu		
				85				90					95				
gca gcg atg gct tat gac cgt ttt gtg gca gtt tgt aaa ccc ttg ctg 336																	
Ala	Ala	Met	Ala	Tyr	Asp	Arg	Phe	Val	Ala	Val	Cys	Lys	Pro	Leu	Leu		
			100					105				110					
tat acc act att atg tct cag aag ctc tgt gct ctt ctg gtg gct ggg 384																	
Tyr	Thr	Thr	Ile	Met	Ser	Gln	Lys	Leu	Cys	Ala	Leu	Leu	Val	Ala	Gly		
		115					120					125					
tcc tat aca tgg ggg ata gtg tgc tcc ctg ata ctc aca tat ttt ctt 432																	
Ser	Tyr	Thr	Trp	Gly	Ile	Val	Cys	Ser	Leu	Ile	Leu	Thr	Tyr	Phe	Leu		
		130				135					140						
ctt gac tta tcg ttt tgt gaa tct acc ttc ata aat aat ttt atc tct 480																	
Leu	Asp	Leu	Ser	Phe	Cys	Glu	Ser	Thr	Phe	Ile	Asn	Asn	Phe	Ile	Ser		
145					150					155				160			
ttc aac tcc acc tta tac tat aaa ata tac cac caa acc ttc tcc tgt 528																	
Phe	Asn	Ser	Thr	Leu	Tyr	Tyr	Lys	Ile	Tyr	His	Gln	Thr	Phe	Ser	Cys		

152/160

165										170					175					
ata	tgt	gag	cac	ttt	ctg	cca	atg	tgt	aca	cta	ctg	atc	atc	ctc	act	576				
Ile	Cys	Glu	His	Phe	Leu	Pro	Met	Cys	Thr	Leu	Leu	Ile	Ile	Leu	Thr					
			180						185				190							
tcc	tat	gtt	ttc	att	ttt	gtg	act	gta	cta	aaa	atc	cgt	tct	gtt	agt	624				
Ser	Tyr	Val	Phe	Ile	Phe	Val	Thr	Val	Leu	Lys	Ile	Arg	Ser	Val	Ser					
		195					200					205								
ggg	cgc	cac	aaa	gcc	ttc	tcc	acc	tgg	gcc	tcc	cac	ctg	act	tct	atc	672				
Gly	Arg	His	Lys	Ala	Phe	Ser	Thr	Trp	Ala	Ser	His	Leu	Thr	Ser	Ile					
		210				215					220									
acc	atc	ttc	cat	ggg	acc	atc	ctt	ttc	ctt	tac	tgt	gta	ccc	aac	tcc	720				
Thr	Ile	Phe	His	Gly	Thr	Ile	Leu	Phe	Leu	Tyr	Cys	Val	Pro	Asn	Ser					
		225				230				235					240					
aaa	aac	tct	cgg	caa	aca	gtc	aaa	gtg	gcc	tct	gta	ttt	tac	aca	gtt	768				
Lys	Asn	Ser	Arg	Gln	Thr	Val	Lys	Val	Ala	Ser	Val	Phe	Tyr	Thr	Val					
			245						250					255						
gtc	aac	ccc	atg	ctg	aac	cct	ctg	atc	tac	agc	cta	agg	aat	aaa	gac	816				
Val	Asn	Pro	Met	Leu	Asn	Pro	Leu	Ile	Tyr	Ser	Leu	Arg	Asn	Lys	Asp					
			260					265					270							
gtg	aag	gat	gct	ttc	tgg	aag	tta	ata	cat	aca	caa	tca	aga	agg	agg	864				
Val	Lys	Asp	Ala	Phe	Trp	Lys	Leu	Ile	His	Thr	Gln	Ser	Arg	Arg	Arg					
		275					280					285								
cag	agc	ttg	agg	agg	tcc	ttg	aga	aat	tcc	cat	tta	atg	acc	acc	agc	912				
Gln	Ser	Leu	Arg	Arg	Ser	Leu	Arg	Asn	Ser	His	Leu	Met	Thr	Thr	Ser					
		290				295					300									
att	gaa	gaa	gga	gtc	acc	cac	acc	agt	acc	att	ctg	gag	ctc	tgc	tca	960				
Ile	Glu	Glu	Gly	Val	Thr	His	Thr	Ser	Thr	Ile	Leu	Glu	Leu	Cys	Ser					
	305				310					315				320						
tcc																963				
Ser																				

<210> 118

<211> 321

<212> PRT

<213> Homo sapiens

<400> 118

Tyr	Pro	Glu	Ile	Gln	Val	Pro	Leu	Phe	Leu	Val	Phe	Leu	Phe	Val	Tyr
1				5					10					15	
Thr	Val	Thr	Val	Val	Gly	Asn	Leu	Gly	Met	Ile	Ile	Ile	Ile	Arg	Leu
			20					25				30			
Asn	Ser	Lys	Leu	His	Thr	Ile	Met	Cys	Phe	Phe	Leu	Ser	His	Leu	Ser
		35				40					45				
Leu	Thr	Asp	Phe	Cys	Phe	Ser	Thr	Val	Val	Thr	Pro	Lys	Leu	Leu	Glu
	50					55				60					
Asn	Leu	Val	Val	Glu	Tyr	Arg	Thr	Ile	Ser	Phe	Ser	Gly	Cys	Ile	Met
	65			70					75					80	
Gln	Phe	Cys	Phe	Ala	Cys	Ile	Phe	Gly	Val	Thr	Glu	Thr	Phe	Met	Leu
			85					90					95		
Ala	Ala	Met	Ala	Tyr	Asp	Arg	Phe	Val	Ala	Val	Cys	Lys	Pro	Leu	Leu
			100				105						110		

153/160

Tyr Thr Thr Ile Met Ser Gln Lys Leu Cys Ala Leu Leu Val Ala Gly
 115 120 125
 Ser Tyr Thr Trp Gly Ile Val Cys Ser Leu Ile Leu Thr Tyr Phe Leu
 130 135 140
 Leu Asp Leu Ser Phe Cys Glu Ser Thr Phe Ile Asn Asn Phe Ile Ser
 145 150 155 160
 Phe Asn Ser Thr Leu Tyr Tyr Lys Ile Tyr His Gln Thr Phe Ser Cys
 165 170 175
 Ile Cys Glu His Phe Leu Pro Met Cys Thr Leu Leu Ile Ile Leu Thr
 180 185 190
 Ser Tyr Val Phe Ile Phe Val Thr Val Leu Lys Ile Arg Ser Val Ser
 195 200 205
 Gly Arg His Lys Ala Phe Ser Thr Trp Ala Ser His Leu Thr Ser Ile
 210 215 220
 Thr Ile Phe His Gly Thr Ile Leu Phe Leu Tyr Cys Val Pro Asn Ser
 225 230 235 240
 Lys Asn Ser Arg Gln Thr Val Lys Val Ala Ser Val Phe Tyr Thr Val
 245 250 255
 Val Asn Pro Met Leu Asn Pro Leu Ile Tyr Ser Leu Arg Asn Lys Asp
 260 265 270
 Val Lys Asp Ala Phe Trp Lys Leu Ile His Thr Gln Ser Arg Arg Arg
 275 280 285
 Gln Ser Leu Arg Arg Ser Leu Arg Asn Ser His Leu Met Thr Thr Ser
 290 295 300
 Ile Glu Glu Gly Val Thr His Thr Ser Thr Ile Leu Glu Leu Cys Ser
 305 310 315 320
 Ser

<210> 119
 <211> 927
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(927)

<400> 119
 cca ctc agg cta agg aca ctc ttt ttt gtg ttc ttt ttt cta atc tac 48
 Pro Leu Arg Leu Arg Thr Leu Phe Phe Val Phe Phe Phe Leu Ile Tyr
 1 5 10 15

 atc ctg act cag ctg gga aac ctg ctt att tta atc act gtc tgg gca 96
 Ile Leu Thr Gln Leu Gly Asn Leu Leu Ile Leu Ile Thr Val Trp Ala
 20 25 30

 gac cca agg ctc cat gcc cgc ccc atg tac atc ttt ctt ggt gtt ctc 144
 Asp Pro Arg Leu His Ala Arg Pro Met Tyr Ile Phe Leu Gly Val Leu
 35 40 45

 tca gtc att gat atg agc atc tcc tcc atc att gtc cct cgc ctc atg 192
 Ser Val Ile Asp Met Ser Ile Ser Ser Ile Ile Val Pro Arg Leu Met
 50 55 60

 atg aac ttc act tta ggt gtc aaa ccc atc cca ttt ggt ggc tgt gtt 240
 Met Asn Phe Thr Leu Gly Val Lys Pro Ile Pro Phe Gly Gly Cys Val
 65 70 75 80

 gct caa ctc tat ttc tat cac ttc ctg ggc agc acc cag tgc ttc ctc 288
 Ala Gln Leu Tyr Phe Tyr His Phe Leu Gly Ser Thr Gln Cys Phe Leu
 85 90 95

154/160

tac acc cta atg gcc tat gac agg tac ctg gca ata tgt cag ccc ctg	336
Tyr Thr Leu Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Gln Pro Leu	
100 105 110	
cgc tac cct gtg ctc atg act gct aag ctg agc gcc ttg ctt gtg gct	384
Arg Tyr Pro Val Leu Met Thr Ala Lys Leu Ser Ala Leu Leu Val Ala	
115 120 125	
gga gcc tgg atg gca gga tcc atc cat ggg gct ctc cag gcc atc cta	432
Gly Ala Trp Met Ala Gly Ser Ile His Gly Ala Leu Gln Ala Ile Leu	
130 135 140	
acc ttc cgc ctg ccc tac tgt ggg ccc aat cag gtg gat tac ttc ttc	480
Thr Phe Arg Leu Pro Tyr Cys Gly Pro Asn Gln Val Asp Tyr Phe Phe	
145 150 155 160	
ttc aac gag ctg gtg acg ttt gta gac att ggg gtg gtg gtt gcc agt	528
Phe Asn Glu Leu Val Thr Phe Val Asp Ile Gly Val Val Val Ala Ser	
165 170 175	
tgc ttc tcc ctg atc ctc ctc tcc tac ata cag atc att cag gcc atc	576
Cys Phe Ser Leu Ile Leu Leu Ser Tyr Ile Gln Ile Ile Gln Ala Ile	
180 185 190	
ctg aga atc cac aca gct gat ggg cgg cgc cgg gct ttt tca act tgt	624
Leu Arg Ile His Thr Ala Asp Gly Arg Arg Arg Ala Phe Ser Thr Cys	
195 200 205	
gga gcc cat gta acc gtg gtc acc gtg tac tat gtg ccc tgt gcc ttc	672
Gly Ala His Val Thr Val Val Thr Val Tyr Tyr Val Pro Cys Ala Phe	
210 215 220	
atc tac ctg agg cct gaa acc aac agc ccc ctg gat ggg gca gct gcc	720
Ile Tyr Leu Arg Pro Glu Thr Asn Ser Pro Leu Asp Gly Ala Ala Ala	
225 230 235 240	
cta gtc ccc acg gcc atc act cct ttc ctc aac ccc ctt atc tac act	768
Leu Val Pro Thr Ala Ile Thr Pro Phe Leu Asn Pro Leu Ile Tyr Thr	
245 250 255	
ctg cgg aac caa gag gtg aag ctg gcc ctg aaa aga atg ctc aga agc	816
Leu Arg Asn Gln Glu Val Lys Leu Ala Leu Lys Arg Met Leu Arg Ser	
260 265 270	
cca aga act ccg agt gag cac ttt ggg agg cca agg cgg gtg gat cac	864
Pro Arg Thr Pro Ser Glu His Phe Gly Arg Pro Arg Arg Val Asp His	
275 280 285	
ctg agg tcg gga gtt cga gac cag cct aac caa cat gga gaa act gca	912
Leu Arg Ser Gly Val Arg Asp Gln Pro Asn Gln His Gly Glu Thr Ala	
290 295 300	
tct tta cca aaa ata	927
Ser Leu Pro Lys Ile	
305	

<210> 120

<211> 309

<212> PRT

<213> Homo sapiens

155/160

<400> 120

```

Pro Leu Arg Leu Arg Thr Leu Phe Phe Val Phe Phe Phe Leu Ile Tyr
 1           5           10           15
Ile Leu Thr Gln Leu Gly Asn Leu Leu Ile Leu Ile Thr Val Trp Ala
           20           25           30
Asp Pro Arg Leu His Ala Arg Pro Met Tyr Ile Phe Leu Gly Val Leu
           35           40           45
Ser Val Ile Asp Met Ser Ile Ser Ser Ile Ile Val Pro Arg Leu Met
           50           55           60
Met Asn Phe Thr Leu Gly Val Lys Pro Ile Pro Phe Gly Gly Cys Val
65           70           75           80
Ala Gln Leu Tyr Phe Tyr His Phe Leu Gly Ser Thr Gln Cys Phe Leu
           85           90           95
Tyr Thr Leu Met Ala Tyr Asp Arg Tyr Leu Ala Ile Cys Gln Pro Leu
           100          105          110
Arg Tyr Pro Val Leu Met Thr Ala Lys Leu Ser Ala Leu Leu Val Ala
           115          120          125
Gly Ala Trp Met Ala Gly Ser Ile His Gly Ala Leu Gln Ala Ile Leu
130          135          140
Thr Phe Arg Leu Pro Tyr Cys Gly Pro Asn Gln Val Asp Tyr Phe Phe
145          150          155          160
Phe Asn Glu Leu Val Thr Phe Val Asp Ile Gly Val Val Val Ala Ser
           165          170          175
Cys Phe Ser Leu Ile Leu Leu Ser Tyr Ile Gln Ile Ile Gln Ala Ile
           180          185          190
Leu Arg Ile His Thr Ala Asp Gly Arg Arg Arg Ala Phe Ser Thr Cys
           195          200          205
Gly Ala His Val Thr Val Val Thr Val Tyr Tyr Val Pro Cys Ala Phe
210          215          220
Ile Tyr Leu Arg Pro Glu Thr Asn Ser Pro Leu Asp Gly Ala Ala Ala
225          230          235          240
Leu Val Pro Thr Ala Ile Thr Pro Phe Leu Asn Pro Leu Ile Tyr Thr
           245          250          255
Leu Arg Asn Gln Glu Val Lys Leu Ala Leu Lys Arg Met Leu Arg Ser
           260          265          270
Pro Arg Thr Pro Ser Glu His Phe Gly Arg Pro Arg Arg Val Asp His
275          280          285
Leu Arg Ser Gly Val Arg Asp Gln Pro Asn Gln His Gly Glu Thr Ala
290          295          300
Ser Leu Pro Lys Ile
305

```

<210> 121

<211> 972

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(972)

<400> 121

```

gat cct ata gtg aca ccc cac tta atc agc ctc tac ttc ata gtg ctt   48
Asp Pro Ile Val Thr Pro His Leu Ile Ser Leu Tyr Phe Ile Val Leu
 1           5           10           15

att ggc ggg ctg gtg ggt gtc att tcc att ctt ttc ctc ctg gtg aaa   96
Ile Gly Gly Leu Val Gly Val Ile Ser Ile Leu Phe Leu Leu Val Lys
           20           25           30

atg aac acc cgg tca gtg acc acc atg gcg gtc att aac ttg gtg gtg   144
Met Asn Thr Arg Ser Val Thr Thr Met Ala Val Ile Asn Leu Val Val

```

156/160

35					40					45						
gtc	cac	agc	gtt	ttt	ctg	ctg	aca	gtg	cca	ttt	cgc	ttg	acc	tac	ctc	192
Val	His	Ser	Val	Phe	Leu	Leu	Thr	Val	Pro	Phe	Arg	Leu	Thr	Tyr	Leu	
	50					55					60					
atc	aag	aag	act	tgg	atg	ttt	ggg	ctg	ccc	ttc	tgc	aaa	ttt	gtg	agt	240
Ile	Lys	Lys	Thr	Trp	Met	Phe	Gly	Leu	Pro	Phe	Cys	Lys	Phe	Val	Ser	
	65				70					75					80	
gcc	atg	ctg	cac	atc	cac	atg	tac	ctc	acg	ttc	cta	ttc	tat	gtg	gtg	288
Ala	Met	Leu	His	Ile	His	Met	Tyr	Leu	Thr	Phe	Leu	Phe	Tyr	Val	Val	
				85					90					95		
atc	ctg	gtc	acc	aga	tac	ctc	atc	ttc	ttc	aag	tgc	aaa	gac	aaa	gtg	336
Ile	Leu	Val	Thr	Arg	Tyr	Leu	Ile	Phe	Phe	Lys	Cys	Lys	Asp	Lys	Val	
			100					105					110			
gaa	ttc	tac	aga	aaa	ctg	cat	gct	gtg	gct	gcc	agt	gct	ggc	atg	tgg	384
Glu	Phe	Tyr	Arg	Lys	Leu	His	Ala	Val	Ala	Ala	Ser	Ala	Gly	Met	Trp	
		115					120					125				
acg	ctg	gtg	att	gtc	att	gtg	gta	ccc	ctg	gtt	gtc	tcc	cgg	tat	gga	432
Thr	Leu	Val	Ile	Val	Ile	Val	Val	Pro	Leu	Val	Val	Ser	Arg	Tyr	Gly	
	130					135					140					
atc	cat	gag	gaa	tac	aat	gag	gag	cac	tgt	ttt	aaa	ttt	cac	aaa	gag	480
Ile	His	Glu	Glu	Tyr	Asn	Glu	Glu	His	Cys	Phe	Lys	Phe	His	Lys	Glu	
	145				150					155					160	
ctt	gct	tac	aca	tat	gtg	aaa	atc	atc	aac	tat	atg	ata	gtc	att	ttt	528
Leu	Ala	Tyr	Thr	Tyr	Val	Lys	Ile	Ile	Asn	Tyr	Met	Ile	Val	Ile	Phe	
				165					170					175		
gtc	ata	gcc	gtt	gct	gtg	att	ctg	ttg	gtc	ttc	cag	gtc	ttc	atc	att	576
Val	Ile	Ala	Val	Ala	Val	Ile	Leu	Leu	Val	Phe	Gln	Val	Phe	Ile	Ile	
		180						185				190				
atg	ttg	atg	gtg	cag	aag	cta	cgc	cac	tct	tta	cta	tcc	cac	cag	gag	624
Met	Leu	Met	Val	Gln	Lys	Leu	Arg	His	Ser	Leu	Leu	Ser	His	Gln	Glu	
		195					200					205				
ttc	tgg	gct	cag	ctg	aaa	aac	cta	ttt	ttt	ata	ggg	gtc	atc	ctt	gtt	672
Phe	Trp	Ala	Gln	Leu	Lys	Asn	Leu	Phe	Phe	Ile	Gly	Val	Ile	Leu	Val	
	210					215					220					
tgt	ttc	ctt	ccc	tac	cag	ccc	cat	tgt	gtg	atg	ttc	ccc	tcc	ctg	tgt	720
Cys	Phe	Leu	Pro	Tyr	Gln	Pro	His	Cys	Val	Met	Phe	Pro	Ser	Leu	Cys	
	225				230					235					240	
cca	tgt	gtt	ttc	att	gtt	caa	ctc	cca	ctt	cta	agt	gag	aac	atg	cgg	768
Pro	Cys	Val	Phe	Ile	Val	Gln	Leu	Pro	Leu	Leu	Ser	Glu	Asn	Met	Arg	
				245					250					255		
tgt	ttg	gtt	ttc	tgt	tcc	tgt	ttg	att	cat	ttt	tta	ttg	tat	ata	ttt	816
Cys	Leu	Val	Phe	Cys	Ser	Cys	Leu	Ile	His	Phe	Leu	Leu	Tyr	Ile	Phe	
			260					265					270			
ata	gtg	cac	aac	atg	agg	tat	tca	tac	atg	tat	aac	ttc	gtc	agc	tgt	864
Ile	Val	His	Asn	Met	Arg	Tyr	Ser	Tyr	Met	Tyr	Asn	Phe	Val	Ser	Cys	
		275					280					285				

157/160

cct ttg cca gca tgt aat gca gtg atg caa tgc tct ggt agt aat ttg 912
Pro Leu Pro Ala Cys Asn Ala Val Met Gln Cys Ser Gly Ser Asn Leu
290 295 300

gaa caa tcc agg aag caa tat tct cag tgt tca agg ccc ggc act gcc 960
Glu Gln Ser Arg Lys Gln Tyr Ser Gln Cys Ser Arg Pro Gly Thr Ala
305 310 315 320

cgg ggg aaa tta
 Arg Gly Lys Leu

972

```
<210> 122
<211> 324
<212> PRT
<213> Homo sapiens
```

<400> 122															
Asp	Pro	Ile	Val	Thr	Pro	His	Leu	Ile	Ser	Leu	Tyr	Phe	Ile	Val	Leu
1				5					10					15	
Ile	Gly	Gly	Leu	Val	Gly	Val	Ile	Ser	Ile	Leu	Phe	Leu	Leu	Val	Lys
			20					25					30		
Met	Asn	Thr	Arg	Ser	Val	Thr	Thr	Met	Ala	Val	Ile	Asn	Leu	Val	Val
		35					40					45			
Val	His	Ser	Val	Phe	Leu	Leu	Thr	Val	Pro	Phe	Arg	Leu	Thr	Tyr	Leu
	50					55					60				
Ile	Lys	Lys	Thr	Trp	Met	Phe	Gly	Leu	Pro	Phe	Cys	Lys	Phe	Val	Ser
65					70					75					80
Ala	Met	Leu	His	Ile	His	Met	Tyr	Leu	Thr	Phe	Leu	Phe	Tyr	Val	Val
				85					90					95	
Ile	Leu	Val	Thr	Arg	Tyr	Leu	Ile	Phe	Phe	Lys	Cys	Lys	Asp	Lys	Val
			100					105					110		
Glu	Phe	Tyr	Arg	Lys	Leu	His	Ala	Val	Ala	Ala	Ser	Ala	Gly	Met	Trp
		115					120					125			
Thr	Leu	Val	Ile	Val	Ile	Val	Val	Pro	Leu	Val	Val	Ser	Arg	Tyr	Gly
	130					135						140			
Ile	His	Glu	Glu	Tyr	Asn	Glu	Glu	His	Cys	Phe	Lys	Phe	His	Lys	Glu
145					150					155					160
Leu	Ala	Tyr	Thr	Tyr	Val	Lys	Ile	Ile	Asn	Tyr	Met	Ile	Val	Ile	Phe
				165					170					175	

[illegible]

158/160

<210> 123
 <211> 933
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(933)

<400> 123
 cat gtt ctt aat ttc caa gaa ctc ttt ttt ctt gtc ttc gga gtt tca 48
 His Val Leu Asn Phe Gln Glu Leu Phe Phe Leu Val Phe Gly Val Ser
 1 5 10 15

aca ctt att gtt gtt ttt tta atg gtg ctc ata att ctg acc aca ctc 96
 Thr Leu Ile Val Val Phe Leu Met Val Leu Ile Ile Leu Thr Thr Leu
 20 25 30

gtt ggc aat ctg ata gtt att gtt tct ata tca cac ttc aaa caa ctt 144
 Val Gly Asn Leu Ile Val Ile Val Ser Ile Ser His Phe Lys Gln Leu
 35 40 45

cat acc cca aca aat tgg ctc att cat tcc atg gcc act gtg gac ttt 192
 His Thr Pro Thr Asn Trp Leu Ile His Ser Met Ala Thr Val Asp Phe
 50 55 60

ctt ctg ggg tgt ctg gtc atg cct tac agt atg gtg aga tct gct gag 240
 Leu Leu Gly Cys Leu Val Met Pro Tyr Ser Met Val Arg Ser Ala Glu
 65 70 75 80

cac tgt tgg tat ttt gga gaa gtc ttc tgt aaa att cac aca agc acc 288
 His Cys Trp Tyr Phe Gly Glu Val Phe Cys Lys Ile His Thr Ser Thr
 85 90 95

gac att atg ctg agc tca gcc tcc att ttc cat ttg tct ttc atc tcc 336
 Asp Ile Met Leu Ser Ser Ala Ser Ile Phe His Leu Ser Phe Ile Ser
 100 105 110

att gac cgc tac tat gct gtg tgt gat cca ctg aga tat aaa gcc aag 384
 Ile Asp Arg Tyr Tyr Ala Val Cys Asp Pro Leu Arg Tyr Lys Ala Lys
 115 120 125

atg aat atc ttg gtt att tgt gtg atg atc ttc att agt tgg agt gtc 432
 Met Asn Ile Leu Val Ile Cys Val Met Ile Phe Ile Ser Trp Ser Val
 130 135 140

cct gct gtt ttt gca ttt gga atg atc ttt ctg gag cta aac ttc aaa 480
 Pro Ala Val Phe Ala Phe Gly Met Ile Phe Leu Glu Leu Asn Phe Lys
 145 150 155 160

ggc gct gaa gag ata tat tac aaa cat gtt cac tgc aga gga ggt tgc 528
 Gly Ala Glu Glu Ile Tyr Tyr Lys His Val His Cys Arg Gly Gly Cys
 165 170 175

tct gtc ttc ttt agc aaa ata tct ggg gta ctg acc ttt atg act tct 576
 Ser Val Phe Phe Ser Lys Ile Ser Gly Val Leu Thr Phe Met Thr Ser
 180 185 190

ttt tat ata cct gga tct att atg tta tgt gtc tat tac aga ata tat 624
 Phe Tyr Ile Pro Gly Ser Ile Met Leu Cys Val Tyr Tyr Arg Ile Tyr
 195 200 205

159/160

ctt atc gct aaa gaa cag gca aga tta att agt gat gcc aat cag aag 672
 Leu Ile Ala Lys Glu Gln Ala Arg Leu Ile Ser Asp Ala Asn Gln Lys
 210 215 220
 ctc caa att gga ttg gaa atg aaa aat gga att tca caa agc aaa gaa 720
 Leu Gln Ile Gly Leu Glu Met Lys Asn Gly Ile Ser Gln Ser Lys Glu
 225 230 235 240
 agg aaa gct gtg aag aca ttg ggg att gtg atg gga gtt ttc cta ata 768
 Arg Lys Ala Val Lys Thr Leu Gly Ile Val Met Gly Val Phe Leu Ile
 245 250 255
 tgc tgg tgc cct ttc ttt atc tgt aca gtc atg gac cct ttt ctt cac 816
 Cys Trp Cys Pro Phe Phe Ile Cys Thr Val Met Asp Pro Phe Leu His
 260 265 270
 tac att att cca cct act ttg aat gat gta ttg att tgg ttt ggc tac 864
 Tyr Ile Ile Pro Pro Thr Leu Asn Asp Val Leu Ile Trp Phe Gly Tyr
 275 280 285
 ttg aac tct aca ttt aat cca atg gtt tat gca ttt ttc tat cct tgg 912
 Leu Asn Ser Thr Phe Asn Pro Met Val Tyr Ala Phe Phe Tyr Pro Trp
 290 295 300
 ttt aga aaa gca ctg aag atg 933
 Phe Arg Lys Ala Leu Lys Met
 305 310

<210> 124

<211> 311

<212> PRT

<213> Homo sapiens

<400> 124

His Val Leu Asn Phe Gln Glu Leu Phe Phe Leu Val Phe Gly Val Ser
 1 5 10 15
 Thr Leu Ile Val Val Phe Leu Met Val Leu Ile Ile Leu Thr Thr Leu
 20 25 30
 Val Gly Asn Leu Ile Val Ile Val Ser Ile Ser His Phe Lys Gln Leu
 35 40 45
 His Thr Pro Thr Asn Trp Leu Ile His Ser Met Ala Thr Val Asp Phe
 50 55 60
 Leu Leu Gly Cys Leu Val Met Pro Tyr Ser Met Val Arg Ser Ala Glu
 65 70 75 80
 His Cys Trp Tyr Phe Gly Glu Val Phe Cys Lys Ile His Thr Ser Thr
 85 90 95
 Asp Ile Met Leu Ser Ser Ala Ser Ile Phe His Leu Ser Phe Ile Ser
 100 105 110
 Ile Asp Arg Tyr Tyr Ala Val Cys Asp Pro Leu Arg Tyr Lys Ala Lys
 115 120 125
 Met Asn Ile Leu Val Ile Cys Val Met Ile Phe Ile Ser Trp Ser Val
 130 135 140
 Pro Ala Val Phe Ala Phe Gly Met Ile Phe Leu Glu Leu Asn Phe Lys
 145 150 155 160
 Gly Ala Glu Glu Ile Tyr Tyr Lys His Val His Cys Arg Gly Gly Cys
 165 170 175
 Ser Val Phe Phe Ser Lys Ile Ser Gly Val Leu Thr Phe Met Thr Ser
 180 185 190
 Phe Tyr Ile Pro Gly Ser Ile Met Leu Cys Val Tyr Tyr Arg Ile Tyr
 195 200 205

160/160

[illegible]